

```
% identity
NCBI Description hypothetical protein - garden snapdragon
                .. 298478
Seq. No.
                  LIB3151-013-Q1-K1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3108252
BLAST score
                  123
                  1.0e-62
E value
                  300
Match length
% identity
NCBI Description Gossypium barbadense clone pXP039 repetitive DNA sequence
                  298479
Seq. No.
                  LIB3151-013-Q1-K1-E11
Seq. ID
Method
                  BLASTX
                  q2995405
NCBI GI
BLAST score
                  474
                  1.0e-47
E value
                  148
Match length
% identity
                  61
NCBI Description (Y12432) polyprotein [Ananas comosus]
Seq. No.
                  298480
                  LIB3151-013-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2995405
BLAST score
                  425
E value
                  7.0e-42
Match length
                  136
% identity
                  59
NCBI Description (Y12432) polyprotein [Ananas comosus]
                  298481
Seq. No.
Seq. ID
                  LIB3151-013-Q1-K1-G1
                  BLASTX
Method
                  q2995405
NCBI GI
BLAST score
                  491
                  1.0e-49
E value
                  119
Match length
                  76
% identity
NCBI Description (Y12432) polyprotein [Ananas comosus]
                  298482
Seq. No.
Seq. ID
                  LIB3151-013-Q1-K1-G9
                  BLASTX
Method
                  g3024122
NCBI GI
                  233
BLAST score
                  1.0e-19
E value
                  51
Match length
                  86
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821
                  (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
```

298483 Seq. ID LIB3151-013-Q1-K1-H4

Seq. No.

```
Method
                  BLASTX
NCBI GI
                   q2995405
BLAST score
                   380
E value
                   1.0e-36
                   140
Match length
                   54
% identity
                  (Y12432) polyprotein [Ananas comosus]
NCBI Description
                   298484
Seq. No.
                  LIB3151-013-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1418990
BLAST score
                   465
                   2.0e-46
E value
                   99
Match length
                   86
% identity
                  (Z75524) unknown [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   298485
                   LIB3151-014-Q1-K1-A1
Seq. ID
Method
                   BLASTX
                   q4539359
NCBI GI
BLAST score
                   222
E value
                   3.0e-18
                   53
Match length
                   74
% identity
                  (AL049525) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   298486
                   LIB3151-014-Q1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141599
BLAST score
                   237
E value
                   5.0e-20
Match length
                   88
% identity
                   59
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
NCBI Description
                   >gi 72316 pir__ZIZMA2 19K zein precursor (clone cZ19A2) -
                   maize (fragment) >gi_168670 (M12142) 19 kDa zein protein
                   [Zea mays]
                   298487
Seq. No.
                   LIB3151-014-Q1-K1-A6
Seq. ID
Method
                   BLASTX
                   g1332579
NCBI GI
BLAST score
                   509
                   9.0e-52
E value
Match length
                   109
% identity
                   10
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                   298488
Seq. No.
Seq. ID
                   LIB3151-014-Q1-K1-A7
                   BLASTX
Method
                   g419803
NCBI GI
                   190
```

BLAST score

E value

8.0e-15

```
Match length
% identity
                  49
                  zein protein - maize >gi 168705 (M72708) zein protein [Zea
NCBI Description
                  298489
Seq. No.
Seq. ID
                  LIB3151-014-Q1-K1-B3
Method
                  BLASTX
                  g224508
NCBI GI
                  429
BLAST score
E value
                  2.0e-42
Match length
                  118
% identity
                  79
NCBI Description
                  zein A20 [Zea mays]
                  298490
Seq. No.
                  LIB3151-014-Q1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22288
BLAST score
                  111
                  9.0e-56
E value
Match length
                  211
                  88
% identity
                  Maize mRNA fragment for endosperm glutelin-2
NCBI Description
                  298491
Seq. No.
                  LIB3151-014-Q1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4185305
BLAST score
                  38
E value
                  4.0e-12
Match length
                  70
                  89
% identity
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
Seq. No.
                  298492
Seq. ID
                  LIB3151-014-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  q100925
BLAST score
                  194
                  2.0e-15
E value
                  55
Match length
% identity
                  65
                  zein, 27K - maize (fragment) >gi 22550 emb_CAA41175_
NCBI Description
                  (X58197) 27kDa storage protein, zein [Zea mays]
```

298493 Seq. No.

Seq. ID LIB3151-014-Q1-K1-E10

Method BLASTX NCBI GI g116333 BLAST score 256 3.0e-27 E value Match length 105 % identity 54



```
ENDOCHITINASE B PRECURSOR (SEED CHITINASE B) >gi_168443
NCBI Description
                   (M84165) chitinase B [Zea mays]
                  298494
Seq. No.
                  LIB3151-014-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g168695
                  303
BLAST score
                  9.0e-28
E value
                  111
Match length
% identity
                   54
                   (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                  zein gamma [Zea mays]
                  298495
Seq. No.
                  LIB3151-014-Q1-K1-F12
Seq. ID
                  BLASTN
Method
NCBI GI
                  g22447
BLAST score
                   40
                   3.0e-13
E value
                   88
Match length
                   86
% identity
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein
                   298496
Seq. No.
                   LIB3151-014-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   q433970
NCBI GI
BLAST score
                   161
                   9.0e-15
E value
Match length
                   81
                   18
% identity
NCBI Description (Z28649) polyubiquitin [Acetabularia cliftonii]
Seq. No.
                   298497
                   LIB3151-014-Q1-K1-G3
Seq. ID
                   BLASTN
Method
                   q168665
NCBI GI
BLAST score
                   217
                   1.0e-119
E value
                   272
Match length
                   97
% identity
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                   298498
Seq. No.
                   LIB3151-014-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g141603
NCBI GI
                   353
BLAST score
                   2.0e-33
E value
                   126
Match length
                   63
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                   >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                   >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
```

298499

Seq. No.

```
Seq. ID
                  LIB3151-014-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g22216
BLAST score
                  207
                  2.0e-16
E value
Match length
                  82
% identity
                  54
NCBI Description (X55722) 22kD zein [Zea mays]
Seq. No.
                  298500
Seq. ID
                  LIB3151-014-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q141597
BLAST score
                  268
                  2.0e-23
E value
                  142
Match length
% identity
                  46
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
Seq. No.
                  298501
Seq. ID
                  LIB3151-014-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  q508545
BLAST score
                   264
                   6.0e-23
E value
Match length
                   65
                  85
% identity
                  (L34340) zein [Zea mays]
NCBI Description
                   298502
Seq. No.
                   LIB3151-015-Q1-K1-A7
Seq. ID
Method
                  BLASTN
                   g168704
NCBI GI
BLAST score
                   93
                   6.0e-45
E value
Match length
                   171
% identity
                   95
NCBI Description Zea mays zein protein gene, complete cds
                   298503
Seq. No.
                   LIB3151-015-Q1-K1-A8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g531828
BLAST score
                   33
                   2.0e-09
E value
                   73
Match length
% identity
                   86
NCBI Description Cloning vector pSport1, complete cds
                   298504
Seq. No.
```

LIB3151-015-Q1-K1-B6 Seq. ID

BLASTX Method NCBI GI g72307 BLAST score 153



```
E value
                  5.0e-10
Match length
                  53
                  66
% identity
                  22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                  298505
Seq. No.
                  LIB3151-015-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  q1167955
NCBI GI
BLAST score
                  156
E value
                  2.0e-10
Match length
                   104
                   39
% identity
                   (U43497) putative 32.7 kDa jasmonate-induced protein
NCBI Description
                   [Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein
                   [Hordeum vulgare]
                   298506
Seq. No.
                  LIB3151-015-Q1-K1-C1
Seq. ID
Method
                   BLASTX
                   q100938
NCBI GI
BLAST score
                   170
E value
                   2.0e-12
Match length
                   64
                   61
% identity
                   zein precursor - maize >gi_22442_emb_CAA32513_ (X14335)
NCBI Description
                   zein precursor (AA -21 to 90) [Zea mays]
                   298507
Seq. No.
                   LIB3151-015-Q1-K1-D4
Seq. ID
Method
                   BLASTX
                   g168695
NCBI GI
BLAST score
                   230
                   5.0e-19
E value
Match length
                   86
% identity
                   (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                   zein gamma [Zea mays]
                   298508
Seq. No.
                   LIB3151-015-Q1-K1-E4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g168694
                   38
BLAST score
                   6.0e-12
E value
                   74
Match length
                   88
% identity
NCBI Description Maize gamma zein mRNA, partial cds
                   298509
Seq. No.
                   LIB3151-015-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g22216
NCBI GI
                   298
BLAST score
                   3.0e-27
E value
```

107

Match length

```
% identity
NCBI Description (X55722) 22kD zein [Zea mays]
                   298510
Seq. No.
                   LIB3151-015-Q1-K1-F7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22537
                   73
BLAST score
                   7.0e-33
E value
Match length
                   105
                   58
% identity
NCBI Description Maize mRNA for zein polypeptide (clone M6)
Seq. No.
                   298511
                   LIB3151-015-Q1-K1-G5
Seq. ID
                   BLASTN
Method
                   q22516
NCBI GI
                   106
BLAST score
                   1.0e-52
E value
                   254
Match length
                   86
% identity
                   Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
NCBI Description
                   298512
Seq. No.
                   LIB3151-015-Q1-K1-G8
Seq. ID
Method
                   BLASTN
                   q22531
NCBI GI
BLAST score
                   165
                   9.0e-88
E value
                   376
Match length
% identity
                   86
                   Zea mays mRNA encoding a zein (clone pZ22.1)
NCBI Description
                   >gi_270688_gb_I03336_ Sequence 10 from Patent US 4885357
>gi_270741_gb_I03273_ Sequence 2 from Patent US
                   298513
Seq. No.
Seq. ID
                   LIB3151-015-Q1-K1-H4
Method
                   BLASTN
NCBI GI
                   g22516
BLAST score
                   258
                   1.0e-143
E value
                   374
Match length
% identity
                   92
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   298514
Seq. No.
                   LIB3151-016-Q1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141617
                   337
BLAST score
                   1.0e-31
E value
                   109
Match length
                    61
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
```

>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]

>gi_100941_pir__S12140 zein Zc1 - maize >gi_100945_pir__B29017 zein 2 - maize



```
>qi 168666 (M16460) 16-kDa zein protein [Zea mays]
                    298515
Seq. No.
                    LIB3151-016-Q1-K1-A12
Seq. ID
                    BLASTX
Method
                     g136063
NCBI GI
BLAST score
                     152
                     2.0e-10
E value
                     50
Match length
                                                4
% identity
                     62
                     TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                     >gi 68426 pir__ISZMT triose-phosphate isomerase (EC
                     5.3.1.1) - maize >gi_168647 (L00371) triosephosphate isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)
                     triosephosphate isomerase [Zea mays]
```

298516 Seq. No. LIB3151-016-Q1-K1-A2 Seq. ID BLASTX Method g141614 NCBI GI BLAST score 148 6.0e-11 E value 80 Match length 54 % identity

NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)

>gi_82662_pir__B22831 22K zein precursor (clone M1) - maize
>gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea

mays] >gi 224510_prf 1107201D zein M1 [Zea mays]

Seq. No. 298517

Seq. ID LIB3151-016-Q1-K1-A3

Method BLASTX
NCBI GI g224508
BLAST score 312
E value 7.0e-29
Match length 92
% identity 73

NCBI Description zein A20 [Zea mays]

Seq. No. 298518

Seq. ID LIB3151-016-Q1-K1-B10

Method BLASTN
NCBI GI g22516
BLAST score 276
E value 1.0e-154
Match length 384
% identity 93

NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298519

Seq. ID LIB3151-016-Q1-K1-B12

Method BLASTX
NCBI GI g224507
BLAST score 185
E value 9.0e-14
Match length 111
% identity 41

Match length

% identity

52

56



```
NCBI Description zein Al [Zea mays]
                   298520
Seq. No.
                  LIB3151-016-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   g141608
NCBI GI
                   191
BLAST score
                   2.0e-27
E value
                   109
Match length
% identity
                   62
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82) \overline{1}9 kDa
                   zein [Zea mays]
                   298521
Seq. No.
                   LIB3151-016-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   q72307
NCBI GI
                   367
BLAST score
                   4.0e-35
E value
Match length
                   101
                   78
% identity
                   22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   298522
Seq. No.
                   LIB3151-016-Q1-K1-D10
Seq. ID
Method
                   BLASTN
                   g4185305
NCBI GI
BLAST score
                   147
                   5.0e-77
E value
                   295
Match length
                   88
% identity
                   Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                   protein, polyprotein, and copia protein genes, complete
                   cds; and unknown genes
                   298523
Seq. No.
                   LIB3151-016-Q1-K1-D11
Seq. ID
Method
                   BLASTN
                   g22549
NCBI GI
                   164
BLAST score
                   3.0e-87
E value
Match length
                   252
                   91
% identity
NCBI Description Maize gene for a 27kDa storage protein, zein
Seq. No.
                   298524
                   LIB3151-016-Q1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4325282
BLAST score
                   163
                   2.0e-11
E value
```

41930

NCBI Description (AF123310) NAC domain protein NAM [Arabidopsis thaliana]

```
>gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]
298525
LIB3151-016-Q1-K1-D7
BLASTX
g419803
```

Method BLASTX
NCBI GI g419803
BLAST score 388
E value 8.0e-38
Match length 92
% identity 77

Seq. No.

Seq. ID

NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea

mays]

Seq. No. 298526

Seq. ID LIB3151-016-Q1-K1-E4

Method BLASTX
NCBI GI g121472
BLAST score 275
E value 2.0e-24
Match length 64
% identity 75

NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir_ ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289 emb_CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi_22517 emb_CAA37594 (X53514) zein Zc2 [Zea

mays] $>gi_1684\overline{8}5$ (M1 $\overline{6}066$) gluteli \overline{n} -2 [Zea mays]

Seq. No. 298527

Seq. ID LIB3151-016-Q1-K1-G10

Method BLASTX
NCBI GI g508545
BLAST score 340
E value 6.0e-32
Match length 119
% identity 61

NCBI Description (L34340) zein [Zea mays]

Seq. No. 298528

Seq. ID LIB3151-016-Q1-K1-G5

Method BLASTX
NCBI GI g141616
BLAST score 216
E value 1.0e-17
Match length 88
% identity 50

NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)

>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 298529

Seq. ID LIB3151-016-Q1-K1-H3

Method BLASTN
NCBI GI g168484
BLAST score 80
E value 3.0e-37
Match length 120

```
% identity 92
NCBI Description Maize endosperm glutelin-2 gene, complete cds
Seq. No. 298530
Seq. ID LIB3151-016-Q1-K1-H7
Method BLASTX
```

NCBI GI g2832246 BLAST score 255 E value 3.0e-22 Match length 95 % identity 58

NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

 Seq. No.
 298531

 Seq. ID
 LIB3151-016-Q1-K1-H9

 Method
 BLASTN

 NCBI GI
 g168681

 BLASTR
 69

NCBI GI g168681
BLAST score 69
E value 1.0e-30
Match length 234
% identity 82

NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.

>gi_270686_gb_I03333_ Sequence 8 from Patent US

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Seq. No. 298532

Seq. ID LIB3151-017-Q1-K1-A12

Method BLASTN
NCBI GI g1037129
BLAST score 183
E value 2.0e-98
Match length 294
% identity 90

NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,

Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298533

Seq. ID LIB3151-017-Q1-K1-A8

Method BLASTN
NCBI GI g2832242
BLAST score 121
E value 1.0e-61
Match length 219
% identity 13

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 298534

Seq. ID LIB3151-017-Q1-K1-B5

Method BLASTX
NCBI GI g16073
BLAST score 331
E value 6.0e-31
Match length 119
% identity 61

NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298535

Seq. ID LIB3151-017-Q1-K1-B8

```
BLASTN
Method
NCBI GI
                  g22514
                   99
BLAST score
                   2.0e-48
E value
                  183
Match length
                  89
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                  298536
Seq. No.
                  LIB3151-017-Q1-K1-C3
Seq. ID
                  BLASTN
Method
                   g22549
NCBI GI
```

Method BLASTN
NCBI GI g22549
BLAST score 100
E value 7.0e-49
Match length 124
% identity 98

NCBI Description Maize gene for a 27kDa storage protein, zein

 Seq. No.
 298537

 Seq. ID
 LIB3151-017-Q1-K1-C7

 Method
 BLASTX

 NCBI GI
 g121472

 BLAST score
 199

 E value
 1.0e-15

 Match length
 77

% identity 52

NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea

mays] >gi 168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298538

Seq. ID LIB3151-017-Q1-K1-C9

Method BLASTX
NCBI GI g419803
BLAST score 224
E value 2.0e-26
Match length 81
% identity 75

NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea

mays]

Seq. No. 298539

Seq. ID LIB3151-017-Q1-K1-D1

Method BLASTX
NCBI GI g135398
BLAST score 282
E value 1.0e-25
Match length 57
% identity 89

NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1

chain - maize >gi_22147_emb_CAA33734_ (X15704)

alpha1-tubulin [Zea mays]

Seq. No. 298540

```
LIB3151-017-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  g141597
NCBI GI
BLAST score
                  308
                  2.0e-28
E value
                  92
Match length
% identity
                   68
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   298541
Seq. No.
                  LIB3151-017-Q1-K1-F11
Seq. ID
Method
                   BLASTN
                   g168663
NCBI GI
BLAST score
                   41
                   8.0e-14
E value
                   101
Match length
                   87
% identity
                  Maize sulfur-rich zein protein of Mr 15,000, complete cds
NCBI Description
                   298542
Seq. No.
                   LIB3151-017-Q1-K1-F5
Seq. ID
                   BLASTN
Method
                   g168661
NCBI GI
BLAST score
                   46
                   4.0e-17
E value
                   113
Match length
                   87
% identity
NCBI Description Maize 15 kDa zein mRNA, clone cZ15A3, complete cds
                   298543
Seq. No.
                   LIB3151-017-Q1-K1-F6
Seq. ID
                   BLASTN
Method
                   g22514
NCBI GI
                   175
BLAST score
                   6.0e - 94
E value
                   247
Match length
```

NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 298544

% identity

Seq. ID LIB3151-017-Q1-K1-G10

93

Method BLASTN
NCBI GI g168665
BLAST score 142
E value 3.0e-74
Match length 206
% identity 92

NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298545

Seq. ID LIB3151-017-Q1-K1-G6

Method BLASTX
NCBI GI g1076678
BLAST score 261

```
6.0e-23 ∴
E value
                                                                                 72
Match length
                   80
                   71
% identity
                   ubiquitin / ribosomal protein S27a - potato (fragment)
NCBI Description
                   298546
Seq. No.
                   LIB3151-017-Q1-K1-G7
Seq. ID
Method
                   BLASTN
                   g22326
NCBI GI
                   65
BLAST score
E value
                   3.0e-28
Match length
                   149
% identity
                   86
NCBI Description Z.mays gene for Hageman factor inhibitor
                   298547
Seq. No.
Seq. ID
                   LIB3151-017-Q1-K1-H5
Method
                   BLASTN
                   g22542
NCBI GI
                    156
BLAST score
                    1.0e-82
E value
                    200
Match length
                    94
% identity
NCBI Description Maize gene for Mr 19000 alpha zein and 5'-flanking region
                    298548
Seq. No.
                    LIB3151-017-Q1-K1-H7
Seq. ID
                    BLASTX
Method
NCBI GI
                    g121472
BLAST score
                    163
                    6.0e-33
E value
Match length
                    97
                    79
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                    maize >gi_22289 emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                    mays] >qi 168485 (M16066) glutelin-2 [Zea mays]
                    298549
Seq. No.
Seq. ID
                    LIB3151-018-Q1-K1-B3
Method
                    BLASTX
NCBI GI
                    g141605
BLAST score
                    530
E value
                    3.0e-54
Match length
                    121
```

90 % identity

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) NCBI Description

>gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

298550 Seq. No.

LIB3151-018-Q1-K1-B9 Seq. ID

Method BLASTN g22516 NCBI GI 137 BLAST score

E value

Match length

1.0e-155

418



```
4.0e-71
E value
Match length
                    269
                    88
% identity
                   Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
NCBI Description
                    298551
Seq. No.
                    LIB3151-018-Q1-K1-C12
Seq. ID
                    BLASTX
Method
NCBI GI
                    g168701
BLAST score
                    403
                    2.0e-39
E value
                    120
Match length
                    72
% identity
NCBI Description
                   (M60837) zein [Zea mays]
                    298552
Seq. No.
                    LIB3151-018-Q1-K1-C3
Seq. ID
                    BLASTX
Method
                    q4096786
NCBI GI
                    223
BLAST score
                    3.0e-18
E value
                    58
Match length
                    74
% identity
                   (U39958) NADP-malic enzyme [Zea mays]
NCBI Description
Seq. No.
                    298553
                    LIB3151-018-Q1-K1-C5
Seq. ID
                    BLASTX
Method
                    g141617
NCBI GI
                    318
BLAST score
                    9.0e-33
E value
                    105
Match length
                    70
% identity
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                    >gi 100941_pir__ S12140 zein Zc1 - maize
>gi 100945_pir__ B29017 zein 2 - maize
>gi 22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                    >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                    298554
Seq. No.
                    LIB3151-018-Q1-K1-D5
Seq. ID
Method
                    BLASTN
NCBI GI
                    g1037129
BLAST score
                    49
E value
                    1.0e-18
Match length
                    109
                    87
% identity
                    (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                    Tuxpeno CMS 450, mRNA Partial, 1889 nt]
Seq. No.
                    298555
Seq. ID
                    LIB3151-018-Q1-K1-F4
Method
                    BLASTN
NCBI GI
                    g1037129
BLAST score
                    279
```

BLAST score

E value

224 5.0e-31



```
% identity
                  (gamma-zeinA) = opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                  298556
Seq. No.
                  LIB3151-018-Q1-K1-F9
Seq. ID
Method
                  BLASTX
                  q4559384
NCBI GI
                  176
BLAST score
                  1.0e-12
E value
Match length
                  79
% identity
                  44
                  (AC006526) unknown protein [Arabidopsis thaliana]
NCBI Description
                  298557
Seq. No.
                  LIB3151-018-Q1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4097690
                  205
BLAST score
                  2.0e-16
E value
                  75
Match length
                  60
% identity
                  (U66592) prohibitin 2 [Arabidopsis thaliana] >gi 4099801
NCBI Description
                   (U89791) prohibitin-like protein [Arabidopsis thaliana]
                  >qi 4204301 (AC003027) prohibitin 2 [Arabidopsis thaliana]
                  298558
Seq. No.
                  LIB3151-018-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  q2832247
NCBI GI
BLAST score
                  223
                  3.0e-18
E value
Match length
                  92
% identity
                  53
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
Seq. No.
                   298559
                  LIB3151-018-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                  g136757
NCBI GI
BLAST score
                   395
                   2.0e-38
E value
                   75
Match length
% identity
                   97
                  GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
NCBI Description
                   >gi 100881 pir S07314 UDPglucose--starch
                   glucosyltransferase (EC 2.4.1.11) precursor - maize
                   >gi 168653 (M24258) amyloplast-specific transit protein
                   [Zea mays] >gi 1644339 emb CAA27574 (X03935) glucosyl
                   transferase [Zea mays]
                   298560
Seq. No.
Seq. ID
                   LIB3151-019-Q1-K1-A6
                   BLASTX
Method
NCBI GI
                   g168701
```

Seq. ID



```
103
Match length
                   69
% identity
                  (M60837) zein [Zea mays]
NCBI Description
                  298561
Seq. No.
                  LIB3151-019-Q1-K1-A8
Seq. ID
                  BLASTX
Method
                   g168701
NCBI GI
                   197
BLAST score
                   2.0e-15
E value
                  78
Match length
                   63
% identity
                  (M60837) zein [Zea mays]
NCBI Description
Seq. No.
                   298562
                   LIB3151-019-Q1-K1-A9
Seq. ID
                   BLASTX
Method
                   q4185308
NCBI GI
                   220
BLAST score
                   4.0e-18
E value
                   83
Match length
                   61
% identity
                  (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
NCBI Description
                   298563
Seq. No.
                   LIB3151-019-Q1-K1-B8
Seq. ID
                   BLASTN
Method
                   g168484
NCBI GI
BLAST score
                   304
                   1.0e-170
E value
                   375
Match length
                   95
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   298564
Seq. No.
                   LIB3151-019-Q1-K1-C6
Seq. ID
                   BLASTN
Method
                   g168681
NCBI GI
                   226
BLAST score
                   1.0e-124
E value
                   298
Match length
                   58
% identity
                   Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                   >gi 270686 gb I03333 Sequence 8 from Patent US
                   298565
Seq. No.
                   LIB3151-019-Q1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4206306
BLAST score
                   650
E value
                   2.0e-68
                   130
Match length
% identity
                   100
NCBI Description
                   (AF049110) prpol [Zea mays]
Seq. No.
                   298566
```

41938

LIB3151-019-Q1-K1-D10

```
Method
                  BLASTX
                  q82660
NCBI GI
                  235
BLAST score
                  1.0e-19
E value
                  119
Match length
% identity
                  46
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >qi 809117 emb CAA24720 (V01473) zein [Zea mays]
Seq. No.
                  298567
                  LIB3151-019-Q1-K1-D11
Seq. ID
Method
                  BLASTX
                  g2832243
NCBI GI
                  167
BLAST score
                  7.0e-12
E value
Match length
                  65
% identity
                  62
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
                  298568
Seq. No.
                  LIB3151-019-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1707924
BLAST score
                  201
                  2.0e-21
E value
Match length
                  81
                  69
% identity
                  GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 1
NCBI Description
                  PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
                  PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE
                  ADENYL TRANSFERASE) (SHRUNKEN-2) >gi_1947182 (M81603)
                  shrunken-2 [Zea mays] >gi 444329 prf_1906378A ADP glucose
                  pyrophosphorylase [Zea mays]
                  298569
Seq. No.
                  LIB3151-019-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  q141605
NCBI GI
                  145
BLAST score
                  3.0e-19
E value
                  94
Match length
                   66
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
                  298570
Seq. No.
Seq. ID
                  LIB3151-019-Q1-K1-E11
                  BLASTX
Method
NCBI GI
                   g2832243
BLAST score
                   253
                  8.0e-22
E value
Match length
                  109
                   56
% identity
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
```

298571

Seq. No.



```
LIB3151-019-Q1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g224513
                  189
BLAST score
                  1.0e-15
E value
                  98
Match length
                  48
% identity
                  zein M6 [Zea mays]
NCBI Description
                  298572
Seq. No.
                  LIB3151-019-Q1-K1-F12
Seq. ID
                  BLASTX
Method
                  g168695
NCBI GI
BLAST score
                  178
                  3.0e-13
E value
                  67
Match length
                  58
% identity
                  (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                  zein gamma [Zea mays]
                  298573
Seq. No.
                  LIB3151-019-Q1-K1-F5
Seq. ID
                  BLASTN
Method
                  g22516
NCBI GI
BLAST score
                  65
                  3.0e-28
E value
                  137
Match length
% identity
                  87
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   298574
Seq. No.
                  LIB3151-019-Q1-K1-G6
Seq. ID
                   BLASTN
Method
                   g168484
NCBI GI
BLAST score
                   96
E value
                   8.0e-47
Match length
                   156
                   90
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   298575
Seq. No.
                   LIB3151-019-Q1-K1-H3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22549
BLAST score
                   281
E value
                   1.0e-157
Match length
                   357
                   95
% identity
NCBI Description Maize gene for a 27kDa storage protein, zein
                   298576
Seq. No.
                   LIB3151-019-Q1-K1-H4
Seq. ID
                   BLASTX
Method
                   g170354
NCBI GI
                   506
BLAST score
```

2.0e-51

109

E value

Match length

```
% identity
NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
                  298577
Seq. No.
                  LIB3151-019-Q1-K1-H6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g168675
                  61
BLAST score
                  1.0e-25
E value
                  182
Match length
                  91
% identity
NCBI Description Maize mutant zein (zE19) gene, complete cds
Seq. No.
                  298578
                  LIB3151-019-Q1-K1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832247
                  181
BLAST score
                  2.0e-13
E value
                  91
Match length
                   49
% identity
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
                  298579
Seq. No.
                  LIB3151-019-Q1-K1-H8
Seq. ID
                  BLASTN
Method
                   q168425
NCBI GI
                   62
BLAST score
                   1.0e-26
E value
Match length
                   154
                   85
% identity
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds
                   298580
Seq. No.
                   LIB3151-020-Q1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q168691
                   245
BLAST score
                   8.0e-21
E value
Match length
                   92
                   60
% identity
                  (M29628) zein [Zea mays]
NCBI Description
Seq. No.
                   298581
```

LIB3151-020-Q1-K1-D4 Seq. ID

Method BLASTX NCBI GI g141603 BLAST score 177 6.0e-13 E value Match length 99

% identity 45

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) NCBI Description

>gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize

647.1

>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

298582 Seq. No.

LIB3151-020-Q1-K1-D8 Seq. ID

Seq. ID

BLAST score

Method NCBI GI

```
BLASTX
Method
                  g629862
NCBI GI
                  162
BLAST score
                  2.0e-11
E value
                  75
Match length
                  48
% identity
                  zein Zdl, 19K - maize >gi_535021_emb_CAA47640_ (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
                  298583
Seq. No.
                  LIB3151-020-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  g508545
NCBI GI
                   235
BLAST score
E value
                   1.0e-19
Match length
                   98
                   54
% identity
                  (L34340) zein [Zea mays]
NCBI Description
Seq. No.
                   298584
                   LIB3151-020-Q1-K1-E10
Seq. ID
Method
                   BLASTX
                   g141613
NCBI GI
BLAST score
                   155
                   2.0e-10
E value
                   81
Match length
% identity
                   44
                   ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                   >gi_72305_pir__ZIZM21 22K zein precursor (clone pZ22.1) -
                   maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]
                   298585
Seq. No.
                   LIB3151-020-Q1-K1-E12
Seq. ID
                   BLASTN
Method
                   g1037129
NCBI GI
BLAST score
                   296
                   1.0e-166
E value
                   392
Match length
                   94
% identity
                   (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   298586
 Seq. No.
                   LIB3151-020-Q1-K1-F1
 Seq. ID
                   BLASTX
Method
NCBI GI
                   g2832247
                   153
BLAST score
                   3.0e-10
 E value
                   77
 Match length
                   45
 % identity
                   (AF031569) 22-kDa alpha zein 10 [Zea mays]
 NCBI Description
                   298587
 Seq. No.
```

41942

LIB3151-020-Q1-K1-F5

BLASTN

42

g4140643

Match length

% identity

70



```
E value
                      2.0e-14
                      82
   Match length
   % identity
                      88
                      Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
   NCBI Description
                      complete sequence
                      298588
   Seq. No.
                      LIB3151-020-Q1-K1-H7
   Seq. ID
   Method
                      BLASTN
   NCBI GI
                      g22549
   BLAST score
                      45
   E value
                      3.0e-16
   Match length
                      49
                      98
   % identity
   NCBI Description Maize gene for a 27kDa storage protein, zein
                      298589
   Seq. No.
                      LIB3151-021-Q1-K1-A11
   Seq. ID
   Method
                      BLASTX
                      q141607
   NCBI GI
                      297
   BLAST score
                      5.0e-27
   E value
   Match length
                      66
   % identity
                      94
                      ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
   NCBI Description
                      >qi 22521 emb CAA24718 (V01471) zein [Zea mays] >gi_168672
                      (J01244) zein 19 kd protein (partial) [Zea mays]
    Seq. No.
                      298590
                      LIB3151-021-Q1-K1-B1
    Seq. ID
                      BLASTX
    Method
    NCBI GI
                      g168691
    BLAST score
                      323
                      4.0e-30
    E value
    Match length
                      95
    %.identity
                      69
                                                                1
                     (M29628) zein [Zea mays]
    NCBI Description
    Seq. No.
                      298591
                      LIB3151-021-Q1-K1-B3
    Seq. ID
                      BLASTX
    Method
                      g629861
    NCBI GI
    BLAST score
                      352
                      2.0e-33
    E value
                      105
    Match length
                      70
    % identity
                      zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
    NCBI Description
                      zein Zd1 (19 kDa zein) [Zea mays]
                      298592
    Seq. No.
                      LIB3151-021-Q1-K1-C1
    Seq. ID
                      BLASTX
    Method
                      g4140644
    NCBI GI
    BLAST score
                      306
                      5.0e-41
    E value
                      133
```

Seq. ID

Method



```
NCBI Description (AF090447) 22-kDa zein protein 12 [Zea mays]
                  298593
Seq. No.
                  LIB3151-021-Q1-K1-C6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g22528
                  47
BLAST score
                  1.0e-17
E value
                  79
Match length
                  91
% identity
NCBI Description Zea mays mRNA encoding a zein (clone A20)
                  298594
Seq. No.
                  LIB3151-021-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  g168701
NCBI GI
                  505
BLAST score
                  3.0e-51
E value
                  126
Match length
                  84
% identity
NCBI Description (M60837) zein [Zea mays]
                  298595
Seq. No.
                  LIB3151-021-Q1-K1-E6
Seq. ID
                  BLASTX
Method
                   g508545
NCBI GI
BLAST score
                   302
                  1.0e-27
E value
                  85
Match length
                  71
% identity
                  (L34340) zein [Zea mays]
NCBI Description
                   298596
Seq. No.
                   LIB3151-021-Q1-K1-G2
Seq. ID
                   BLASTN
Method
NCBI, GI
                   g22516
BLAST score
                   183
                   2.0e-98
E value
                   386
Match length
                   88
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   298597
Seq. No.
Seq. ID
                   LIB3151-021-Q1-K1-G3
Method
                   BLASTX
NCBI GI
                   g141608
BLAST score
                   269
E value
                   9.0e-24
Match length
                   101
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                   zein [Zea mays]
                   298598
Seq. No.
```

41944

LIB3151-021-Q1-K1-H3

BLASTX



```
q100925
NCBI GI
BLAST score
                  144
                  3.0e-09
E value
                   38
Match length
% identity
                  zein, 27K - maize (fragment) >gi_22550_emb_CAA41175
NCBI Description
                   (X58197) 27kDa storage protein, zein [Zea mays]
                  298599
Seq. No.
                  LIB3151-021-Q1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g141600
BLAST score
                   144
                   1.0e-09
E value
                   56
Match length
                   55
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                   >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                   maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]
                   298600
Seq. No.
                   LIB3151-021-Q1-K1-H7
Seq. ID
                   BLASTN
Method
NCBI GI
                   q168685
BLAST score
                   43
                   3.0e-15
E value
                   59
Match length
                   93
% identity
NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA
                   298601
Seq. No.
                   LIB3151-022-Q1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g72307
BLAST score
                   198
                   2.0e-15
E value
Match length
                   100
                   49
% identity
                   22K zein precursor (clone pZ22.3) - maize >gi 168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   298602
Seq. No.
                   LIB3151-022-Q1-K1-A5
Seq. ID
Method
                   BLASTX
                   g4519539
NCBI GI
                   158
BLAST score
E value
                   2.0e-12
Match length
                   83
 % identity
                   (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
NCBI Description
                   domestica]
                   298603
 Seq. No.
                   LIB3151-022-Q1-K1-A6
 Seq. ID
                   BLASTN
Method
                   g168665
NCBI GI
```

BLAST score

Method

NCBI GI

BLASTX g224509

```
1.0e-13
E value
                  101
Match length
                  85
% identity
                  Maize 16-kDa zein-2 mRNA, complete cds
NCBI Description
                  298604
Seq. No.
                  LIB3151-022-Q1-K1-C8
Seq. ID
                  BLASTN
Method
                  g1037129
NCBI GI
BLAST score
                  285
                  1.0e-159
E value
                  425
Match length
% identity
                  92
                  (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                  298605
Seq. No.
                  LIB3151-022-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                   g136757
NCBI GI
BLAST score
                   242
                   1.0e-20
E value
                   80
Match length
                   68
% identity
                  GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
NCBI Description
                   >gi 100881 pir S07314 UDPglucose--starch
                   glucosyltransferase (EC 2.4.1.11) precursor - maize
                   >gi_168653 (M24258) amyloplast-specific transit protein
                   [Zea mays] >gi_1644339_emb_CAA27574_ (X03935) glucosyl
                   transferase [Zea mays]
                   298606
Seq. No.
                   LIB3151-022-Q1-K1-E8
Seq. ID
                   BLASTN
Method
                   g1037129
NCBI GI
                   350
BLAST score
                   0.0e + 00
E value
                   426
Match length
                   96
% identity
                   (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   298607
Seq. No.
                   LIB3151-022-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g168695
NCBI GI
                   239
BLAST score
                   4.0e-20
 E value
                   103
Match length
                   50
 % identity
                   (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                   zein gamma [Zea mays]
                   298608
 Seq. No.
                   LIB3151-022-Q1-K1-G1
 Seq. ID
```



NCBI Description (L34340) zein [Zea mays]

% identity

```
BLAST score
                  4.0e-14
E value
                  82
Match length
% identity
                  54
NCBI Description zein E19 [Zea mays]
                  298609
Seq. No.
                  LIB3151-022-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82660
BLAST score
                  252
E value
                  1.0e-21
                  77
Match length
                   68
% identity
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
Seq. No.
                   298610
                  LIB3151-022-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g16073
BLAST score
                   353
E value
                   1.0e-33
Match length
                   99
                   77
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                   298611
Seq. No.
                   LIB3151-022-Q1-K1-H7
Seq. ID
Method
                   BLASTX
                   g224514
NCBI GI
BLAST score
                   281
E value
                   5.0e-25
Match length
                   66
% identity
                   89
NCBI Description zein M8 [Zea mays]
                   298612
Seq. No.
                   LIB3151-022-Q1-K1-H9
Seq. ID
                   BLASTX
Method
                   g224508
NCBI GI
                   284
BLAST score
                   2.0e-25
E value
Match length
                   113
% identity
                   60
NCBI Description zein A20 [Zea mays]
Seq. No.
                   298613
                   LIB3151-023-Q1-K1-A11
Seq. ID
Method
                   BLASTX
                   q508545
NCBI GI
                   208
BLAST score
                   1.0e-16
E value
Match length
                   94
```



```
298614
Seq. No.
                  LIB3151-023-Q1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g224508
BLAST score
                  151
                  8.0e-15
E value
                  81
Match length
                  63
% identity
                  zein A20 [Zea mays]
NCBI Description
                  298615
Seq. No.
                  LIB3151-023-Q1-K1-A4
Seq. ID
Method
                  BLASTX
                  g224513
NCBI GI
BLAST score
                  219
                  2.0e-18
E value
Match length
                  73
% identity
                   64
NCBI Description
                  zein M6 [Zea mays]
                   298616
Seq. No.
                   LIB3151-023-Q1-K1-A7
Seq. ID
                   BLASTN
Method
                   g168681
NCBI GI
BLAST score
                   92
                   2.0e-44
E value
                   148
Match length
                   92
% identity
                   Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                   >gi 270686_gb_I03333_ Sequence 8 from Patent US
                   298617
Seq. No.
                   LIB3151-023-Q1-K1-A9
Seq. ID
                   BLASTX
Method
                   g141597
NCBI GI
                   400
BLAST score
                   6.0e-39
E value
                   102
Match length
                   79
 % identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   298618
 Seq. No.
                   LIB3151-023-Q1-K1-B10
 Seq. ID
                   BLASTX
 Method
                   g508545
 NCBI GI
                   393
 BLAST score
                   4.0e-38
 E value
 Match length
                   128
 % identity
                   66
                   (L34340) zein [Zea mays]
 NCBI Description
```

298619

BLASTX

LIB3151-023-Q1-K1-B11

Seq. No.

Seq. ID Method

```
g224514
NCBI GI
BLAST score
                  201
                  8.0e-16
E value
                  60
Match length
                  72
% identity
NCBI Description zein M8 [Zea mays]
                  298620
Seq. No.
                  LIB3151-023-Q1-K1-B12
Seq. ID
                  BLASTN
Method
                  g168484
NCBI GI
                  129
BLAST score
                  2.0e-66
E value
Match length
                  217
                  92
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                  298621
Seq. No.
                  LIB3151-023-Q1-K1-B5
Seq. ID
                  BLASTX
Method
                  g419803
NCBI GI
                  258
BLAST score
                  1.0e-22
E value
                  80
Match length
                  65
% identity
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
                  mays]
                  298622
Seq. No.
                  LIB3151-023-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  g100940
NCBI GI
                  226
BLAST score
                  1.0e-18
E value
Match length
                  100
                   52
% identity
```

NCBI Description zein zA1 - maize

Seq. No. 298623

Seq. ID LIB3151-023-Q1-K1-C6

Method BLASTX
NCBI GI g141603
BLAST score 281
E value 5.0e-25
Match length 121
% identity 53

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)

>gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize

>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 298624

Seq. ID LIB3151-023-Q1-K1-C8

Method BLASTX
NCBI GI g121472
BLAST score 155
E value 2.0e-18
Match length 89

```
% identity
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                   [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
                   mays] >gi_1684\overline{8}5 (M1\overline{6}066\overline{)} gluteli\overline{n}-2 [Zea mays]
                   298625
Seq. No.
                   LIB3151-023-Q1-K1-D10
Seq. ID
                   BLASTN
Method
                   g2832242
NCBI GI
                   123
BLAST score
                   6.0e-63
E value
Match length
                   143
% identity
                   11
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                   298626
Seq. No.
                   LIB3151-023-Q1-K1-D3
Seq. ID
Method
                   BLASTN
                   g535019
NCBI GI
                   55
BLAST score
                   4.0e-22
E value
                   131
Match length
% identity
                   43
NCBI Description Z.mays Zdl tandem genes for zein Zdl (19 kDa Zein)
Seq. No.
                   298627
                   LIB3151-023-Q1-K1-D5
Seq. ID
                   BLASTX
Method
                   g2832246
NCBI GI
                   341
BLAST score
                   3.0e - 32
E value
                   98
Match length
                   76
% identity
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]
                   298628
Seq. No.
                   LIB3151-023-Q1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q508545
BLAST score
                    322
E value
                   8.0e-30
Match length
                   126
% identity
                    56
NCBI Description (L34340) zein [Zea mays]
                    298629
Seq. No.
                   LIB3151-023-Q1-K1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                    q535019
BLAST score
                    63
E value
                    6.0e-27
Match length
                    139
 % identity
                    44
```

NCBI Description Z.mays Zdl tandem genes for zein Zdl (19 kDa Zein)

```
298630
Seq. No.
                  LIB3151-023-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q168664
BLAST score
                  217
                  5.0e-18
E value
                  51
Match length
                  86
% identity
NCBI Description (M13507) zein protein precursor [Zea mays]
                  298631
Seq. No.
                  LIB3151-023-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g16073
NCBI GI
BLAST score
                   451
                   6.0e-45
E value
Match length
                   121
                   79
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                   298632
Seq. No.
                   LIB3151-023-Q1-K1-H11
Seq. ID
                   BLASTX
Method
                   g1710521
NCBI GI
BLAST score
                   223
E value
                   2.0e-18
                   67
Match length
                   75
% identity
                   60S RIBOSOMAL PROTEIN L24 >gi_1154859_emb_CAA63960_
NCBI Description
                   (X94296) L24 ribosomal protein [Hordeum vulgare]
                   298633
Seq. No.
                   LIB3151-023-Q1-K1-H3
Seq. ID
                   BLASTX
Method
                   g132584
NCBI GI
                   231
BLAST score
                   2.0e-19
E value
                   77
Match length
                   58
 % identity
                   RIBOSOME-INACTIVATING PROTEIN 3 (RRNA N-GLYCOSIDASE) (B-32
 NCBI Description
                   PROTEIN) >gi 168451 (M83926) ribosome-inactivating protein
                    [Zea mays]
                   298634
 Seq. No.
                   LIB3151-023-Q1-K1-H7
 Seq. ID
                   BLASTX
 Method
                   g141616
 NCBI GI
                   179
 BLAST score
                   1.0e-13
 E value
                    41
 Match length
                    78
 % identity
                   ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
 NCBI Description
                    >gi_168662 (M12147) 15 kDa zein protein [Zea mays]
                    298635
 Seq. No.
                    LIB3151-023-Q1-K1-H9
 Seq. ID
```

Match length

311

```
BLASTX
Method
NCBI GI
                  g141616
BLAST score
                  157
E value
                  1.0e-10
Match length
                  98
% identity
                  43
                  ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                  >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
                  298636
Seq. No.
Seq. ID
                  LIB3151-024-Q1-K1-A9
Method
                  BLASTN
                  g168484
NCBI GI
BLAST score
                  192
                   1.0e-104
E value
Match length
                   316
% identity
                   95
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   298637
Seq. No.
                  LIB3151-024-Q1-K1-B2
Seq. ID
Method
                   BLASTX
                   g3970823
NCBI GI
BLAST score
                   293
                   2.0e-26
E value
Match length
                   98
% identity
                   63
NCBI Description (X17555) pyruvate decarboxylase [Zea mays]
Seq. No.
                   298638
                   LIB3151-024-Q1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q168691
BLAST score
                   290
E value
                   3.0e-26
Match length
                   103
% identity
                   59
                  (M29628) zein [Zea mays]
NCBI Description
                   298639
Seq. No.
                   LIB3151-024-Q1-K1-B7
Seq. ID
Method
                   BLASTX
                   q629862
NCBI GI
                   216
BLAST score
                   1.0e-17
E value
Match length
                   79
 % identity
                   58
                   zein Zd1, 19K - maize >gi_535021_emb_CAA47640_ (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
                   298640
Seq. No.
 Seq. ID
                   LIB3151-024-Q1-K1-C7
                   BLASTN
Method
NCBI GI
                   g22516
BLAST score
                   160
E value
                   7.0e-85
```



```
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                    298641
Seq. No.
                    LIB3151-024-Q1-K1-C8
Seq. ID
Method
                    BLASTN
NCBI GI
                    q22516
                    110
BLAST score
                    3.0e-55
E value
                    182
Match length
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                    298642
Seq. No.
Seq. ID
                    LIB3151-024-Q1-K1-C9
Method
                    BLASTN
                    q22516
NCBI GI
BLAST score
                    71
                    7.0e-32
E value
Match length
                    119
                    91
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.
                    298643
                    LIB3151-024-Q1-K1-D1
Seq. ID
Method
                    BLASTN
NCBI GI
                    q168661
BLAST score
                    120
E value
                    8.0e-61
                    184
Match length
                    96
% identity
NCBI Description Maize 15 kDa zein mRNA, clone cZ15A3, complete cds
                    298644
Seq. No.
                    LIB3151-024-Q1-K1-D12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q141600
BLAST score
                    167
                    5.0e-12
E value
Match length
                    64
                    58
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                    >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                    maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
                    298645
Seq. No.
Seq. ID
                    LIB3151-024-Q1-K1-D2
Method
                    BLASTX
                    g1076708
NCBI GI
BLAST score
                    704
                    1.0e-74
E value
Match length
                    148
% identity
                    27
                    seed tetraubiquitin - common sunflower
NCBI Description
                    >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max]
>gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max]
>gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin
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[Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092)
Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044)
putative polyubiquitin [Arabidopsis thaliana]
>gi_1096513_prf__2111434A tetraubiquitin [Helianthus
```

annuus] 298646 Seq. No. LIB3151-024-Q1-K1-D8 Seq. ID Method BLASTX g2832247 NCBI GI 167 BLAST score 7.0e-12 E value 88 Match length % identity 51 NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays] 298647 Seq. No. LIB3151-024-Q1-K1-E4 Seq. ID BLASTX Method g2832243 NCBI GI 185 BLAST score 2.0e-15 E value Match length 97 57 % identity (AF031569) 22-kDa alpha zein 4 [Zea mays] NCBI Description Seq. No. 298648 LIB3151-024-Q1-K1-E8 Seq. ID BLASTX Method g4185308 NCBI GI 156 BLAST score 2.0e-10 E value 86 Match length 45 % identity (AF090446) 22-kDa alpha zein protein 21 [Zea mays] NCBI Description 298649 Seq. No. LIB3151-024-Q1-K1-F6 Seq. ID BLASTN Method NCBI GI q168694 48 BLAST score 5.0e-18 E value 140 Match length 84 % identity

NCBI Description Maize gamma zein mRNA, partial cds

298650 Seq. No.

LIB3151-024-Q1-K1-G11 Seq. ID

Method BLASTN NCBI GI g22288 BLAST score 219 1.0e-120 E value 323 Match length % identity 92

NCBI Description Maize mRNA fragment for endosperm glutelin-2

298651 Seq. No.

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Y d a y parame
```

```
LIB3151-024-Q1-K1-G8
Seq. ID
                   BLASTN
Method
NCBI GI
                   q16072
                   68
BLAST score
                   4.0e-30
E value
                   140
Match length
                   87
% identity
NCBI Description Acetabularia mediterranea zein gene
                   298652
Seq. No.
                   LIB3151-024-Q1-K1-H11
Seq. ID
                   BLASTN
Method
                   q168669
NCBI GI
BLAST score
                   43
                   6.0e-15
E value
                   107
Match length
                   85
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19A2, partial cds
                   298653
Seq. No.
                   LIB3151-024-Q1-K1-H12
Seq. ID
                   BLASTX
Method
                   g121472
NCBI GI
                    226
BLAST score
                    1.0e-18
E value
                    110
Match length
                    40
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                    maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
                    mays] >gi_1684\overline{8}5 (M1\overline{6}066) glutelin-2 [Zea mays]
                    298654
Seq. No.
                    LIB3151-024-Q1-K1-H2
 Seq. ID
Method
                    BLASTX
                    q462195
NCBI GI
                    145
BLAST score
                    3.0e-09
E value
                    39
Match length
                    74
 % identity
                    PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
 NCBI Description
                    >gi_100682_pir__S21636 GOS2 protein - rice
                    >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                    >gi 3789950 (AF094774) translation initiation factor [Oryza
                    sativa]
                    298655
 Seq. No.
                    LIB3151-024-Q1-K1-H6
 Seq. ID
                    BLASTX
 Method
                    q462195
 NCBI GI
                    361
 BLAST score
                    2.0e-34
 E value
                    98
 Match length
                    74
 % identity
 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
```



```
>gi_100682_pir__S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza sativa]
```

 Seq. No.
 298656

 Seq. ID
 LIB3151-025-Q1-K1-A10

 Method
 BLASTX

 NCBI GI
 g629861

 BLAST score
 478

 E value
 4.0e-48

 Match length
 133

% identity 75
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)

zein Zdl (19 kDa zein) [Zea mays]

Seq. No. 298657

Seq. ID LIB3151-025-Q1-K1-B9

Method BLASTX
NCBI GI g22216
BLAST score 222
E value 4.0e-18
Match length 88
% identity 60

NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 298658

Seq. ID LIB3151-025-Q1-K1-C11

Method BLASTX
NCBI GI g141615
BLAST score 164
E value 3.0e-13
Match length 85
% identity 58

NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)

>gi 22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 298659

Seq. ID LIB3151-025-Q1-K1-C12

Method BLASTN
NCBI GI g168652
BLAST score 87
E value 3.0e-41
Match length 267
% identity 88

NCBI Description Maize amyloplast-specific transit protein (waxy; wx+

locus), complete cds

Seq. No. 298660

Seq. ID LIB3151-025-Q1-K1-D11

Method BLASTX
NCBI GI g419803
BLAST score 146
E value 2.0e-16
Match length 102
% identity 51

NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea

Seq. ID



mays]

```
298661
Seq. No.
                  LIB3151-025-Q1-K1-E11
Seq. ID
                  BLASTX
Method
                  g629861
NCBI GI
                  379
BLAST score
                  2.0e-36
E value
                  138
Match length
                  59
% identity
                  zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
                  298662
Seq. No.
                  LIB3151-025-Q1-K1-F11
Seq. ID
Method
                  BLASTX
                  g595775
NCBI GI
                  156
BLAST score
                  2.0e-10
E value
                  85
Match length
% identity
                   48
                  (U13869) lacZ alpha peptide [Cloning vector]
NCBI Description
                   298663
Seq. No.
                  LIB3151-025-Q1-K1-G10
Seq. ID
                  BLASTX
Method
                   g168703
NCBI GI
                   157
BLAST score
                   6.0e-11
E value
                   58
Match length
                   57
% identity
                  (M86591) 22 kDa zein protein [Zea mays]
NCBI Description
                   298664
Seq. No.
                   LIB3151-026-Q1-K1-A6
Seq. ID
                   BLASTN
Method
                   g168681
NCBI GI
BLAST score
                   111
                   1.0e-55
E value
                   319
Match length
                   84
% identity
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                   >gi_270686_gb_I03333_ Sequence 8 from Patent US
                   298665
Seq. No.
                   LIB3151-026-Q1-K1-B10
Seq. ID
Method
                   BLASTX
                   g100925
NCBI GI
BLAST score
                   142
                   4.0e-09
E value
Match length
                   57
                   49
% identity
                   zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_
NCBI Description
                   (X58197) 27kDa storage protein, zein [Zea mays]
 Seq. No.
                   298666
```

41957

LIB3151-026-Q1-K1-C5



```
Method
                    BLASTX
NCBI GI
                    g121472
BLAST score
                    416
E value
                    7.0e-41
Match length
                    124
                    60
% identity
                    GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289 emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                    mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
Seq. No.
                    298667
Seq. ID
                    LIB3151-026-Q1-K1-D2
Method
                    BLASTX
NCBI GI
                    g2832243
BLAST score
                    278
                    7.0e-25
E value
Match length
                    84
                    76
% identity
NCBI Description
                    (AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.
                    298668
Seq. ID
                    LIB3151-026-Q1-K1-E9
Method
                    BLASTX
NCBI GI
                    q141612
BLAST score
                    420
E value
                    3.0e-41
Match length
                    120
% identity
NCBI Description
                    ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)
                    >gi 72306 pir ZIZMC2 22K zein precursor (clone cZ22C2) -
                    maize (fragment) >gi 168688 (M12141) 22 kDa zein protein
                    [Zea mays]
                    298669
Seq. No.
Seq. ID
                    LIB3151-027-Q1-K1-B3
Method
                    BLASTX
NCBI GI
                    q141609
BLAST score
                    173
                    2.0e-12
E value
Match length
                    114
% identity
                    38
                    ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi 100944 pir S15656
NCBI Description
                    zein, 19K - maize >gi_22448_emb_CAA41543_ (X58700) 19 kDa
                    zein [Zea mays]
                    298670
Seq. No.
Seq. ID
                    LIB3151-027-Q1-K1-B8
                    BLASTN
Method
NCBI GI
                    g168681
BLAST score
                    126
```

E value 2.0e-64 Match length 282

% identity 86

NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.

Seq. ID

```
>gi 270686_gb_I03333_ Sequence 8 from Patent US
```

```
Seq. No.
                  298671
                  LIB3151-027-Q1-K1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1037129
BLAST score
                  201
                  1.0e-109
E value
                  377
Match length
% identity
                  88
                  (gamma-zeinA) = opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                  298672
Seq. No.
Seq. ID
                  LIB3151-027-Q1-K1-D6
Method
                  BLASTX
                  g4490333
NCBI GI
BLAST score
                  154
                  3.0e-10
E value
Match length
                  95
% identity
                  40
                  (AL035656) EF-Hand containing protein-like [Arabidopsis
NCBI Description
                  thaliana]
                  298673
Seq. No.
Seq. ID
                  LIB3151-027-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g4314378
BLAST score
                  247
                  5.0e-21
E value
                  134
Match length
% identity
                  34
                  (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
                  298674
Seq. No.
                  LIB3151-027-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832247
BLAST score
                  394
                  3.0e-38
E value
Match length
                  105
% identity
                  79
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
                  298675
Seq. No.
Seq. ID
                  LIB3151-027-Q1-K1-E7
Method
                  BLASTN
NCBI GI
                  g1037129
BLAST score
                  110
E value
                  4.0e-55
Match length
                  233
% identity
                  88
NCBI Description
                   (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
Seq. No.
                  298676
```

41959

LIB3151-027-Q1-K1-F3



```
Method
                   BLASTN
NCBI GI
                   q22549
BLAST score
                   56
E value
                   1.0e-22
Match length
                   262
                   84
% identity
NCBI Description Maize gene for a 27kDa storage protein, zein
                   298677
Seq. No.
Seq. ID
                   LIB3151-027-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   g629861
BLAST score
                   178
E value
                   3.0e-20
Match length
                   99
                   64
% identity
                   zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                   298678
Seq. ID
                   LIB3151-027-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   q629861
BLAST score
                   257
E value
                   2.0e-22
Match length
                   87
                   63
% identity
NCBI Description
                   zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
                   zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                   298679
Seq. ID
                   LIB3151-027-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   g141617
BLAST score
                   295
                   1.0e-26
E value
                   74
Match length
                   77
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
                   >gi 22515 emb CAA37595_ (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                   298680
Seq. No.
Seq. ID
                   LIB3151-027-Q1-K1-G6
Method
                   BLASTX
                   g141598
NCBI GI
                   150
BLAST score
E value
                   2.0e-13
                   123
Match length
                   39
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
NCBI Description
                   >gi 72313 pir ZIZM99 19K zein precursor (clone ZG99) -
                   maize >gi 22519 emb CAA24717 (V01470) zein [Zea mays]
```

>gi 22534 emb CAA24726 (V01479) zein [Zea mays]

```
298681
Seq. No.
                  LIB3151-027-Q1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g141617
                   318
BLAST score
                   2.0e-29
E value
                   65
Match length
                   91
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
                   >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                   >gi_168666 (M16460) 16-kDa zein protein [Zea mays]
Seq. No.
                   298682
                   LIB3151-028-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   q1663724
NCBI GI
                   271
BLAST score
                   6.0e-24
E value
Match length
                   103
                   53
% identity
NCBI Description (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
                   298683
Seq. No.
                   LIB3151-028-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   g508545
NCBI GI
BLAST score
                   239
                   4.0e-20
E value
                   91
Match length
                   58
% identity
NCBI Description (L34340) zein [Zea mays]
                   298684
Seq. No.
                   LIB3151-028-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   q141597
NCBI GI
BLAST score
                   187
                   2.0e-14
E value
Match length
                   69
                   57
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   298685
Seq. No.
Seq. ID
                   LIB3151-029-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   q121472
BLAST score
                   218
                   4.0e-18
E value
                   52
Match length
```

GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

81

% identity

NCBI Description

% identity

85

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298686 Seq. ID LIB3151-029-Q1-K1-A8 Method BLASTX NCBI GI g168695 BLAST score 169 2.0e-12 E value Match length 67 58 % identity NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A zein gamma [Zea mays] Seq. No. 298687 Seq. ID LIB3151-029-Q1-K1-B11 Method BLASTX NCBI GI g1184774 BLAST score 407 6.0e-40 E value 96 Match length 81 % identity NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays] Seq. No. 298688 Seq. ID LIB3151-029-Q1-K1-B3 Method BLASTX NCBI GI g168701 BLAST score 348 E value 5.0e-33 94 Match length 79 % identity NCBI Description (M60837) zein [Zea mays] Seq. No. 298689 LIB3151-029-Q1-K1-B6 Seq. ID Method BLASTX NCBI GI q224513 BLAST score 317 E value 3.0e-29 Match length 101 % identity 67 NCBI Description zein M6 [Zea mays] 298690 Seq. No. LIB3151-029-Q1-K1-B7 Seq. ID Method BLASTN NCBI GI g22537 BLAST score 114 E value 3.0e-57 Match length 313

NCBI Description Maize mRNA for zein polypeptide (clone M6)

Method

NCBI GI

BLASTX

g100925



```
298691
Seq. No.
                  LIB3151-029-Q1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832247
BLAST score
                  165
                  2.0e-20
E value
Match length
                  116
                  54
% identity
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.
                  298692
                  LIB3151-029-Q1-K1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22149
                  56
BLAST score
                  9.0e-23
E value
                  96
Match length
                  90
% identity
NCBI Description Z.mays mRNA for alpha-tubulin
                  298693
Seq. No.
Seq. ID
                  LIB3151-029-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q141608
BLAST score
                  176
E value
                  6.0e-24
Match length
                  80
% identity
                  75
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
                  zein, 19K - maize >gi 22446 emb CAA37651 (X53582) 19 kDa
                  zein [Zea mays]
                  298694
Seq. No.
Seq. ID
                  LIB3151-029-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  q224513
BLAST score
                  305
E value
                  8.0e-28
Match length
                  111
% identity
                  65
NCBI Description zein M6 [Zea mays]
                  298695
Seq. No.
                  LIB3151-029-Q1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1037129
BLAST score
                  251
                  1.0e-139
E value
Match length
                   371
% identity
                   92
                  (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                  298696
Seq. No.
Seq. ID
                  LIB3151-029-Q1-K1-D12
```

NCBI GI

g16073



```
BLAST score
                   227
                   6.0e-19
E value
Match length
                   86
% identity
                   47
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175
                   (X58197) 27kDa storage protein, zein [Zea mays]
Seq. No.
                   298697
Seq. ID
                   LIB3151-029-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   g419803
BLAST score
                   415
                   1.0e-40
E value
                   144
Match length
                   60
% identity
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
                   mays]
Seq. No.
                   298698
Seq. ID
                   LIB3151-029-Q1-K1-D8
Method
                   BLASTX
                   g121472
NCBI GI
BLAST score
                   324
E value
                   5.0e-30
Match length
                   101
% identity
                   59
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289 emb CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi_22517 emb CAA37594 (X53514) zein Zc2 [Zea
                   mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
Seq. No.
                   298699
Seq. ID
                   LIB3151-029-Q1-K1-E10
Method
                   BLASTX
                   g22220
NCBI GI
BLAST score
                   149
                   1.0e-09
E value
Match length
                   63
% identity
NCBI Description (X55723) 22 kD zein [Zea mays]
                   298700
Seq. No.
                   LIB3151-029-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   g168691
NCBI GI
BLAST score
                   202
E value
                   5.0e-16
Match length
                   61
% identity
                   69
NCBI Description (M29628) zein [Zea mays]
Seq. No.
                   298701
Seq. ID
                   LIB3151-029-Q1-K1-E3
Method
                   BLASTX
```



```
BLAST score 158
E value 7.0e-11
Match length 54
% identity 72
```

NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298702

Seq. ID LIB3151-029-Q1-K1-F1

Method BLASTX
NCBI GI g168701
BLAST score 217
E value 1.0e-17
Match length 79
% identity 62

NCBI Description (M60837) zein [Zea mays]

Seq. No. 298703

Seq. ID LIB3151-029-Q1-K1-F6

Method BLASTX
NCBI GI g468515
BLAST score 152
E value 1.0e-11
Match length 58
% identity 72

NCBI Description (X55726) zein [Zea mays]

Seq. No. 298704

Seq. ID LIB3151-029-Q1-K1-F8

Method BLASTX
NCBI GI g121472
BLAST score 174
E value 7.0e-15
Match length 77
% identity 56

NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea

mays] >gi 168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298705

Seq. ID LIB3151-029-Q1-K1-G1

Method BLASTX
NCBI GI g121472
BLAST score 329
E value 1.0e-30
Match length 127
% identity 53

NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea

mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298706



```
LIB3151-029-Q1-K1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q141608
BLAST score
                   289
E value
                   4.0e-26
Match length
                   81
% identity
                   74
NCBI Description
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
                   zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                   zein [Zea mays]
Seq. No.
                   298707
Seq. ID
                   LIB3151-029-Q1-K1-H8
Method
                   BLASTN
NCBI GI
                   g168484
BLAST score
                   86
E value
                   1.0e-40
Match length
                   238
% identity
                   84
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   298708
Seq. No.
                   LIB3151-030-Q1-K1-A11
Seq. ID
Method
                   BLASTX
                   g141603
NCBI GI
BLAST score
                   336
                   1.0e-31
E value
Match length
                   98
% identity
                   79
NCBI Description
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                   >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
                   298709
Seq. No.
Seq. ID
                   LIB3151-030-Q1-K1-B11
Method
                   BLASTX
                   g141605
NCBI GI
BLAST score
                   282
E value
                   2.0e-25
Match length
                   85
% identity
                   73
NCBI Description
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                   298710
                   LIB3151-030-Q1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g100938
BLAST score
                   261
E value
                   1.0e-22
Match length
                   104
% identity
                   54
                   zein precursor - maize >gi_22442_emb_CAA32513_ (X14335)
NCBI Description
                   zein precursor (AA -21 to 90) [Zea mays]
```

Seq. No.

NCBI GI

BLAST score

g168690

74



```
LIB3151-030-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q629861
BLAST score
                  273
                  3.0e-24
E value
                  72
Match length
                  74
% identity
NCBI Description zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
                  298712
Seq. No.
Seq. ID
                  LIB3151-030-Q1-K1-D12
                  BLASTX
Method
NCBI GI
                  g16073
                  371
BLAST score
E value
                  1.0e-35
Match length
                  112
% identity
                  66
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
Seq. No.
                  298713
                  LIB3151-030-Q1-K1-E10
Seq. ID
Method
                  BLASTX
                  g16073
NCBI GI
BLAST score
                  205
                  3.0e-16
E value
Match length
                  104
                  51
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                  298714
Seq. No.
                  LIB3151-030-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141608
BLAST score
                  147
                  4.0e-21
E value
                  99
Match length
                  57
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
                  zein, 19K - maize >gi_22446 emb_CAA37651_ (X53582) 19 kDa
                  zein [Zea mays]
Seq. No.
                  298715
Seq. ID
                  LIB3151-030-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q168691
BLAST score
                  402
E value
                  3.0e-39
Match length
                  123
% identity
                  68
NCBI Description (M29628) zein [Zea mays]
                  298716
Seq. No.
Seq. ID
                  LIB3151-030-Q1-K1-F10
Method
                  BLASTN
```



```
E value
                  1.0e-33
Match length
                  242
                  83
% identity
NCBI Description Maize zein mRNA, complete cds, clone ZG124
Seq. No.
                  298717
                  LIB3151-030-Q1-K1-H11
Seq. ID
Method
                  BLASTN
                  g1037129
NCBI GI
BLAST score
                  95
                  3.0e-46
E value
Match length
                  200
% identity
                  92
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
```

(gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, NCBI Description

298718 Seq. No. LIB3151-031-Q1-K1-B7 Seq. ID Method BLASTN NCBI GI g168685 BLAST score 191

E value 1.0e-103 Match length 327 % identity 91

NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA

298719 Seq. No. Seq. ID LIB3151-031-01-K1-D1 Method BLASTX

NCBI GI g141605 BLAST score 554 5.0e-57 E value Match length 135 % identity 85

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) NCBI Description

> >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298720

LIB3151-031-Q1-K1-D4 Seq. ID

Method BLASTX NCBI GI g121472 BLAST score 232 2.0e-19 E value Match length 71 % identity 61

GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) NCBI Description

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi_ $\overline{22517}$ _emb_CAA $\overline{37594}$ _ (X53514) zein Zc2 [Zea

mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298721

Seq. ID LIB3151-031-Q1-K1-D5

Method BLASTX NCBI GI g2832243

```
252
BLAST score
                  1.0e-21
E value
                  95
Match length
                  59
% identity
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
                  298722
Seq. No.
                  LIB3151-031-Q1-K1-E5
Seq. ID
                  BLASTX
Method
                   g141600
NCBI GI
                   226
BLAST score
                   2.0e-38
E value
                   138
Match length
% identity
                   67
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
```

>gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -

maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

298723 Seq. No. LIB3151-031-Q1-K1-F7 Seq. ID Method BLASTX g168699 NCBI GI 158 BLAST score

1.0e-10 E value Match length 55 % identity 67

(M60836) zein [Zea mays] NCBI Description

298724 Seq. No.

LIB3151-031-Q1-K1-F9 Seq. ID

BLASTN Method g22549 NCBI GI 257 BLAST score 1.0e-142 E value 257 Match length 53 % identity

NCBI Description Maize gene for a 27kDa storage protein, zein

298725 Seq. No.

LIB3151-031-Q1-K1-H11 Seq. ID

BLASTN Method g22549 NCBI GI 150 BLAST score 5.0e-79 E value 174 Match length 97 % identity

NCBI Description Maize gene for a 27kDa storage protein, zein

298726 Seq. No.

LIB3151-033-Q1-K1-A2 Seq. ID

Method BLASTX q141605 NCBI GI BLAST score 202 6.0e-16 E value 97 Match length 59 % identity

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)



>gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

298727
LIB3151-033-Q1-K1-A3
BLASTN
g4582786
94

BLAST score 94 E value 1.0e-45 Match length 178 % identity 88

Seq. No.

Seq. ID

NCBI GI

Method

NCBI Description Zea mays mRNA for adenosine kinase, putative

Seq. No. 298728

Seq. ID LIB3151-033-Q1-K1-A4

Method BLASTN
NCBI GI g2832242
BLAST score 268
E value 1.0e-149
Match length 460
% identity 14

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 298729

Seq. ID LIB3151-033-Q1-K1-B1

Method BLASTX
NCBI GI g22216
BLAST score 322
E value 8.0e-30
Match length 101
% identity 67

NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 298730

Seq. ID LIB3151-033-Q1-K1-B2

Method BLASTX
NCBI GI g2832243
BLAST score 344
E value 2.0e-32
Match length 102
% identity 73

NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298731

Seq. ID LIB3151-033-Q1-K1-B3

Method BLASTX
NCBI GI g2832243
BLAST score 237
E value 2.0e-23
Match length 78
% identity 77

NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298732

Seq. ID LIB3151-033-Q1-K1-B7

Method BLASTX NCBI GI g141614



```
BLAST score
                  160
                  3.0e-11
E value
                  61
Match length
                  61
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
NCBI Description
                  >gi_82662_pir__B22831 22K zein precursor (clone M1) - maize
                  >qi 22527 emb CAA24722 (V01475) reading frame zein [Zea
                  mays] >gi_224510_prf_ 1107201D zein M1 [Zea mays]
                  298733
Seq. No.
Seq. ID
                  LIB3151-033-Q1-K1-C2
Method
                  BLASTN
                  g2832242
NCBI GI
BLAST score
                  95
                  2.0e-46
E value
Match length
                  163
% identity
                  19
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                  298734
Seq. No.
                  LIB3151-033-Q1-K1-C5
Seq. ID
Method
                  BLASTX
                  g141605
NCBI GI
                  386
BLAST score
                  2.0e-37
E value
                  94
Match length
% identity
                  83
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                   298735
                  LIB3151-033-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                   g168697
NCBI GI
BLAST score
                  150
E value
                   8.0e-10
Match length
                   44
                   77
% identity
                  (M60835) zein [Zea mays]
NCBI Description
                   298736
Seq. No.
                  LIB3151-033-Q1-K1-F5
Seq. ID
                  BLASTN
Method
                   q22549
NCBI GI
                   70
BLAST score
                   2.0e-31
E value
Match length
                   130
                   88
% identity
NCBI Description Maize gene for a 27kDa storage protein, zein
Seq. No.
                   298737
```

LIB3151-034-Q1-K1-C12 Seq. ID

BLASTX Method g141617 NCBI GI BLAST score 287 E value 4.0e-26

```
Match length
                  85
% identity
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                  >gi_100941_pir__S12140 zein Zc1 - maize
                  >gi_100945_pir__B29017 zein 2 - maize
                  >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                  >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                  298738
Seq. No.
Seq. ID
                  LIB3151-035-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  q100940
BLAST score
                  211
E value
                  5.0e-17
Match length
                  79
% identity
                  62
                  zein zAl - maize
NCBI Description
                  298739
Seq. No.
                  LIB3151-035-Q1-K1-B5
Seq. ID
Method
                  BLASTX
                  g168664
NCBI GI
BLAST score
                  144
                  2.0e-14
E value
Match length
                  101
                  50
% identity
NCBI Description
                  (M13507) zein protein precursor [Zea mays]
                  298740
Seq. No.
                  LIB3151-035-01-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100925
BLAST score
                  175
E value
                  1.0e-12
Match length
                  65
% identity
                  52
NCBI Description
                  zein, 27K - maize (fragment) >gi 22550 emb CAA41175
                   (X58197) 27kDa storage protein, zein [Zea mays]
Seq. No.
                  298741
Seq. ID
                  LIB3151-035-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g121472
BLAST score
                  217
E value
                  2.0e-17
Match length
                  127
% identity
                  41
                  GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
```

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea

mays] >gi 168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298742 Seq. ID LIB3151-035-Q1-K1-E9

Method BLASTX

```
4 100
```

```
g141615
NCBI GI
BLAST score
                  368
                  2.0e-35
E value
                  110
Match length
                  72
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
NCBI Description
                  >gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]
                  298743
Seq. No.
                  LIB3151-035-Q1-K1-F12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q141605
                  277
BLAST score
                   6.0e-25
E value
                   69
Match length
                   83
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize > gi_168\overline{68}0 (M12145) 19 kDa zein protein [Zea mays]
                   298744
Seq. No.
Seq. ID
                   LIB3151-035-Q1-K1-F3
Method
                   BLASTX
                   g3023275
NCBI GI
                   393
BLAST score
                   1.0e-46
E value
                   135
Match length
                   67
% identity
                  ALPHA-GLUCOSIDASE PRECURSOR (MALTASE)
NCBI Description
                   >gi_2130027_pir__S65057 alpha-glucosidase (EC 3.2.1.20) -
                   barley >gi 944901 (U22450) alpha-glucosidase [Hordeum
                   vulgare]
                   298745
Seq. No.
                   LIB3151-035-Q1-K1-G4
Seq. ID
                   BLASTN
Method
                   g22447
NCBI GI
BLAST score
                   62
                   1.0e-26
E value
                   169
Match length
                   85
% identity
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein
Seq. No.
                   298746
                   LIB3151-035-Q1-K1-G6
Seq. ID
                   BLASTX
Method
                   q141615
NCBI GI
BLAST score
                   221
E value
                   3.0e-18
Match length
                   71
 % identity
                   72
                   ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
NCBI Description
                   >qi 22536 emb CAA24727 (V01480) zein protein 3 [Zea mays]
                   298747
 Seq. No.
                   LIB3151-035-Q1-K1-H1
 Seq. ID
```

BLASTN

Method



```
g22100
NCBI GI
                  54
BLAST score
                  1.0e-21
E value
                  82
Match length
                  91
% identity
NCBI Description Z.mays 27kDa zein locus DNA
                  298748
Seq. No.
                  LIB3151-035-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                  q224513
NCBI GI
                  155
BLAST score
                  1.0e-10
E value
                  63
Match length
                  57
% identity
NCBI Description zein M6 [Zea mays]
                   298749
Seq. No.
                  LIB3151-037-Q1-K1-A11
Seq. ID
                  BLASTX
Method
                   g2832243
NCBI GI
                   233
BLAST score
                   2.0e-19
E value
                   84
Match length
                   62
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                   298750
Seq. No.
                   LIB3151-037-Q1-K1-A3
Seq. ID
                   {\tt BLASTX}
Method
                   q419803
NCBI GI
                   182
BLAST score
                   5.0e-14
E value
Match length
                   45
                   78
% identity
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
                   mays]
                   298751
Seq. No.
Seq. ID
                   LIB3151-037-Q1-K1-A8
                   BLASTN
Method
NCBI GI
                   g22537
BLAST score
                   37
E value
                   1.0e-11
                   61
Match length
                   90
 % identity
NCBI Description Maize mRNA for zein polypeptide (clone M6)
 Seq. No.
                   298752
Seq. ID
                   LIB3151-037-Q1-K1-B5
                   BLASTX
Method
                   g141603
 NCBI GI
 BLAST score
                   485
 E value
                   6.0e-49
                   129
 Match length
                   83
 % identity
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
```

```
>gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                   298753
Seq. No.
Seq. ID
                  LIB3151-037-Q1-K1-B8
Method
                  BLASTX
                   q16073
NCBI GI
                   340
BLAST score
                   4.0e-32
E value
Match length
                   101
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                   298754
Seq. No.
                   LIB3151-037-Q1-K1-C6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q629861
BLAST score
                   296
                   6.0e-37
E value
                   130
Match length
                   65
% identity
                   zein Zdl, 19K - maize >gi_535020 emb_CAA47639 (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
                   298755
Seq. No.
                   LIB3151-037-Q1-K1-E6
Seq. ID
Method
                   BLASTX
                   g419803
NCBI GI
                   160
BLAST score
                   6.0e-11
E value
                   87
Match length
% identity
                   37
                   zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                   mays]
                   298756
Seq. No.
                   LIB3151-037-Q1-K1-F4
Seq. ID
Method
                   BLASTX
                   g121472
NCBI GI
BLAST score
                   176
E value
                   7.0e-13
Match length
                   86
% identity
                   44
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                    [Zea mays] >gi \overline{22517} emb CAA\overline{37594} (X53\overline{514}) zein Zc2 [Zea
                   mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
                   298757
Seq. No.
                   LIB3151-037-Q1-K1-F8
Seq. ID
Method
                   BLASTX
                   g482985
NCBI GI
                   164
BLAST score
                   9.0e-12
E value
```

>qi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize

41975

57

Match length

```
% identity
NCBI Description chitinase (EC 3.2.1.14) precursor - maize (fragment)
                  298758
Seq. No.
                  LIB3151-037-Q1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g141608
                   301
BLAST score
                   4.0e-31
E value
                   137
Match length
                   56
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                   zein [Zea mays]
                   298759
Seq. No.
Seq. ID
                   LIB3151-037-Q1-K1-G12
                   BLASTX
Method
                   g168701
NCBI GI
                   269
BLAST score
                   1.0e-23
E value
                   76
Match length
% identity
NCBI Description (M60837) zein [Zea mays]
                   298760
Seq. No.
Seq. ID
                   LIB3151-037-Q1-K1-H8
                   BLASTX
Method
                   q419803
NCBI GI
                   273
BLAST score
                   1.0e-24
E value
Match length
                   64
 % identity
                   zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                   mays]
                   298761
 Seq. No.
                   LIB3151-038-Q1-K1-A4
 Seq. ID
                   BLASTX
 Method
                   g72307
 NCBI GI
 BLAST score
                   334
                   3.0e - 31
 E value
 Match length
                   109
 % identity
                   67
                   22K zein precursor (clone pZ22.3) - maize >gi_168686
 NCBI Description
                    (J01246) 26.99 kd zein protein [Zea mays]
```

298762 Seq. No.

LIB3151-038-Q1-K1-B5 Seq. ID

BLASTN Method g1037129 NCBI GI 114 BLAST score 2.0e-57 E value 326 Match length 84 % identity

(gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, NCBI Description

Tuxpeno CMS 450, mRNA Partial, 1889 nt]

```
298763
Seq. No.
                  LIB3151-038-Q1-K1-E7
Seq. ID
                  BLASTN
Method
                  q168681
NCBI GI
BLAST score
                  71
                  1.0e-31
E value
                  231
Match length
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
                  >gi_270686_gb_I03333_ Sequence 8 from Patent US
Seq. No.
                  298764
                  LIB3151-038-Q1-K1-F1
Seq. ID
                  BLASTX
Method
                  q4510430
NCBI GI
BLAST score
                  254
                  8.0e-22
E value
                  70
Match length
                  67
% identity
NCBI Description (AC006929) unknown protein, 3' partial [Arabidopsis
                  thaliana]
Seq. No.
                  298765
                  LIB3151-038-Q1-K1-G2
Seq. ID
Method
                  BLASTX
                  q508545
NCBI GI
                   413
BLAST score
                   2.0e-40
E value
                   99
Match length
                   81
% identity
NCBI Description (L34340) zein [Zea mays]
Seq. No.
                   298766
                   LIB3151-038-Q1-K1-G3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168484
BLAST score
                   203
E value
                   1.0e-110
Match length
                   367
                   89
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   298767
Seq. No.
                   LIB3151-038-Q1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832243
BLAST score
                   431
                   2.0e-42
E value
Match length
                   128
                   73
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                   298768
Seq. No.
                   LIB3151-039-Q1-K1-B8
Seq. ID
                   BLASTN
Method
NCBI GI
                   g18053
```

```
BLAST score
                      46
                      7.0e-17
    E value
                      66
    Match length
                      92
    % identity
    NCBI Description C.lacryma-jobi L. mRNA for gamma-coixin (22KDa)
    Seq. No.
                      298769
                      LIB3151-039-Q1-K1-C3
    Seq. ID
    Method
                      BLASTN
    NCBI GI
                      g1037129
    BLAST score
                      309
    E value
                      1.0e-173
    Match length
                      375
                      95
    % identity
    NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
                      Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                      298770
    Seq. No.
                      LIB3151-039-Q1-K1-D9
    Seq. ID
    Method
                      BLASTN
    NCBI GI
                      g168484
    BLAST score
                      174
                      3.0e-93
    E value
    Match length
                      294
    % identity
                      90
    NCBI Description Maize endosperm glutelin-2 gene, complete cds
                      298771
    Seq. No.
    Seq. ID
                      LIB3151-039-Q1-K1-E12
    Method
                      BLASTX
    NCBI GI
                      g584706
    BLAST score
                      191
    E value
                      7.0e-15
                      38
    Match length
                      100
    % identity
    NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
                      >gi 2130066 pir JC5124 aspartate transaminase (EC
                      2.6.1.1), cytoplasmic - rice >gi 287298 dbj BAA03504
                      (D14673) aspartate aminotransferase [Oryza sativa]
    Seq. No.
                      298772
    Seq. ID
                      LIB3151-039-Q1-K1-E7
    Method
                      BLASTX
    NCBI GI
                      g141614
    BLAST score
                      220
    E value
                      5.0e-18
                      96
    Match length
                      52
    % identity
    NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
                      >gi_82662_pir_B22831 22K zein precursor (clone M1) - maize
                      >gi_22527_emb_CAA24722 (V01475) reading frame zein [Zea
mays] >gi 224510 prf 1107201D zein M1 [Zea mays]
```

Seq. No. 298773

Seq. ID LIB3151-039-Q1-K1-F6

Method BLASTX NCBI GI g141597



```
BLAST score
                  249
E value
                  2.0e-24
                  103
Match length
                  66
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                  [Zea mays]
                  298774
Seq. No.
Seq. ID
                  LIB3151-039-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  q141600
BLAST score
                  161
E value
                  3.0e-11
Match length
                  51
% identity
                  69
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                  >gi 72315 pir ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
                  298775
Seq. No.
                  LIB3151-039-Q1-K1-G2
Seq. ID
Method
                  BLASTX
                  g2827712
NCBI GI
BLAST score
                  206
                  3.0e-16
E value
Match length
                  82
% identity
                  51
                  (AL021684) endoxyloglucan tranferase-like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  298776
Seq. ID
                  LIB3151-039-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q141603
BLAST score
                  200
E value
                  1.0e-20
Match length
                  103
                  56
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                  298777
Seq. ID
                  LIB3151-039-Q1-K1-H4
Method
                  BLASTN
NCBI GI
                  g168679
BLAST score
                  57
E value
                  1.0e-23
```

Match length 120 % identity 88

NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.

>gi_270687 gb I03334 Sequence 9 from Patent US

298778 Seq. No.

Seq. ID LIB3151-039-Q1-K1-H7



```
Method
                  BLASTN
                  g3057119
NCBI GI
BLAST score
                  111
E value
                  9.0e-56
Match length
                  175
                  91
% identity
NCBI Description Zea mays starch synthase DULL1 (dull1) mRNA, complete cds
Seq. No.
                  298779
                  LIB3151-039-Q1-K1-H9
Seq. ID
                  BLASTN
Method
NCBI GI
                  q22549
BLAST score
                  241
E value
                  1.0e-133
                  279
Match length
                  97
% identity
NCBI Description Maize gene for a 27kDa storage protein, zein
Seq. No.
                  298780
Seq. ID
                  LIB3151-040-Q1-K1-B4
Method
                  BLASTN
NCBI GI
                  q168685
BLAST score
                  63
E value
                  6.0e-27
Match length
                  119
% identity
                  88
NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA
                  298781
Seq. No.
Seq. ID
                  LIB3151-040-Q1-K1-D2
                  BLASTX
Method
                  g419803
NCBI GI
BLAST score
                  151
E value
                  2.0e-10
Match length
                  51
% identity
                  67
NCBI Description
                  zein protein - maize >gi 168705 (M72708) zein protein [Zea
                  298782
Seq. No.
Seq. ID
                  LIB3151-040-Q1-K1-E6
                  BLASTX
Method
NCBI GI
                  g2832243
BLAST score
                  209
E value
                  3.0e-17
                  58
Match length
% identity
                  78
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.
                  298783
Seq. ID
                  LIB3151-040-Q1-K1-F7
                                                            Ē
Method
                  BLASTX
NCBI GI
                  g419803
BLAST score
                  362
                  1.0e-34
E value
```

54

Match length

% identity

115

% identity

96

NCBI Description Z.mays ZSF4C1 gene for zein



```
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
                   mays]
                   298784
Seq. No.
                   LIB3151-040-Q1-K1-G7
Seq. ID
                   BLASTN
Method
                   g168484
NCBI GI
                    38
BLAST score
                    6.0e-12
E value
                   86
Match length
                    86
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                    298785
Seq. No.
                    LIB3151-040-Q1-K1-H3
Seq. ID
                    BLASTN
Method
                    g2832242
NCBI GI
                    57
BLAST score
                    2.0e-23
E value
                    127
Match length
                    10
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                    298786
Seq. No.
                    LIB3151-040-Q1-K1-H9
Seq. ID
Method
                    BLASTX
                    g121472
NCBI GI
BLAST score
                    168
                    7.0e-12
E value
                    97
Match length
                    41
% identity
                    GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
                    maize >gi_22289 emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                    mays] >gi_1684\overline{8}5 (M1\overline{6}066) gluteli\overline{n}-2 [Zea mays]
                    298787
 Seq. No.
                    LIB3151-041-Q1-K1-A3
 Seq. ID
 Method
                    BLASTX
                    q2655029
 NCBI GI
 BLAST score
                    636
                    8.0e-67
 E value
                    113
 Match length
                    100
 % identity
 NCBI Description (AF019296) starch synthase isoform zSTSII-1 [Zea mays]
                     298788
 Seq. No.
                    LIB3151-041-Q1-K1-A8
 Seq. ID
 Method
                     BLASTN
                     q22215
 NCBI GI
                     46
 BLAST score
                     8.0e-17
 E value
                     54
 Match length
```

```
298789
Seq. No.
                  LIB3151-041-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                  g508545
NCBI GI
BLAST score
                  175
                   9.0e-13
E value
                  66
Match length
% identity
NCBI Description (L34340) zein [Zea mays]
                   298790
Seq. No.
                  LIB3151-041-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                   q100925
NCBI GI
                   168
BLAST score
                   7.0e-12
E value
                   42
Match length
                   64
% identity
                   zein, 27K - maize (fragment) >gi_22550_emb_CAA41175
NCBI Description
                   (X58197) 27kDa storage protein, zein [Zea mays]
                   298791
Seq. No.
                   LIB3151-041-Q1-K1-E1
Seq. ID
                   BLASTN
Method
                   g625147
NCBI GI
                   97
BLAST score
                   3.0e-47
E value
Match length
                   345
                   83
% identity
                   Zea mays protein disulfide isomerase (pdi) mRNA, complete
NCBI Description
                   298792
Seq. No.
                   LIB3151-041-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   g121472
NCBI GI
BLAST score
                   151
                   2.0e-10
E value
                   55
Match length
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi 72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                    [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                   mays] >gi_1684\overline{8}5 (M1\overline{6}066) glutelin-2 [Zea mays]
Seq. No.
                   298793
                   LIB3151-041-Q1-K1-F12
Seq. ID
Method
                   BLASTN
                    g168484
NCBI GI
BLAST score
                   273
```

NCBI Description Maize endosperm glutelin-2 gene, complete cds

1.0e-152

377

94

E value

Match length

% identity

```
Seq. No.
                  298794
                  LIB3151-041-Q1-K1-F9
Seq. ID
                  {\tt BLASTX}
Method ·
NCBI GI
                  g141615
BLAST score
                  173
E value
                  1.0e-12
                  83
Match length
                  49
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
                  >gi 22536 emb CAA24727_ (V01480) zein protein 3 [Zea mays]
                  298795
Seq. No.
Seq. ID
                  LIB3151-041-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  q141603
BLAST score
                  436
E value
                  3.0e-43
Match length
                  119
                  77
% identity
                 ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >qi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                  298796
Seq. No.
                  LIB3151-041-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g508545
BLAST score
                  205
                  3.0e-16
E value
Match length
                  87
                  52
% identity
NCBI Description (L34340) zein [Zea mays]
Seq. No.
                  298797
                  LIB3151-042-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3426039
BLAST score
                  513
                  3.0e-52
E value
                  126
Match length
                  71
% identity
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                  298798
                  LIB3151-042-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141608
BLAST score
                  170
E value
                  4.0e-12
Match length
                  47
                  72
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir_ S15655
                  zein, 19K - maize >gi 22446 emb CAA37651 (X53582) 19 kDa
```

zein [Zea mays]

298799

Seq. No.

```
LIB3151-042-Q1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168665
                  88
BLAST score
                  4.0e-42
E value
                  95
Match length
% identity
                  98
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
Seq. No.
                  298800
Seq. ID
                  LIB3151-043-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g100925
                  168
BLAST score
                  4.0e-12
E value
Match length
                  51
% identity
                  63
NCBI Description zein, 27K - maize (fragment) >qi 22550 emb CAA41175
                  (X58197) 27kDa storage protein, zein [Zea mays]
Seq. No.
                  298801
                  LIB3151-043-Q1-K1-B4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g168679
BLAST score
                  59
E value
                  1.0e-24
Match length
                  186
% identity
                  85
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
                  >gi_270687_gb_I03334_ Sequence 9 from Patent US
Seq. No.
                  298802
Seq. ID
                  LIB3151-043-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  q1707924
BLAST score
                  141
E value
                  3.0e-09
Match length
                  55
                  56
% identity
NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 1
                  PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
                  PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE
                  ADENYL TRANSFERASE) (SHRUNKEN-2) >gi 1947182 (M81603)
                  shrunken-2 [Zea mays] >gi 444329 prf 1906378A ADP glucose
                  pyrophosphorylase [Zea mays]
                  298803
Seq. No.
```

 Seq. No.
 298803

 Seq. ID
 LIB3151-043-Q1-K1-D2

 Method
 BLASTX

NCBI GI g419803
BLAST score 216
E value 1.0e-17
Match length 89
% identity 52

NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

```
298804
Seq. No.
Seq. ID
                   LIB3151-043-Q1-K1-D4
                   BLASTX
Method
NCBI GI
                   g584706
BLAST score
                   222
E value
                   3.0e-18
Match length
                   87
                   54
% identity
NCBI Description
                  ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
                   >gi 2130066 pir JC5124 aspartate transaminase (EC
                   2.6.1.1), cytoplasmic - rice >gi 287298 dbj BAA03504
                   (D14673) aspartate aminotransferase [Oryza sativa]
Seq. No.
                   298805
Seq. ID
                   LIB3151-043-Q1-K1-E1
Method
                   BLASTX
NCBI GI
                   g141617
                   393
BLAST score
E value
                   3.0e-38
Match length
                   109
% identity
                   66
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                  >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
                   >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                   298806
Seq. No.
Seq. ID
                   LIB3151-043-01-K1-E4
Method
                   BLASTN
NCBI GI
                   g168484
BLAST score
                   34
E value
                   6.0e-10
Match length
                   90
% identity
                   84
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   298807
Seq. No.
Seq. ID
                   LIB3151-043-Q1-K1-E6
Method
                   BLASTN
NCBI GI
                   g22516
BLAST score
                   109
E value
                   2.0e-54
                   164
Match length
% identity
                   93
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.
                   298808
                   LIB3151-043-Q1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141597
BLAST score
                   245
E value
                   6.0e-21
                   66
Match length
                   76
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
```

>gi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize

```
[Zea mays]
                  298809
Seq. No.
Seq. ID
                  LIB3151-044-Q1-K1-A4
Method
                  BLASTX
                  q141610
NCBI GI
                  217
BLAST score
                  4.0e-18
E value
                  55
Match length
                  82
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)
                  298810
Seq. No.
                  LIB3151-044-Q1-K1-A5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1037129
BLAST score
                  40
                   1.0e-13
E value
                  117
Match length
                   82
% identity
                  (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   298811
Seq. No.
                   LIB3151-044-Q1-K1-B3
Seq. ID
                   BLASTN
Method
                   q829147
NCBI GI
                   111
BLAST score
E value
                   1.0e-55
                   167
Match length
                   92
% identity
                   Z.mays gene for cyclophilin
NCBI Description
                   298812
Seq. No.
                   LIB3151-044-Q1-K1-B6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141597
BLAST score
                   275
                   9.0e-25
E value
                   81
Match length
% identity
                   70
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi 72314 pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
                   298813
Seq. No.
                   LIB3151-044-Q1-K1-C2
 Seq. ID
                   BLASTN
Method
                   g168681
NCBI GI
                   139
BLAST score
                   2.0e-72
E value
                   249
Match length
                   90
 % identity
                   Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
 NCBI Description
                   >gi 270686 gb I03333 Sequence 8 from Patent US
```

>gi 22545_emb_CAA24728_ (V01481) reading frame zein [2]

```
298814
Seq. No.
                   LIB3151-044-Q1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q100939
                   215
BLAST score
                   2.0e-17
E value
Match length
                   67
% identity
                   69
NCBI Description zein precursor - maize
                   298815
Seq. No.
                   LIB3151-044-Q1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141608
BLAST score
                   179
E value
                   2.0e-22
Match length
                   131
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82)\overline{1}9 kDa
                   zein [Zea mays]
                   298816
Seq. No.
                   LIB3151-044-Q1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g419803
BLAST score
                   301
E value
                   2.0e-27
Match length
                   110
% identity
                   zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                   mays]
                   298817
Seq. No.
                   LIB3151-044-Q1-K1-F2
Seq. ID
Method
                   BLASTX
                   g141608
NCBI GI
BLAST score
                    306
                    4.0e-28
E value
                    102
Match length
% identity
                    66
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
NCBI Description
                    zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82)\overline{1}9 kDa
                    zein [Zea mays]
                    298818
Seq. No.
                    LIB3151-044-Q1-K1-G2
Seq. ID
                    BLASTX
Method
NCBI GI
                    q141600
BLAST score
                    181
                    1.0e-13
E value
                    49
Match length
                    82
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                    >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                    maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]
```

NCBI GI

g82660

```
Seq. No.
                  298819
Seq. ID
                  LIB3151-044-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g22216
BLAST score
                  163
E value
                  8.0e-12
Match length
                  46
                  78
% identity
NCBI Description (X55722) 22kD zein [Zea mays]
                  298820
Seq. No.
Seq. ID
                  LIB3151-045-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g141607
BLAST score
                  290
E value
                  4.0e-26
                  114
Match length
% identity
                  58
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
                  >gi 22521 emb CAA24718 (V01471) zein [Zea mays] >gi 168672
                  (J01244) zein 19 kd protein (partial) [Zea mays]
Seq. No.
                  298821
Seq. ID
                  LIB3151-045-Q1-K1-B2
Method
                  BLASTN
NCBI GI
                  q168704
BLAST score
                  76
                  1.0e-34
E value
Match length
                  208
% identity
                  92
NCBI Description Zea mays zein protein gene, complete cds
                  298822
Seq. No.
Seq. ID
                  LIB3151-045-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2642163
BLAST score
                  345
E value
                  1.0e-32
Match length
                  93
% identity
                  67
NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  298823
Seq. ID
                  LIB3151-045-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g168699
BLAST score
                  244
E value
                  8.0e-21
Match length
                  72
% identity
                  71
NCBI Description (M60836) zein [Zea mays]
Seq. No.
                  298824
Seq. ID
                  LIB3151-045-Q1-K1-C4
Method
                  BLASTX
```



```
BLAST score
                  216
E value
                  1.0e-17
Match length
                  100
% identity
                  53
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
Seq. No.
Seq. ID
                  LIB3151-045-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g72307
BLAST score
                  163
E value
                  3.0e-11
Match length
                  75
                  52
% identity
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
                  (J01246) 26.99 kd zein protein [Zea mays]
                  298826
Seq. No.
Seq. ID
                  LIB3151-045-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g114974
BLAST score
                  165
                  2.0e-11
E value
Match length
                  52
% identity
NCBI Description
                  NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR
                  >gi 67491 pir GLJY31 beta-glucosidase (EC 3.2.1.21)
                  precursor (clone TRE361) - white clover
                  >gi_21955_emb_CAA40058.1_ (X56734) beta-glucosidase
                  [Trifolium repens]
                  298827
Seq. No.
Seq. ID
                  LIB3151-045-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g224508
BLAST score
                  214
E value
                  1.0e-17
Match length
                  57
% identity
                  87
NCBI Description zein A20 [Zea mays]
                  298828
Seq. No.
Seq. ID
                  LIB3151-045-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1705678
BLAST score
                  321
E value
                  8.0e-30
Match length
                  78
                  83
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                  PROTEIN HOMOLOG) (VCP) >gi 862480 (U20213)
                  valosin-containing protein [Glycine max]
```

Seq. No. 298829

Seq. ID LIB3151-045-Q1-K1-H6

Method BLASTX

```
g2058311
NCBI GI
                  231
BLAST score
                  2.0e-19
E value
Match length
                  62
% identity
                  73
NCBI Description (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]
                  298830
Seq. No.
```

LIB3151-046-Q1-K1-C4

E value 132 Match length % identity NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

298831 Seq. No.

Seq. ID

Method

NCBI GI

BLAST score

LIB3151-046-Q1-K1-D5 Seq. ID

BLASTX

438

q3786009

2.0e-43

BLASTX Method q1182065 NCBI GI BLAST score 165 5.0e-21E value 87 Match length 72 % identity

NCBI Description (X55661) 22 kD zein [Zea mays]

298832 Seq. No.

LIB3151-046-Q1-K1-F1 Seq. ID

Method BLASTX g2668744 NCBI GI BLAST score 478 3.0e-48 E value 92 Match length 97 % identity

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

298833 Seq. No.

LIB3151-046-Q1-K1-F4 Seq. ID

BLASTN Method g168681 NCBI GI 73 BLAST score 3.0e-33 E value 160 Match length 86 % identity

Maize 19 kDa zein mRNA, clone cZ19D1, complete cds. NCBI Description

>gi_270686_gb_I03333_ Sequence 8 from Patent US

298834 Seq. No.

LIB3151-046-Q1-K1-G1 Seq. ID

BLASTX Method a141617 NCBI GI 337 BLAST score 1.0e-31 E value 100 Match length -67 % identity

NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)



```
>gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666 (M16460) 16-kDa zein protein [Zea mays]
298835
LIB3151-046-Q1-K1-G11
BLASTX
```

Method BLASTX
NCBI GI g224514
BLAST score 310
E value 2.0e-28
Match length 62
% identity 98

Seq. No.

Seq. ID

NCBI Description zein M8 [Zea mays]

Seq. No. 298836

Seq. ID LIB3151-046-Q1-K1-G7

Method BLASTX
NCBI GI g100925
BLAST score 185
E value 4.0e-14
Match length 72
% identity 44

NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_

(X58197) 27kDa storage protein, zein [Zea mays]

Seq. No. 298837

Seq. ID LIB3151-046-Q1-K1-H11

Method BLASTX
NCBI GI g141608
BLAST score 178
E value 2.0e-13
Match length 63
% identity 63

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655

zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa

zein [Zea mays]

Seq. No. 298838

Seq. ID LIB3151-047-P1-K1-D1

Method BLASTN
NCBI GI g168696
BLAST score 60
E value 3.0e-25
Match length 92
% identity 91

NCBI Description Z.mays zein mRNA, 3' end

Seq. No. 298839

Seq. ID LIB3151-047-P1-K1-D4

Method BLASTN
NCBI GI g22549
BLAST score 197
E value 1.0e-107
Match length 337
% identity 90

NCBI Description Maize gene for a 27kDa storage protein, zein

```
298840
Seq. No.
                   LIB3151-047-P1-K1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141597
BLAST score
                   488
                   2.0e-50
E value
                   142
Match length
                   77
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   298841
Seq. No.
Seq. ID
                   LIB3151-047-P1-K1-F2
Method
                   BLASTN
NCBI GI
                   g168690
                   77
BLAST score
                   3.0e-35
E value
                   173
Match length
                   87
% identity
NCBI Description Maize zein mRNA, complete cds, clone ZG124
                   298842
Seq. No.
Seq. ID
                   LIB3151-047-P1-K1-F6
Method
                   BLASTN
                   q22537
NCBI GI
                   81
BLAST score
E value
                   9.0e-38
Match length
                   117
                   58
% identity
NCBI Description Maize mRNA for zein polypeptide (clone M6)
                   298843
Seq. No.
                   LIB3151-047-P1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141609
BLAST score
                   195
E value
                    5.0e-15
Match length
                   112
% identity
                    46
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir__S15656
NCBI Description
                    zein, 19K - maize >gi_22448_emb_CAA4154\overline{3}_ (X58\overline{7}00) \overline{1}9 kDa
                    zein [Zea mays]
                    298844
Seq. No.
                   LIB3151-047-P1-K1-H10
Seq. ID
                    BLASTX
Method
                    g16073
NCBI GI
                    293
BLAST score
                    1.0e-26
E value
Match length
                    104
                    64
% identity
                   (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
```

298845

Seq. No.



```
LIB3151-048-P1-K1-A1
Seq. ID
                  BLASTX
Method
                  q2832247
NCBI GI
                  274
BLAST score
                  2.0e-24
E value
Match length
                  101
% identity
                   61
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
                  298846
Seq. No.
                  LIB3151-048-P1-K1-A12
Seq. ID
                  BLASTN
Method
                   g22516
NCBI GI
                   150
BLAST score
                   8.0e-79
E value
                   298
Match length
                   88
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   298847
Seq. No.
                   LIB3151-048-P1-K1-B7
Seq. ID
                   BLASTN
Method
                   q22516
NCBI GI
                   92
BLAST score
                   2.0e-44
E value
                   168
Match length
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   298848
Seq. No.
                   LIB3151-048-P1-K1-B9
Seq. ID
                   BLASTN
Method
NCBI GI
                   q168573
                   93
BLAST score
                   5.0e-45
E value
                   183
Match length
                   93
 % identity
                   Zea mays tryptophan synthase beta-subunit (TSB2) mRNA,
NCBI Description
                   complete cds
 Seq. No.
                   298849
                   LIB3151-048-P1-K1-C6
 Seq. ID
 Method
                   BLASTX
                   q100940
 NCBI GI
                   166
 BLAST score
                   1.0e-11
 E value
                   74
 Match length
                   49
 % identity
 NCBI Description zein zA1 - maize
                   298850
 Seq. No.
                   LIB3151-048-P1-K1-C7
 Seq. ID
 Method
                   BLASTX
                    g2832243
 NCBI GI
                    183
 BLAST score
```

7.0e-14

54

E value

Match length



```
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                   298851
Seq. No.
                   LIB3151-048-P1-K1-D5
Seq. ID
Method
                   BLASTN
                   q22516
NCBI GI
BLAST score
                   133
                   1.0e-68
E value
Match length
                   303
% identity
                   89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   298852
Seq. No.
                   LIB3151-048-P1-K1-E11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168484
BLAST score
                   135
                   6.0e-70
E value
                   159
Match length
                   96
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   298853
Seq. No.
                   LIB3151-048-P1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141605
BLAST score
                   224
                   2.0e-18
E value
Match length
                   95
                    55
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                    >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   \overline{\text{maize}} > \overline{\text{gi}}_{168} = 0 (M12145) 19 kDa zein protein [Zea mays]
                    298854
Seq. No.
                   LIB3151-048-P1-K1-F8
Seq. ID
                   BLASTX
Method
                   g629861
NCBI GI
                    178
BLAST score
                    4.0e-13
E value
                    97
Match length
                    47
% identity
                   zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
NCBI Description
                    zein Zdl (19 kDa zein) [Zea mays]
                    298855
Seq. No.
                    LIB3151-048-P1-K1-F9
 Seq. ID
                    BLASTN
Method
                    g22447
NCBI GI
BLAST score
                    61
E value
                    5.0e-26
                    93
Match length
                    91
 % identity
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein
```

Seq. No. 298856



```
LIB3151-048-P1-K1-G11
Seq. ID
                  BLASTN
Method
                  q168652
NCBI GI
                  66
BLAST score
                  3.0e-29
E value
Match length
                  118
                  89
% identity
NCBI Description Maize amyloplast-specific transit protein (waxy; wx+
                  locus), complete cds
                  298857
Seq. No.
                  LIB3151-048-P1-K1-G5
Seq. ID
                  BLASTN
Method
                  q168484
NCBI GI
                  76
BLAST score
                  6.0e-35
E value
Match length
                  148
                  88
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   298858
Seq. No.
Seq. ID
                  LIB3151-048-P1-K1-G7
                  BLASTX
Method
                   q16073
NCBI GI
                   233
BLAST score
                   2.0e-19
E value
                   112
Match length
                   49
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                   298859
Seq. No.
                   LIB3151-048-P1-K1-G9
Seq. ID
Method
                   BLASTX
                   q72307
NCBI GI
                   185
BLAST score
                   2.0e-28
E value
                   87
Match length
% identity
                   86
                   22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   298860
 Seq. No.
                   LIB3151-048-P1-K1-H10
 Seq. ID
Method
                   BLASTN
                   g168484
NCBI GI
BLAST score
                   260
                   1.0e-144
E value
Match length
                   363
                   93
 % identity
                   Maize endosperm glutelin-2 gene, complete cds
 NCBI Description
                   298861
 Seq. No.
                   LIB3151-048-P1-K1-H12
 Seq. ID
                   BLASTX
 Method
                   g168701
 NCBI GI
```

427

3.0e-42

BLAST score

E value

Seq. ID

Method

```
99
Match length
                  89
% identity
NCBI Description (M60837) zein [Zea mays]
                  298862
Seq. No.
                  LIB3151-049-P1-K1-A1
Seq. ID
                  BLASTN
Method
                  q22537
NCBI GI
                  89
BLAST score
                  1.0e-42
E value
                  157
Match length
                  89
% identity
NCBI Description Maize mRNA for zein polypeptide (clone M6)
                  298863
Seq. No.
                  LIB3151-049-P1-K1-A10
Seq. ID
Method
                  BLASTN
                  g168673
NCBI GI
BLAST score
                  39
                   1.0e-12
E value
Match length
                   91
% identity
                   86
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
                   298864
Seq. No.
                   LIB3151-049-P1-K1-A12
Seq. ID
Method
                   BLASTN
                   g168665
NCBI GI
BLAST score
                   203
                   1.0e-110
E value
                   267
Match length
% identity
                   94
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                   298865
Seq. No.
                   LIB3151-049-P1-K1-A3
Seq. ID
                   BLASTX
Method
                   g168701
NCBI GI
BLAST score
                   252
                   1.0e-21
E value
                   111
Match length
% identity
                   50
NCBI Description (M60837) zein [Zea mays]
                   298866
 Seq. No.
                   LIB3151-049-P1-K1-A7
 Seq. ID
                   BLASTX
 Method
                   g224508
 NCBI GI
                   167
 BLAST score
                   8.0e-12
 E value
Match length
                   55
                   69
 % identity
 NCBI Description zein A20 [Zea mays]
                   298867
 Seq. No.
```

41996

LIB3151-049-P1-K1-B10

BLASTX



```
- 2
                   q168699
NCBI GI
                   144
BLAST score
                   4.0e-11
E value
                   76
Match length
                   63
% identity
NCBI Description (M60836) zein [Zea mays]
                   298868
Seq. No.
                   LIB3151-049-P1-K1-B2
Seq. ID
                   BLASTX
Method
                   g141608
NCBI GI
                   150
BLAST score
                   2.0e-18
E value
                   65
Match length
                   86
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
                   zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82) \overline{1}9 kDa
                   zein [Zea mays]
                   298869
Seq. No.
                   LIB3151-049-P1-K1-B5
Seq. ID
                   BLASTN
Method
                   g22514
NCBI GI
                   37
BLAST score
                   5.0e-12
E value
                   45
Match length
                   96
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                   298870
Seq. No.
                   LIB3151-049-P1-K1-C4
Seq. ID
                   BLASTN
Method
                   g168484
NCBI GI
                   321
BLAST score
                   0.0e + 00
E value
                    392
Match length
                    95
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                    298871
Seq. No.
                   LIB3151-049-P1-K1-D12
Seq. ID
Method
                    BLASTX
NCBI GI
                    g141605
BLAST score
                    360
                    4.0e-36
E value
                    123
Match length
                    73
 % identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                    >gi 72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                    maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
                    298872
 Seq. No.
                    LIB3151-049-P1-K1-D8
 Seq. ID
                    BLASTX
 Method
                    g3851003
 NCBI GI
                    369
 BLAST score
```

2.0e-35

E value



```
Match length
                  81
% identity
                  94
                  (AF069910) pyruvate dehydrogenase El beta subunit isoform 3
NCBI Description
                  [Zea mays]
                  298873
Seq. No.
Seq. ID
                  LIB3151-049-P1-K1-E3
                  BLASTN
Method
                  g22549
NCBI GI
BLAST score
                  100
E value
                  6.0e-49
Match length
                  120
                  96
% identity
NCBI Description Maize gene for a 27kDa storage protein, zein
                  298874
Seq. No.
Seq. ID
                  LIB3151-049-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  q168652
BLAST score
                  103
                  7.0e-51
E value
Match length
                  167
                  91
% identity
NCBI Description Maize amyloplast-specific transit protein (waxy; wx+
                  locus), complete cds
                  298875
Seq. No.
Seq. ID
                  LIB3151-049-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  q585338
BLAST score
                  247
                  6.0e-24
E value
Match length
                  85
                  74
% identity
                  ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                  >gi 391879 dbj BAA01181 (D10335) adenylate kinase-b [Oryza
                  sativa]
Seq. No.
                  298876
Seq. ID
                  LIB3151-049-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  g168665
BLAST score
                  164
                  2.0e-87
E value
                  196
Match length
                  96
% identity
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                  298877
Seq. No.
Seq. ID
                  LIB3151-049-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q629861
```

Method BLASTX
NCBI GI g629861
BLAST score 242
E value 9.0e-21
Match length 84
% identity 68

NCBI Description zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)



```
zein Zdl (19 kDa zein) [Zea mays]
```

```
298878
Seq. No.
                   LIB3151-049-P1-K1-G2
Seq. ID
                   BLASTN
Method
                   g22544
NCBI GI
                   69
BLAST score
E value
                   2.0e-30
                   69
Match length
                   100
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                   298879
Seq. No.
                   LIB3151-049-P1-K1-H7
Seq. ID
                   BLASTX
Method
                   g121472
NCBI GI
                   223
BLAST score
                   2.0e-18
E value
                   101
Match length
                   45
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                   [Zea mays] >gi_\overline{2}251\overline{7}_emb_CAA\overline{3}7594_ (X53\overline{5}14) zein Zc2 [Zea
                   mays] >gi_168485 (M16066) glutelin-2 [Zea mays]
                   298880
Seq. No.
                   LIB3151-049-P1-K1-H8
Seq. ID
                   BLASTX
Method
                   g629861
NCBI GI
                   166
BLAST score
                    3.0e-12
E value
                   78
Match length
                    63
% identity
                   zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
NCBI Description
                    zein Zd1 (19 kDa zein) [Zea mays]
                    298881
Seq. No.
                    LIB3151-050-P1-K1-C10
Seq. ID
                    BLASTN
Method
NCBI GI
                    q168484
BLAST score
                    38
E value
                    3.0e-12
                    98
Match length
                    85
 % identity
                    Maize endosperm glutelin-2 gene, complete cds
NCBI Description
 Seq. No.
                    298882
                    LIB3151-050-P1-K1-C11
 Seq. ID
                    BLASTX
 Method
                    g141601
 NCBI GI
 BLAST score
                    187
 E value
                    4.0e-14
                    106
 Match length
                    45
 % identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
 NCBI Description
```



>gi_82657_pir__S03417 19K zein precursor (clone gZ19AB11) maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA 1 - 234) [Zea mays]

Seq. No. 298883 LIB3151-050-P1-K1-C12 Seq. ID Method BLASTN NCBI GI g168484 36 BLAST score 1.0e-10 E value 36 Match length 100

NCBI Description Maize endosperm glutelin-2 gene, complete cds

298884 Seq. No.

% identity

Seq. ID LIB3151-050-P1-K1-C3

BLASTX Method NCBI GI q141608 BLAST score 248 E value 2.0e-21 Match length 93 % identity 59

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655

zein, 19K - maize >gi 22446 emb CAA37651 (X53582) 19 kDa

zein [Zea mays]

298885 Seq. No.

LIB3151-050-P1-K1-C9 Seq. ID

Method BLASTN NCBI GI q168484 BLAST score 219 E value 1.0e-120 Match length 278 95 % identity

NCBI Description Maize endosperm glutelin-2 gene, complete cds

298886 Seq. No.

Seq. ID LIB3151-050-P1-K1-D1

Method BLASTX NCBI GI g266398 BLAST score 189 7.0e-15 E value Match length 56 % identity

NCBI Description TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR

INHIBITOR) (CHFI) >gi 68849 pir TIZM1 trypsin/factor XIIa

inhibitor precursor - maize >gi 22327 emb CAA37998 (X54064) corn Hageman factor inhibitor [Zea mays]

298887 Seq. No.

Seq. ID LIB3151-050-P1-K1-D10

Method BLASTN NCBI GI q22549 BLAST score 115 E value 4.0e-58 Match length 131 97 % identity

NCBI GI

g168652



```
NCBI Description Maize gene for a 27kDa storage protein, zein
                    298888
  Seq. No.
                    LIB3151-050-P1-K1-D8
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g22216
                    144
  BLAST score
                    2.0e-14
  E value
                    99
 Match length
  % identity
  NCBI Description (X55722) 22kD zein [Zea mays]
                    298889
  Seq. No.
                    LIB3151-050-P1-K1-E3
  Seq. ID
                    BLASTN
  Method
  NCBI GI
                    q22516
  BLAST score
                    308
                    1.0e-173
  E value
                    381
  Match length
                    95
  % identity
  NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                    298890
  Seq. No.
                    LIB3151-050-P1-K1-E5
  Seq. ID
                    BLASTN
  Method
  NCBI GI
                    g1037129
  BLAST score
                    58
                     3.0e-24
  E value
                     78
  Match length
                     95
  % identity
                    (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
  NCBI Description
                     Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                     298891
  Seq. No.
                     LIB3151-050-P1-K1-F10
  Seq. ID
                     BLASTX
  Method
                     g2832243
  NCBI GI
  BLAST score
                     277
                     1.0e-24
  E value
                     105
  Match length
                     58
  % identity
                    (AF031569) 22-kDa alpha zein 4 [Zea mays]
  NCBI Description
                     298892
  Seq. No.
                     LIB3151-050-P1-K1-G12
  Seq. ID
                     BLASTN
  Method
                     g168673
  NCBI GI
  BLAST score
                     119
                     1.0e-60
  E value
                     143
  Match length
                     97
  % identity
  NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
                     298893
  Seq. No.
                     LIB3151-050-P1-K1-H5
  Seq. ID
                     BLASTN
  Method
```

BLAST score

E value

91 1.0e-43

```
BLAST score
                  4.0e-53
E value
                  207
Match length
% identity
                  88
                  Maize amyloplast-specific transit protein (waxy; wx+
NCBI Description
                  locus), complete cds
                  298894
Seq. No.
                  LIB3151-050-P1-K1-H6
Seq. ID
Method
                  BLASTX
                  q100675
NCBI GI
                  239
BLAST score
                  2.0e-20
E value
Match length
                  59
% identity
                  78
                  glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)
NCBI Description
                  precursor - rice >gi_169759 (J04960) ADP-glucose
                  pyrophosphorylase 51\overline{k}D subunit (EC 2.7.7.27) [Oryza sativa]
                   298895
Seq. No.
                  LIB3151-052-Q1-K1-A2
Seq. ID
Method
                  BLASTN
                   g1037129
NCBI GI
BLAST score
                   151
                   1.0e-79
E value
Match length
                   158
% identity
                   99
                   (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   298896
Seq. No.
                   LIB3151-052-Q1-K1-A5
Seq. ID
                   BLASTN
Method
                   g168484
NCBI GI
                   190
BLAST score
                   1.0e-102
E value
                   222
Match length
                   96
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   298897
Seq. No.
                   LIB3151-052-Q1-K1-A8
Seq. ID
                   BLASTN
Method
                   q4140643
NCBI GI
                   118
BLAST score
                   9.0e-60
E value
                   138
Match length
                   24
% identity
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   298898
Seq. No.
                   LIB3151-052-Q1-K1-B6
Seq. ID
                   BLASTN
Method
                   q2832242
NCBI GI
```

```
Match length
                  98
                  10
% identity
                  Zea mays 22-kDa alpha zein gene cluster, complete sequence
NCBI Description
                  298899
Seq. No.
                  LIB3151-052-Q1-K1-B7
Seq. ID
                  BLASTN
Method
                  q168675
```

NCBI GI BLAST score 89 2.0e-42 E value Match length 139 94 % identity

NCBI Description Maize mutant zein (zE19) gene, complete cds

298900 Seq. No. Seq. ID LIB3151-052-Q1-K1-C2 Method BLASTX NCBI GI q16073 339 BLAST score 7.0e-32

E value 92 Match length 79 % identity

NCBI Description (X59526) zein protein [Acetabularia mediterranea]

298901 Seq. No.

LIB3151-052-Q1-K1-C9 Seq. ID

Method BLASTX q4185308 NCBI GI 286 BLAST score E value 2.0e-35 91 Match length 93 % identity

(AF090446) 22-kDa alpha zein protein 21 [Zea mays] NCBI Description

298902 Seq. No.

Seq. ID LIB3151-052-Q1-K1-E5

Method BLASTN NCBI GI g3747049 BLAST score 58 5.0e-24E value Match length 124 % identity 89

Zea mays ribosomal protein L26 mRNA, partial cds NCBI Description

298903 Seq. No.

LIB3151-052-Q1-K1-E8 Seq. ID

Method BLASTN NCBI GI g168484 BLAST score 96 9.0e-47 E value 124 Match length 97 % identity

NCBI Description Maize endosperm glutelin-2 gene, complete cds

298904 Seq. No.

LIB3151-052-Q1-K1-F1 Seq. ID

BLASTN Method

Match length

NCBI Description

% identity

86 91



```
g22542
NCBI GI
                  109
BLAST score
E value
                  2.0e-54
Match length
                  182
% identity
                  91
NCBI Description Maize gene for Mr 19000 alpha zein and 5'-flanking region
                  298905
Seq. No.
                  LIB3151-052-Q1-K1-F5
Seq. ID
Method
                  BLASTN
                  g22549
NCBI GI
BLAST score
                  160
                  6.0e-85
E value
Match length
                  181
                  63
% identity
NCBI Description Maize gene for a 27kDa storage protein, zein
                  298906
Seq. No.
                  LIB3151-052-Q1-K1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q340933
BLAST score
                  104
E value
                   8.0e-52
Match length
                   139
                   94
% identity
NCBI Description Zea mays 10-kDa zein gene, complete cds
                   298907
Seq. No.
                   LIB3151-054-Q1-K1-A12
Seq. ID
Method
                   BLASTN
                   q22549
NCBI GI
BLAST score
                   61
                   9.0e-26
E value
                   292
Match length
                   80
% identity
NCBI Description Maize gene for a 27kDa storage protein, zein
                   298908
Seq. No.
                   LIB3151-054-Q1-K1-A2
Seq. ID
                   BLASTX
Method
                   g16073
NCBI GI
BLAST score
                   203
                   4.0e-16
E value
                   63
Match length
                   68
% identity
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   298909
Seq. No.
                   LIB3151-054-Q1-K1-A5
Seq. ID
Method
                   BLASTX
                   g141603
NCBI GI
                   372
BLAST score
                   9.0e-36
E value
```

42004

>gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)

```
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
```

298910 Seq. No. Seq. ID LIB3151-054-Q1-K1-A8 Method BLASTX NCBI GI g141603 BLAST score 448 1.0e-44 E value 107 Match length 92 % identity ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) NCBI Description >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays] 298911 Seq. No. Seq. ID LIB3151-054-Q1-K1-B11 Method BLASTN NCBI GI g22544 BLAST score 124 2.0e-63 E value 272 Match length % identity 87 NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein) 298912 Seq. No. LIB3151-054-Q1-K1-B8 Seq. ID Method BLASTX NCBI GI g2832243 BLAST score 365 5.0e-35 E value 106 Match length % identity 71 (AF031569) 22-kDa alpha zein 4 [Zea mays] NCBI Description 298913 Seq. No. LIB3151-054-Q1-K1-B9 Seq. ID Method BLASTN g22516 NCBI GI BLAST score 86 1.0e-40 E value 210 Match length % identity 85 NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2) 298914 Seq. No. LIB3151-054-Q1-K1-C10 Seq. ID BLASTX Method g16073 NCBI GI

Method BLASTX
NCBI GI g16073
BLAST score 286
E value 1.0e-25
Match length 108
% identity 60

NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298915

Seq. ID LIB3151-054-Q1-K1-C2

Method BLASTX



```
q2130089
NCBI GI
BLAST score
                  218
                  8.0e-18
E value
                  78
Match length
% identity
                  2-oxoglutarate/malate translocator (clone OMT103),
NCBI Description
                  mitochondrial membrane - proso millet
                  >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate
                  translocator [Panicum miliaceum]
Seq. No.
                  298916
Seq. ID
                  LIB3151-054-Q1-K1-C9
Method
                  BLASTN
NCBI GI
                  g22516
BLAST score
                  285
E value
                   1.0e-159
Match length
                   369
% identity
                   95
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   298917
Seq. No.
                   LIB3151-054-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   q4033424
NCBI GI
BLAST score
                   362
                   1.0e-34
E value
Match length
                   84
% identity
                   SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                   PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                   pyrophosphatase [Zea mays]
                   298918
Seq. No.
                   LIB3151-054-Q1-K1-D9
Seq. ID
                   BLASTX
Method
                   g541546
NCBI GI
                   248
BLAST score
                   3.0e-21
E value
                   101
Match length
                   13
% identity
                   ubiquitin precursor - Volvox carteri
NCBI Description
                   >gi 395295 emb CAA52290_ (X74214) polyubiquitin [Volvox
                   carteri]
                   298919
Seq. No.
                   LIB3151-054-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   g141601
NCBI GI
                   385
BLAST score
E value
                   2.0e-37
Match length
                   120
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                   >gi_82657_pir__S03417 19K zein precursor (clone gZ19AB11) -
```

1 - 234) [Zea mays]

 $maize > gi_225\overline{43}_emb_CAA29340_ (X05911)$ 19 kd alpha zein (AA



```
298920
Seq. No.
                  LIB3151-054-Q1-K1-E5
Seq. ID
                  BLASTN
Method
                   g984524
NCBI GI
BLAST score
                   75
                   3.0e-34
E value
                   250
Match length
                   86
% identity
                   Zea mays high-methionine zein DZS18 (dzs18) gene, complete
NCBI Description
                   298921
Seq. No.
                   LIB3151-054-Q1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141603
BLAST score
                   285
                   1.0e-25
E value
Match length
                   103
                   66
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
                   298922
Seq. No.
                   LIB3151-054-Q1-K1-E9
Seq. ID
Method
                   BLASTX
                   g141608
NCBI GI
BLAST score
                   208
                   3.0e-25
E value
                   104
Match length
                   67
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82)\overline{1}9 kDa
                   zein [Zea mays]
                   298923
Seq. No.
                   LIB3151-054-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   g22220
NCBI GI
                   234
BLAST score
                   1.0e-19
E value
                   91
Match length
                   56
% identity
                   (X55723) 22 kD zein [Zea mays]
NCBI Description
                   298924
Seq. No.
                   LIB3151-054-Q1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q82660
BLAST score
                   304
E value
                   7.0e-28
```

80 Match length 78 % identity

19K zein precursor (clone ZG31A) - maize (fragment) NCBI Description >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

298925 Seq. No.

```
LIB3151-054-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2735840
                  318
BLAST score
                  2.0e-29
E value
                  116
Match length
% identity
                  57
                  (AF010283) ADP-glucose pyrophosphorylase subunit SH2
NCBI Description
                  [Sorghum bicolor]
Seq. No.
                  298926
                  LIB3151-054-Q1-K1-H10
Seq. ID
Method
                  BLASTX
                  q419803
NCBI GI
                  247
BLAST score
                  4.0e-21
E value
                  112
Match length
                   46
% identity
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
                  mays]
Seq. No.
                   298927
                  LIB3151-054-Q1-K1-H12
Seq. ID
Method
                  BLASTX
                   g22220
NCBI GI
                   280
BLAST score
                   4.0e-25
E value
                   70
Match length
                   80
% identity
NCBI Description (X55723) 22 kD zein [Zea mays]
                   298928
Seq. No.
Seq. ID
                   LIB3151-054-Q1-K1-H7
Method
                   BLASTX
NCBI GI
                   g2832246
BLAST score
                   468
E value
                   5.0e-47
Match length
                   120
                   82
% identity
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]
                   298929
Seq. No.
                   LIB3151-054-Q1-K1-H8
Seq. ID
Method
                   BLASTX
                   g2832246
NCBI GI
                   143
BLAST score
E value
                   2.0e-09
Match length
                   60
% identity
                   58
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]
                   298930
Seq. No.
Seq. ID
                   LIB3151-055-Q1-K1-C10
```

BLASTN

g22537

70 5.0e-31

Method

NCBI GI BLAST score

E value



Match length 140 % identity 89

NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 298931

Seq. ID LIB3151-055-Q1-K1-D10

Method BLASTN
NCBI GI g22445
BLAST score 44
E value 8.0e-16
Match length 94
% identity 85

NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 298932

Seq. ID LIB3151-055-Q1-K1-D9

Method BLASTX
NCBI GI g141608
BLAST score 265
E value 3.0e-23
Match length 63
% identity 86

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655

zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa

zein [Zea mays]

Seq. No. 298933

Seq. ID LIB3151-056-Q1-K1-C11

Method BLASTN
NCBI GI g168704
BLAST score 58
E value 4.0e-24
Match length 90
% identity 91

NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 298934

Seq. ID LIB3151-057-Q1-K1-A1

Method BLASTX
NCBI GI g2832243
BLAST score 230
E value 4.0e-19
Match length 106
% identity 49

NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298935

Seq. ID LIB3151-057-Q1-K1-A12

Method BLASTN
NCBI GI g22516
BLAST score 110
E value 5.0e-55
Match length 282
% identity 85

NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298936

```
LIB3151-057-Q1-K1-A9
Seq. ID
Method
                   BLASTN
                    g168484
NCBI GI
                    218
BLAST score
                    1.0e-119
E value
                    365
Match length
                    90
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                    298937
Seq. No.
                    LIB3151-057-Q1-K1-B1
Seq. ID
                    BLASTX
Method
                    g121472
NCBI GI
                    179
BLAST score
                    3.0e-13
E value
                    70
Match length
                    50
% identity
                    GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                    maize >gi_22289 emb_CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
                    mays] >gi_1684\overline{8}5 (M1\overline{6}066) glutelin-2 [Zea mays]
Seq. No.
                    298938
                    LIB3151-057-Q1-K1-B5
Seq. ID
                    BLASTX
Method
                    g2832247
NCBI GI
BLAST score
                    225
                    1.0e-18
E value
Match length
                    93
                    53
% identity
                   (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
                    298939
Seq. No.
                    LIB3151-057-Q1-K1-C5
Seq. ID
                    BLASTN
Method
NCBI GI
                    q218340
BLAST score
                    45
                    2.0e-16
E value
Match length
                    65
                    92
% identity
NCBI Description Triticum aestivum mRNA for elongation factor 1 beta'
                    298940
Seq. No.
                    LIB3151-057-Q1-K1-C9
Seq. ID
                    BLASTN
Method
                     g22514
NCBI GI
BLAST score
                     227
                     1.0e-125
E value
```

Match length 343 % identity 92

NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

298941 Seq. No.

LIB3151-057-Q1-K1-D11 Seq. ID

Method BLASTX

E value

Match length

1.0e-143

304



```
g168701
NCBI GI
BLAST score
                  370
E value
                  2.0e-35
Match length
                  98
% identity
                  79
                  (M60837) zein [Zea mays]
NCBI Description
                  298942
Seq. No.
                  LIB3151-057-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                  g168691
NCBI GI
BLAST score
                  200
                  7.0e-16
E value
Match length
                  60
                  70
% identity
                  (M29628) zein [Zea mays]
NCBI Description
                  298943
Seq. No.
                  LIB3151-057-Q1-K1-D9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1184775
BLAST score
                  62
                  1.0e-26
E value
                  90
Match length
                   92
% identity
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4
NCBI Description
                   (gpc4) mRNA, complete cds
                  298944
Seq. No.
                  LIB3151-057-Q1-K1-E11
Seq. ID
                  BLASTX
Method
                   q141608
NCBI GI
                   271
BLAST score
                   7.0e-24
E value
                   114
Match length
                   55
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA37651 (X53582) 19 kDa
                   zein [Zea mays]
                   298945
Seq. No.
                   LIB3151-057-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   g1542941
NCBI GI
                   148
BLAST score
                   9.0e-10
E value
                   70
Match length
                   47
% identity
                  (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
NCBI Description
                   298946
Seq. No.
                   LIB3151-057-Q1-K1-F2
Seq. ID
                   BLASTN
Method
                   g1037129
NCBI GI
                   258
BLAST score
```

```
% identity
                  (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                  298947
Seq. No.
                  LIB3151-057-Q1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2130065
                  146
BLAST score
                  3.0e-09
E value
                  90
Match length
                  42
% identity
                  alpha-globulin precursor - rice >gi_1783206_dbj_BAA09308_
NCBI Description
                  (D50643) 26 kDa globulin [Oryza sativa]
                  298948
Seq. No.
                  LIB3151-057-Q1-K1-G11
Seq. ID
                  BLASTX
Method
                  q168701
NCBI GI
BLAST score
                  316
                  3.0e-29
E value
                  79
Match length
                  82
% identity
                  (M60837) zein [Zea mays]
NCBI Description
                  298949
Seq. No.
                  LIB3151-057-Q1-K1-H11
Seq. ID
                  BLASTN
Method
                  g22516
NCBI GI
BLAST score
                  155
                  8.0e-82
E value
                  279
Match length
                  89
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                  298950
                  LIB3151-057-Q1-K1-H12
Seq. No.
Seq. ID
                  BLASTN
Method
                  q508544
NCBI GI
BLAST score
                   43
                   6.0e-15
E value
                  162
Match length
% identity
NCBI Description Zea mays 24-kD alpha-zein gene (floury2), complete cds
```

298951 Seq. No.

LIB3151-058-Q1-K1-B11 Seq. ID

Method BLASTX NCBI GI g99688 BLAST score 317 2.0e-29 E value 72 Match length % identity 88

translation elongation factor eEF-1 alpha chain (gene A4) -NCBI Description Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432)

elongation factor 1-alpha [Arabidopsis thaliana]

```
Seq. No.
                  LIB3151-058-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g451193
NCBI GI
BLAST score
                  143
E value
                  9.0e-20
                  87
Match length
                  63
% identity
                  (L28008) wali7 [Triticum aestivum]
NCBI Description
                  >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
Seq. No.
                  298953
                  LIB3151-058-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q629861
BLAST score
                   226
E value
                  1.0e-18
Match length
                   100
% identity
                  zein Zd1, 19K - maize >gi 535020 emb_CAA47639_ (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                   298954
                  LIB3151-058-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3643607
BLAST score
                   317
E value
                   2.0e-29
Match length
                   113
                   58
% identity
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   298955
Seq. ID
                   LIB3151-058-Q1-K1-D6
Method
                   BLASTX
                   q1684855
NCBI GI
BLAST score
                   422
                   1.0e-41
E value
                   85
Match length
                   21
% identity
                  (U77939) ubiquitin-like protein [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   298956
                   LIB3151-058-Q1-K1-E12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141608
                   177
BLAST score
                   5.0e-17
E value
                   78
Match length
                   71
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943_pir__S15655
NCBI Description
                   zein, 19K - maize >gi 22446 emb CAA37651 (X53582) 19 kDa
                   zein [Zea mays]
                   298957
Seq. No.
Seq. ID
                   LIB3151-058-Q1-K1-H4
Method
                   BLASTN
```

```
NCBI GI
                   q168675
BLAST score
                  59
E value
                  1.0e-24
Match length
                  79
                  94
% identity
NCBI Description Maize mutant zein (zE19) gene, complete cds
                  298958
Seq. No.
                  LIB3151-058-Q1-K1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2832243
BLAST score
                  242
E value
                  1.0e-20
                   98
Match length
                   56
% identity
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
                   298959
Seq. No.
                  LIB3151-058-Q1-K1-H9
Seq. ID
Method
                  BLASTX
                  g168691
NCBI GI
                   186
BLAST score
E value
                   5.0e-14
Match length
                   96
% identity
                   46
NCBI Description (M29628) zein [Zea mays]
                   298960
Seq. No.
                   LIB3151-059-Q1-K1-A8
Seq. ID
Method
                   BLASTX
                   q141616
NCBI GI
BLAST score
                   240
                   2.0e-20
E value
Match length
                   71
                   62
% identity
                   ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                   >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
                   298961
Seq. No.
                   LIB3151-059-Q1-K1-B1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1037129
BLAST score
                   41
E value
                   6.0e-14
Match length
                   216
                   82
% identity
                   (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
```

Seq. No. 298962

Seq. ID LIB3151-059-Q1-K1-B6 Method BLASTN

Method BLASTN
NCBI GI g168704
BLAST score 54
E value 5.0e-22
Match length 82
% identity 91



```
NCBI Description Zea mays zein protein gene, complete cds
```

Seq. No. 298963 Seq. ID LIB3151-059-Q1-K1-B9

Method BLASTX
NCBI GI g2832243
BLAST score 192
E value 9.0e-15
Match length 105

% identity 47 NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298964

Seq. ID LIB3151-059-Q1-K1-C2

Method BLASTN
NCBI GI g168425
BLAST score 37
E value 1.0e-11
Match length 61
% identity 90

NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 298965

Seq. ID LIB3151-059-Q1-K1-C5

Method BLASTN
NCBI GI g168425
BLAST score 60
E value 1.0e-25
Match length 87
% identity 93

NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 298966

Seq. ID LIB3151-059-Q1-K1-C9

Method BLASTN
NCBI GI g1037129
BLAST score 287
E value 1.0e-160
Match length 362
% identity 95

NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,

Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298967

Seq. ID LIB3151-059-Q1-K1-D3

Method BLASTX
NCBI GI g4539370
BLAST score 151
E value 3.0e-10
Match length 58
% identity 60

NCBI Description (AL049525) UDP-galactose 4-epimerase-like protein

[Arabidopsis thaliana]

Seq. No. 298968

Seq. ID LIB3151-059-Q1-K1-D4

Method BLASTN

```
NCBI GI
BLAST score
                  140
                  4.0e-73
E value
                  195
Match length
% identity
                  93
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                  298969
Seq. No.
                  LIB3151-059-Q1-K1-D8
Seq. ID
                  BLASTX
Method
                  g141610
NCBI GI
BLAST score
                  198
E value
                  2.0e-15
Match length
                  98
                  48
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)
                  298970
Seq. No.
                  LIB3151-059-Q1-K1-E4
Seq. ID
Method
                  BLASTN
                  g2832242
NCBI GI
                  168
BLAST score
E value
                  1.0e-89
Match length
                  204
% identity
                  10
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                  298971
Seq. No.
                  LIB3151-059-Q1-K1-F3
Seq. ID
Method
                  BLASTX
                  g2832246
NCBI GI
                   229
BLAST score
                   5.0e-19
E value
Match length
                   107
                   50
% identity
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]
                   298972
Seq. No.
                   LIB3151-059-Q1-K1-F5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2341060
BLAST score
                   33
                   4.0e-09
E value
Match length
                   61
% identity
                   89
                  Zea mays translational initiation factor eIF-4A (tif-4A3)
NCBI Description
                   mRNA, complete cds
                   298973
Seq. No.
Seq. ID
                   LIB3151-059-Q1-K1-G9
Method
                   BLASTX
                   q2996096
NCBI GI
                   140
BLAST score
                   4.0e-09
E value
Match length
                   31
                   87
% identity
```

NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1



alpha [Oryza sativa]

```
298974
Seq. No.
                  LIB3151-059-Q1-K1-H1
Seq. ID
Method
                  BLASTX
                  q100925
NCBI GI
BLAST score
                  156
E value
                  1.0e-10
Match length
                  96
                  22
% identity
                  zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_
NCBI Description
                  (X58197) 27kDa storage protein, zein [Zea mays]
Seq. No.
                  298975
                  LIB3151-059-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q16073
BLAST score
                  153
                  3.0e-10
E value
                  53
Match length
                  62
% identity
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
Seq. No.
                  298976
                  LIB3151-061-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141616
BLAST score
                  141
                  8.0e-09
E value
Match length
                  53
                  49
% identity
                  ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                  >gi_168662 (M12147) 15 kDa zein protein [Zea mays]
                  298977
Seq. No.
                  LIB3151-061-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141603
BLAST score
                   434
E value
                   5.0e-43
                   120
Match length
                   79
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi 22529_emb_CAA24723_ (V01476) zein [Zea mays]
                   298978
Seq. No.
Seq. ID
                  LIB3151-061-Q1-K1-B5
Method
                   BLASTN
NCBI GI
                   g22485
                   82
BLAST score
                   1.0e-38
E value
                   146
Match length
                   90
% identity
NCBI Description Maize mRNA for sucrose synthase (EC 2.4.1.13)
```

298979

Seq. No.

Seq. No.

```
LIB3151-061-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                  g141605
NCBI GI
                  504
BLAST score
                  4.0e-51
E value
Match length
                  127
                  82
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >qi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  298980
                  LIB3151-061-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141616
BLAST score
                  142
E value
                  4.0e-09
Match length
                  28
% identity
                  89
                  ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                  >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
Seq. No.
                  298981
Seq. ID
                  LIB3151-061-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g2501354
BLAST score
                  206
E value
                  3.0e-16
Match length
                   44
% identity
                  84
                  TRANSKETOLASE 7 (TK) >gi 1084441 pir S54301 transketolase
NCBI Description
                   (EC 2.2.1.1) 7 - Craterostigma plantagineum
                  >gi 664903 emb CAA86609 (Z46648) transketolase
                   [Craterostigma plantagineum]
                  298982
Seq. No.
                  LIB3151-061-Q1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q168693
                  220
BLAST score
                  7.0e-25
E value
                  104
Match length
                   70
% identity
NCBI Description
                  (M29627) zein [Zea mays]
Seq. No.
                  298983
                  LIB3151-061-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3021357
                  152
BLAST score
                   6.0e-10
E value
                   39
Match length
                   74
% identity
                   (AJ005082) UDP-galactose 4-epimerase [Cyamopsis
NCBI Description
                   tetragonoloba]
```

298984



```
Seq. ID
                  LIB3151-061-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q541816
BLAST score
                  196
E value
                  5.0e-23
Match length
                  56
% identity
                  90
NCBI Description
                  protein kinase - common ice plant >gi_457689_emb_CAA82990_
                  (Z30329) protein kinase [Mesembryanthemum crystallinum]
Seq. No.
                  298985
Seq. ID
                  LIB3151-061-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  q2282584
BLAST score
                  332
E value
                  5.0e-31
Match length
                  122
% identity
                  62
                  (U76259) elongation factor 1-alpha [Zea mays]
NCBI Description
                  298986
Seq. No.
Seq. ID
                  LIB3151-061-Q1-K1-G10
Method
                  BLASTN
                  q168652
NCBI GI
BLAST score
                  83
                  5.0e-39
E value
Match length
                  123
                  92
% identity
NCBI Description
                  Maize amyloplast-specific transit protein (waxy; wx+
                  locus), complete cds
Seq. No.
                  298987
Seq. ID
                  LIB3151-061-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  q2832243
BLAST score
                  220
E value
                  5.0e-18
Match length
                  66
% identity
                  76
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
Seq. No.
                  298988
Seq. ID
                  LIB3151-061-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g141603
BLAST score
                  190
                  1.0e-14
E value
Match length
                  72
% identity
                  61
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                  298989
```

Seq. ID LIB3151-062-Q1-K1-A2

Method BLASTN NCBI GI g168704



```
BLAST score
                   4.0e-27
E value
Match length
                  115
% identity
                  89
NCBI Description Zea mays zein protein gene, complete cds
                  298990
Seq. No.
Seq. ID
                  LIB3151-062-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g82660
                  221
BLAST score
E value
                   4.0e-18
Match length
                   61
                  74
% identity
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi 809117_emb_CAA24720_ (V01473) zein [Zea mays]
Seq. No.
                   298991
Seq. ID
                  LIB3151-062-Q1-K1-C9
Method
                  BLASTN
NCBI GI
                  q168704
BLAST score
                   56
E value
                  7.0e-23
Match length
                  107
                   89
% identity
NCBI Description Zea mays zein protein gene, complete cds
Seq. No.
                  298992
Seq. ID
                  LIB3151-062-Q1-K1-E10
Method
                  BLASTN
NCBI GI
                   g168665
                  198
BLAST score
E value
                   1.0e-107
                   279
Match length
% identity
                   92
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
Seq. No.
                   298993
Seq. ID
                  LIB3151-062-Q1-K1-F6
                  BLASTX
Method
                   g1449179
NCBI GI
BLAST score
                   214
E value
                   3.0e-17
Match length
                   94
                   51
% identity
                   (D86506) N-ethylmaleimide sensitive fusion protein
NCBI Description
                   [Nicotiana tabacum]
                   298994
Seq. No.
Seq. ID
                   LIB3151-062-Q1-K1-G8
                   BLASTX
Method
NCBI GI
                   g141617
```

NCBI GI g141617 BLAST score 279 E value 7.0e-25 Match length 112 % identity 54

NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)



```
298995
Seq. No.
Seq. ID
                  LIB3152-001-Q1-K1-A3
Method
                  BLASTN
                  q168484
NCBI GI
BLAST score
                  168
E value
                  1.0e-89
Match length
                  264
% identity
                  91
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                  298996
Seq. No.
                  LIB3152-001-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4193320
BLAST score
                  324
                  2.0e-30
E value
Match length
                  77
                  78
% identity
NCBI Description
                  (AF045473) histone deacetylase [Zea mays]
                  298997
Seq. No.
                  LIB3152-001-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141615
                  248
BLAST score
                  2.0e-21
E value
Match length
                  84
                  65
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
                  >gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]
Seq. No.
                  298998
                  LIB3152-001-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141602
BLAST score
                  343
                  3.0e-32
E value
Match length
                  120
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
NCBI Description
                  >gi 82658 pir A22831 19K zein precursor (clone M6) - maize
                  >gi 22538 emb CAA26294 (X02450) zein precursor [Zea mays]
Seq. No.
                  298999
Seq. ID
                  LIB3152-001-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2832243
BLAST score
                  285
```

>gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize

>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666 (M16460) 16-kDa zein protein [Zea mays]

42021

2.0e-25

NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

129

53

E value Match length

% identity



```
299000
Seq. No.
Seq. ID
                  LIB3152-001-Q1-K1-C3
Method
                  BLASTX
                  g224508
NCBI GI
BLAST score
                  330
                  4.0e-31
E value
Match length
                  88
% identity
                  81
NCBI Description zein A20 [Zea mays]
Seq. No.
                  299001
Seq. ID
                  LIB3152-001-Q1-K1-C4
Method
                  BLASTN
NCBI GI
                  q168681
BLAST score
                  147
E value
                  4.0e-77
Match length
                  255
                  89
% identity
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                  >gi_270686_gb_I03333_ Sequence 8 from Patent US
Seq. No.
                  299002
Seq. ID
                  LIB3152-001-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q100939
BLAST score
                  215
E value
                  1.0e-26
Match length
                  98
% identity
                  63
NCBI Description zein precursor - maize
Seq. No.
                  299003
Seq. ID
                  LIB3152-001-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  q141608
BLAST score
                  155
E value
                  1.0e-10
                  63
Match length
                  62
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
NCBI Description
                  zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                  zein [Zea mays]
                  299004
Seq. No.
Seq. ID
                  LIB3152-001-Q1-K1-E1
Method
                  BLASTN
NCBI GI
                  g22441
BLAST score
                  69
                  1.0e-30
E value
Match length
                  192
                  84
% identity
NCBI Description Maize pML2 gene for zein
```

299005

BLASTN

LIB3152-001-Q1-K1-E3

Seq. No. Seq. ID

Method

```
NCBI GI
                  q22514
                                                                           34
BLAST score
                  150
E value
                  6.0e-79
                  257
Match length
% identity
                  91
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                  299006
Seq. No.
                  LIB3152-001-Q1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                  69
E value
                  1.0e-30
Match length
                  158
% identity
                  10
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  299007
                  LIB3152-001-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g419803
BLAST score
                  229
E value
                  3.0e-19
Match length
                  69
% identity
                  70
NCBI Description
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
                  mays]
Seq. No.
                  299008
Seq. ID
                  LIB3152-001-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2832246
BLAST score
                  186
E value
                  4.0e-14
Match length
                  84
% identity
                  46
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]
Seq. No.
                  299009
Seq. ID
                  LIB3152-001-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g168691
BLAST score
                  237
E value
                  5.0e-20
Match length
                  98
                  52
% identity
NCBI Description (M29628) zein [Zea mays]
                  299010
Seq. No.
Seq. ID
                  LIB3152-001-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g141603
BLAST score
                  258
                  1.0e-22
E value
Match length
                  75
                  76
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
```

Seq. No. Seq. ID

Method



>gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize >gi_22529 emb CAA24723 (V01476) zein [Zea mays]

```
299011
Seq. No.
Seq. ID
                  LIB3152-002-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g224507
BLAST score
                  160
                  5.0e-11
E value
Match length
                  41
% identity
                  83
NCBI Description zein Al [Zea mays]
                  299012
Seq. No.
Seq. ID
                  LIB3152-002-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  q82660
BLAST score
                  189
E value
                  2.0e-14
Match length
                  54
                  70
% identity
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
                  299013
Seq. No.
Seq. ID
                  LIB3152-002-01-K1-E6
Method
                  BLASTX
NCBI GI
                  q2281089
BLAST score
                  292
E value
                  2.0e-26
Match length
                  63
% identity
                  87
NCBI Description (AC002333) Sm protein F isolog [Arabidopsis thaliana]
Seq. No.
                  299014
Seq. ID
                  LIB3152-002-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2832243
BLAST score
                  201
                  5.0e-16
E value
Match length
                  70
% identity
                   63
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
                  299015
Seq. No.
Seq. ID
                  LIB3152-002-Q1-K1-F11
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                  86
                  6.0e-41
E value
Match length
                  186
                  10
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                  299016
```

42024

LIB3152-002-Q1-K1-F3

BLASTX

```
NCBI GI
                  q419803
BLAST score
                  361
                  2.0e-34
E value
                  116
Match length
% identity
                  66
NCBI Description zein protein - maize >gi 168705 (M72708) zein protein [Zea
                  mays]
                  299017
Seq. No.
                  LIB3152-002-Q1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168679
BLAST score
                  62
                  1.0e-26
E value
                  134
Match length
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
                  >gi 270687_gb_I03334_ Sequence 9 from Patent US
Seq. No.
                  299018
                  LIB3152-002-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g224509
                  243
BLAST score
                  1.0e-20
E value
Match length
                  105
                  54
% identity
NCBI Description zein E19 [Zea mays]
                  299019
Seq. No.
                  LIB3152-002-Q1-K1-H8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22514
BLAST score
                  104
E value
                  1.0e-51
Match length
                  164
% identity
                  91
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                  299020
Seq. No.
                  LIB3152-003-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g224508
BLAST score
                  174
                  2.0e-12
E value
Match length
                  67
% identity
                  55
NCBI Description zein A20 [Zea mays]
```

Seq. No. 299021

Seq. ID LIB3152-003-P1-K1-B11

Method BLASTX
NCBI GI g168691
BLAST score 239
E value 3.0e-20
Match length 107
% identity 54



```
NCBI Description
                  (M29628) zein [Zea mays]
                  299022
Seq. No.
                  LIB3152-003-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q168699
BLAST score
                  183
                  2.0e-18
E value
                  81
Match length
                  72
% identity
NCBI Description
                  (M60836) zein [Zea mays]
Seq. No.
                  299023
Seq. ID
                  LIB3152-003-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q629861
                  281
BLAST score
E value
                  3.0e-25
                  107
Match length
                  61
% identity
                  zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  299024
                  LIB3152-003-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  g141603
NCBI GI
                  222
BLAST score
                   3.0e-18
E value
Match length
                  82
% identity
                   66
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
Seq. No.
                   299025
Seq. ID
                   LIB3152-003-P1-K1-E6
Method
                  BLASTN
NCBI GI
                   q168681
BLAST score
                   157
E value
                   4.0e-83
Match length
                   300
                   89
% identity
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                   >gi_270686_gb_I03333_ Sequence 8 from Patent US
Seq. No.
                   299026
Seq. ID
                   LIB3152-003-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g168699
BLAST score
                   269
                   9.0e-24
E value
                   75
Match length
                   75
% identity
                  (M60836) zein [Zea mays]
NCBI Description
```

299027

Seq. No.

```
LIB3152-003-P1-K1-F12
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                    g22537
                    48
 BLAST score
                    4.0e-18
. E value
 Match length
                    84
 % identity
                    90
 NCBI Description Maize mRNA for zein polypeptide (clone M6)
 Seq. No.
                    299028
                    LIB3152-003-P1-K1-F6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g224509
 BLAST score
                    168
                    9.0e-12
 E value
 Match length
                    119
                    45
 % identity
 NCBI Description zein E19 [Zea mays]
                    299029
 Seq. No.
                    LIB3152-003-P1-K1-F7
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q629861
 BLAST score
                    259
                    9.0e-23
 E value
 Match length
                    73
                    75
 % identity
                   zein Zd1, 19K - maize >qi 535020 emb CAA47639 (X67203)
 NCBI Description
                    zein Zd1 (19 kDa zein) [Zea mays]
                    299030
 Seq. No.
                    LIB3152-003-P1-K1-G10
 Seq. ID
 Method
                    BLASTN
                    g22516
 NCBI GI
 BLAST score
                    169
                    3.0e-90
 E value
 Match length
                    322
 % identity
                    72
 NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                    299031
 Seq. No.
                    LIB3152-003-P1-K1-G7
 Seq. ID
                    BLASTN
 Method
                    g22516
 NCBI GI
 BLAST score
                    305
                    1.0e-171
 E value
 Match length
                    361
                    96
 % identity
 NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                    299032
 Seq. No.
 Seq. ID
                    LIB3152-003-P1-K1-H10
                    BLASTX
 Method
                    g141597
 NCBI GI
 BLAST score
                    352
```

1.0e-34

111

E value Match length



% identity 75

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)

>gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize

>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]

[Zea mays]

Seq. No. 299033

Seq. ID LIB3152-003-P1-K1-H5

Method BLASTX
NCBI GI g141616
BLAST score 364
E value 9.0e-35
Match length 125
% identity 67

NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)

>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 299034

Seq. ID LIB3152-005-P1-K1-A10

Method BLASTN
NCBI GI g22516
BLAST score 150
E value 6.0e-79
Match length 255
% identity 89

NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 299035

Seq. ID LIB3152-005-P1-K1-A2

Method BLASTX
NCBI GI g2827524
BLAST score 151
E value 6.0e-10
Match length 36
% identity 69

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 299036

Seq. ID LIB3152-005-P1-K1-A3

Method BLASTN
NCBI GI g168673
BLAST score 92
E value 4.0e-44
Match length 131
% identity 95

NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 299037

Seq. ID LIB3152-005-P1-K1-A7

Method BLASTX
NCBI GI g602076
BLAST score 452
E value 3.0e-45
Match length 98
% identity 21

NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]

BLAST score

E value Match length 320 9.0e-30

82



```
Seq. No.
                    299038
                    LIB3152-005-P1-K1-C10
Seq. ID
Method
                    BLASTX
NCBI GI
                    g141617
BLAST score
                    249
E value
                    2.0e-21
Match length
                    89
% identity
                    60
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                    >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
                    >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                    >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                    299039
Seq. No.
Seq. ID
                    LIB3152-005-P1-K1-D11
Method
                    BLASTX
NCBI GI
                    q508545
BLAST score
                    147
E value
                    3.0e-15
                    91
Match length
                    59
% identity
NCBI Description
                   (L34340) zein [Zea mays]
                    299040
Seq. No.
Seq. ID
                    LIB3152-005-P1-K1-D3
Method
                    BLASTX
NCBI GI
                    q141617
BLAST score
                    512
                    3.0e-52
E value
Match length
                    128
% identity
                    74
NCBI Description
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
                    >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                    >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                    299041
Seq. No.
                    LIB3152-005-P1-K1-D4
Seq. ID
Method
                    BLASTX
                    g141606
NCBI GI
BLAST score
                    188
E value
                    3.0e-14
                    95
Match length
                    49
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
NCBI Description
                    >gi 72309 pir ZIZMD1 19K zein precursor (clone cZ19D1) -
                    maize >gi 168682 (M12144) 19 kDa zein protein [Zea mays]
                    299042
Seq. No.
Seq. ID
                    LIB3152-005-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    g141617
```

Method

NCBI GI

BLAST score

BLASTX

228

q224514



```
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                   299043
Seq. No.
Seq. ID
                   LIB3152-005-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g508545
BLAST score
                   168
E value
                   5.0e-12
Match length
                   38
% identity
                   89
NCBI Description (L34340) zein [Zea mays]
                   299044
Seq. No.
                   LIB3152-005-P1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g72307
BLAST score
                   330
E value
                   8.0e-31
Match length
                   107
% identity
                   65
                   22K zein precursor (clone pZ22.3) - maize >gi 168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   299045
Seq. No.
Seq. ID
                   LIB3152-005-P1-K1-F3
Method
                   BLASTN
NCBI GI
                   q168661
BLAST score
                   107
E value
                   4.0e-53
Match length
                   206
% identity
                   94
NCBI Description Maize 15 kDa zein mRNA, clone cZ15A3, complete cds
                   299046
Seq. No.
                   LIB3152-005-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141617
                   246
BLAST score
E value
                   5.0e-21
                   109
Match length
                   50
% identity
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
                   >gi 100941 pir S12140 zein Zc1 - maize
                   >gi 100945 pir B29017 zein 2 - maize
                   >qi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
Seq. No.
                   299047
Seq. ID
                   LIB3152-005-P1-K1-F7
```



E value 2.0e-19
Match length 53
% identity 87

NCBI Description zein M8 [Zea mays]

Seq. No. 299048

Seq. ID LIB3152-005-P1-K1-G2

Method BLASTX
NCBI GI g141608
BLAST score 154
E value 2.0e-12
Match length 86
% identity 50

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655

zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa

zein [Zea mays]

Seq. No. 299049

Seq. ID LIB3152-006-P1-K1-B9

Method BLASTN
NCBI GI g168675
BLAST score 219
E value 1.0e-120
Match length 339
% identity 92

NCBI Description Maize mutant zein (zE19) gene, complete cds

Seq. No. 299050

Seq. ID LIB3152-006-P1-K1-D7

Method BLASTX
NCBI GI g135060
BLAST score 232
E value 2.0e-19
Match length 57
% identity 84

NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)

(SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose

synthase [Zea mays] >gi 22488 emb CAA26229 (X02382)

sucrose synthase [Zea mays]

Seq. No. 299051

Seq. ID LIB3152-006-P1-K1-E8

Method BLASTX
NCBI GI g508545
BLAST score 184
E value 5.0e-20
Match length 71
% identity 80

NCBI Description (L34340) zein [Zea mays]

Seq. No. 299052

Seq. ID LIB3152-006-P1-K1-F12

Method BLASTX
NCBI GI g2832246
BLAST score 207
E value 2.0e-16



```
Match length
% identity
                  98
NCBI Description
                  (AF031569) 22-kDa alpha zein 8 [Zea mays]
                  299053
Seq. No.
Seq. ID
                  LIB3152-006-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  g22514
BLAST score
                  38
E value
                  2.0e-12
Match length
                  98
% identity
                  85
NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)
                  299054
Seq. No.
                  LIB3152-006-P1-K1-G5
Seq. ID
Method
                  BLASTN
                  g4185305
NCBI GI
BLAST score
                  195
                  1.0e-105
E value
                  315
Match length
% identity
                  91
NCBI Description
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
                  299055
Seq. No.
Seq. ID
                  LIB3152-006-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g2832243
BLAST score
                  234
E value
                  8.0e-20
Match length
                  58
% identity
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
                  299056
Seq. No.
Seq. ID
                  LIB3152-006-P1-K1-H12
Method
                  BLASTX
                  g322870
NCBI GI
BLAST score
                   144
                  7.0e-21
E value
Match length
                   57
                   93
% identity
                  glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
NCBI Description
                  maize (fragment)
```

Seq. ID LIB3152-006-P1-K1-H5

BLASTN Method NCBI GI g22514 BLAST score 80 3.0e-37 E value 204 Match length 85 % identity

NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. ID

Method NCBI GI



```
299058
Seq. No.
                  LIB3152-006-P1-K1-H7
Seq. ID
Method
                  BLASTN
                  q22516
NCBI GI
                  67
BLAST score
E value
                  2.0e-29
                  115
Match length
                  90
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                  299059
Seq. No.
Seq. ID
                  LIB3152-007-P1-K1-A3
Method
                  BLASTN
                  q22549
NCBI GI
BLAST score
                  268
E value
                  1.0e-149
Match length
                  396
% identity
                  71
NCBI Description Maize gene for a 27kDa storage protein, zein
                  299060
Seq. No.
                  LIB3152-007-P1-K1-B10
Seq. ID
Method
                  BLASTX
                  g141616
NCBI GI
                  154
BLAST score
                  1.0e-10
E value
Match length
                  48
                  60
% identity
                  ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                  >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
                  299061
Seq. No.
Seq. ID
                  LIB3152-007-P1-K1-C2
Method
                  BLASTX
NCBI GI
                   q22216
BLAST score
                   195
                   3.0e-15
E value
Match length
                   61
% identity
                   66
NCBI Description (X55722) 22kD zein [Zea mays]
                   299062
Seq. No.
Seq. ID
                   LIB3152-007-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g419803
BLAST score
                   230
E value
                   3.0e-19
Match length
                   83
% identity
                   54
                  zein protein - maize >gi 168705 (M72708) zein protein [Zea
NCBI Description
                   299063
Seq. No.
```

42033

LIB3152-007-P1-K1-C5

BLASTN

g168484



BLAST score E value 1.0e-116 Match length 277 94 % identity

NCBI Description Maize endosperm glutelin-2 gene, complete cds

299064 Seq. No.

LIB3152-007-P1-K1-D12 Seq. ID

Method BLASTN NCBI GI g2832242 BLAST score 60 E value 3.0e-25 Match length 191 % identity 15

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

299065 Seq. No.

LIB3152-007-P1-K1-D4 Seq. ID

Method BLASTX NCBI GI g22216 BLAST score 266 E value 2.0e-23 105 Match length % identity 55

NCBI Description (X55722) 22kD zein [Zea mays]

299066 Seq. No.

LIB3152-007-P1-K1-G1 Seq. ID

Method BLASTX NCBI GI q231654 250 BLAST score 1.0e-21 E value 94 Match length

% identity 59

BRITTLE-1 PROTEIN PRECURSOR >gi 82676_pir__JQ1459 Bt1 NCBI Description protein precursor - maize >gi_168426 (M79333) brittle-1

protein [Zea mays]

Seq. No. 299067

Seq. ID LIB3152-007-P1-K1-G3

Method BLASTN NCBI GI g168698 BLAST score 132 E value 4.0e-68 Match length 174 % identity

NCBI Description Z.mays zein mRNA, complete cds

299068 Seq. No.

Seq. ID LIB3152-007-P1-K1-G6

Method BLASTX NCBI GI q100940 BLAST score 209 E value 8.0e-17 Match length 65 71 % identity

NCBI Description zein zA1 - maize

Method

NCBI GI

BLAST score

BLASTX

245

g168701



```
Seq. No.
                  299069
Seq. ID
                  LIB3152-007-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g16073
BLAST score
                  261
E value
                  9.0e-23
Match length
                  62
% identity
                  82
NCBI Description
                 (X59526) zein protein [Acetabularia mediterranea]
Seq. No.
                  299070
                  LIB3152-008-P1-K1-A2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168690
BLAST score
                  116
E value
                  1.0e-58
Match length
                  124
% identity
NCBI Description Maize zein mRNA, complete cds, clone ZG124
Seq. No.
                  299071
Seq. ID
                  LIB3152-008-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q82660
BLAST score
                  169
E value
                  5.0e-12
Match length
                  75
% identity
                  59
NCBI Description
                  19K zein precursor (clone ZG31A) - maize (fragment)
                  >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
Seq. No.
                  299072
Seq. ID
                  LIB3152-008-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  q168692
BLAST score
                  120
E value
                  8.0e-61
Match length
                  206
                  64
% identity
NCBI Description Maize zein mRNA, complete cds, clone ZG7
                  299073
Seq. No.
Seq. ID
                  LIB3152-008-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2832243
BLAST score
                  226
E value
                  6.0e-19
                  68
Match length
                  72
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.
                  299074
Seq. ID
                  LIB3152-008-P1-K1-H10
```



```
E value 7.0e-21
Match length 100
% identity 57
```

NCBI Description (M60837) zein [Zea mays]

Seq. No. 299075

Seq. ID LIB3152-008-P1-K1-H2

Method BLASTN
NCBI GI g2832242
BLAST score 228
E value 1.0e-125
Match length 343
% identity 12

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299076

Seq. ID LIB3152-008-P1-K1-H6

Method BLASTX
NCBI GI g4586107
BLAST score 313
E value 8.0e-29
Match length 114
% identity 16

NCBI Description (AL049638) putative disease resistance protein [Arabidopsis

thaliana]

Seq. No. 299077

Seq. ID LIB3152-009-P1-K1-A7

Method BLASTX
NCBI GI g121472
BLAST score 188
E value 4.0e-14
Match length 60
% identity 63

NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289 emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea

mays] >qi 168485 (M16066) qlutelin-2 [Zea mays]

Seq. No. 299078

Seq. ID LIB3152-009-P1-K1-B8

Method BLASTX
NCBI GI g508545
BLAST score 241
E value 2.0e-20
Match length 109
% identity 50

NCBI Description (L34340) zein [Zea mays]

Seq. No. 299079

Seq. ID LIB3152-009-P1-K1-D12

Method BLASTN
NCBI GI g168690
BLAST score 99
E value 2.0e-48



```
Match length
% identity
                  90
                  Maize zein mRNA, complete cds, clone ZG124
NCBI Description
                  299080
Seq. No.
Seq. ID
                  LIB3152-009-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q419803
BLAST score
                  351
                  2.0e-33
E value
Match length
                  98
% identity
                  66
NCBI Description
                  zein protein - maize >gi 168705 (M72708) zein protein [Zea
                  299081
Seq. No.
                  LIB3152-009-P1-K1-D9
Seq. ID
Method
                  BLASTN
                  g4185305
NCBI GI
                  112
BLAST score
                  3.0e-56
E value
Match length
                  220
% identity
                  89
NCBI Description
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
Seq. No.
                  299082
Seq. ID
                  LIB3152-009-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g168699
BLAST score
                  166
                  2.0e-25
E value
Match length
                  93
% identity
                  60
NCBI Description
                 (M60836) zein [Zea mays]
Seq. No.
                  299083
Seq. ID
                  LIB3152-009-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g16073
BLAST score
                  452
E value
                  3.0e-45
Match length
                  101
% identity
                  89
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
```

299084

Seq. ID Method

LIB3152-009-P1-K1-G1

BLASTX NCBI GI g141612 BLAST score 430 1.0e-42 E value 107 Match length 82 % identity

NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)



69

64

NCBI Description (M86591) 22 kDa zein protein [Zea mays]

Match length % identity

>gi_72306_pir__ZIZMC2 22K zein precursor (clone cZ22C2) maize (fragment) >gi_168688 (M12141) 22 kDa zein protein
[Zea mays]

```
299085
Seq. No.
Seq. ID
                  LIB3152-010-P1-K1-B11
Method
                  BLASTX
                  q168693
NCBI GI
                  306
BLAST score
                  3.0e-28
E value
Match length
                  88
% identity
                  74
NCBI Description
                  (M29627) zein [Zea mays]
Seq. No.
                  299086
                  LIB3152-010-P1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168698
BLAST score
                  120
E value
                  6.0e-61
Match length
                  291
                  87
% identity
NCBI Description Z.mays zein mRNA, complete cds
                  299087
Seq. No.
                  LIB3152-010-P1-K1-D3
Seq. ID
Method
                  BLASTX
                  a141612
NCBI GI
BLAST score
                   340
                   6.0e-32
E value
                  135
Match length
                   67
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)
NCBI Description
                  >gi_72306_pir__ZIZMC2 22K zein precursor (clone cZ22C2) -
                  maize (fragment) >gi_168688 (M12141) 22 kDa zein protein
                   [Zea mays]
                   299088
Seq. No.
Seq. ID
                  LIB3152-010-P1-K1-E11
Method
                  BLASTN
NCBI GI
                   q168681
BLAST score
                   144
                   3.0e-75
E value
Match length
                   311
% identity
                   88
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                   >gi 270686 gb I03333 Sequence 8 from Patent US
                   299089
Seq. No.
Seq. ID
                   LIB3152-010-P1-K1-G5
                   BLASTX
Method
                   q168703
NCBI GI
BLAST score
                   205
E value
                   3.0e-16
```



```
299090
Seq. No.
Seq. ID
                  LIB3152-010-P1-K1-G8
Method
                  BLASTX
                  g2244785
NCBI GI
BLAST score
                  369
                  2.0e-35
E value
Match length
                  104
% identity
                  65
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  299091
                  LIB3152-010-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g72307
BLAST score
                  261
E value
                  8.0e-23
Match length
                  102
                  57
% identity
                  22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                  (J01246) 26.99 kd zein protein [Zea mays]
Seq. No.
                  299092
Seq. ID
                  LIB3152-012-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q2832247
BLAST score
                  148
                  2.0e-10
E value
Match length
                  58
                  61
% identity
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.
                  299093
Seq. ID
                  LIB3152-012-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  g168681
BLAST score
                  89
                  2.0e-42
E value
Match length
                  149
% identity
                  90
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                  >gi 270686 gb I03333 Sequence 8 from Patent US
Seq. No.
                  299094
Seq. ID
                  LIB3152-012-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g1345587
BLAST score
                  255
                  3.0e-22
E value
Match length
                  92
% identity
                  63
                  14-3-3-LIKE PROTEIN GF14-6 >gi 998430 bbs 164522 (S77133)
NCBI Description
                  GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261
                  aa] [Zea mays]
```

Seq. ID LIB3152-012-P1-K1-D7



Method BLASTX
NCBI GI g141597
BLAST score 316
E value 3.0e-29
Match length 72
% identity 86

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)

>gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize

>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]

[Zea mays]

Seq. No. 299096

Seq. ID LIB3152-012-P1-K1-F6

Method BLASTX
NCBI GI g22216
BLAST score 282
E value 3.0e-25
Match length 79
% identity 76

NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 299097

Seq. ID LIB3152-012-P1-K1-F7

Method BLASTN
NCBI GI g168702
BLAST score 69
E value 1.0e-30
Match length 161
% identity 86

NCBI Description Corn 22 kDa zein protein gene, complete cds

Seq. No. 299098

Seq. ID LIB3152-012-P1-K1-G11

Method BLASTX
NCBI GI g141605
BLAST score 258
E value 1.0e-22
Match length 73
% identity 75

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)

>gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 299099

Seq. ID LIB3152-014-P1-K1-A1

Method BLASTX
NCBI GI g16073
BLAST score 184
E value 3.0e-27
Match length 120
% identity 63

NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 299100

Seq. ID LIB3152-014-P1-K1-A11

Method BLASTX NCBI GI g468516



BLAST score 5.0e-09 E value Match length 34 85 % identity

NCBI Description (X55724) zein [Zea mays]

Seq. No. 299101

Seq. ID LIB3152-014-P1-K1-B12

Method BLASTN NCBI GI q168681 BLAST score 61 E value 5.0e-26 Match length 153 % identity 85

NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.

>gi 270686 gb I03333 Sequence 8 from Patent US

Seq. No. 299102

LIB3152-014-P1-K1-C11 Seq. ID

Method BLASTX NCBI GI g168699 171 BLAST score E value 1.0e-18 Match length 81 % identity 74

NCBI Description (M60836) zein [Zea mays]

299103 Seq. No.

LIB3152-014-P1-K1-D2 Seq. ID

Method BLASTX g16073 NCBI GI BLAST score 293 1.0e-26 E value Match length 68

% identity 88

NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 299104

Seq. ID LIB3152-014-P1-K1-E9

Method BLASTN NCBI GI q168665 BLAST score 94 E value 1.0e-45 Match length 225 % identity 88

NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 299105

Seq. ID LIB3152-014-P1-K1-G11

Method BLASTN NCBI GI g2832242 BLAST score 56 8.0e-23 E value Match length 158 % identity 16

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence



```
Seq. No.
                  299106
Seq. ID
                  LIB3152-014-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g168699
BLAST score
                  354
E value
                  1.0e-33
Match length
                  73
                  99
% identity
NCBI Description (M60836) zein [Zea mays]
Seq. No.
                  299107
Seq. ID
                  LIB3152-014-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  q168675
BLAST score
                  60
E value
                  4.0e-25
                  128
Match length
% identity
                  88
NCBI Description Maize mutant zein (zE19) gene, complete cds
                  299108
Seq. No.
                  LIB3152-014-P1-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168398
BLAST score
                  226
                  1.0e-124
E value
                  234
Match length
% identity
                  99
NCBI Description Zea mays auxin-binding protein (abp4) gene, exons 1-5 and
                  complete cds
Seq. No.
                  299109
Seq. ID
                  LIB3152-015-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g141608
BLAST score
                  188
E value
                  2.0e-15
Match length
                  98
% identity
                  54
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >qi 100943 pir S15655
NCBI Description
                  zein, 19K - maize >gi 22446 emb CAA37651 (X53582) 19 kDa
                  zein [Zea mays]
Seq. No.
                  299110
Seq. ID
                  LIB3152-015-P1-K1-D9
Method
                  BLASTX
                  g168699
NCBI GI
BLAST score
                  267
                  2.0e-23
E value
Match length
                  82
% identity
                  71
NCBI Description (M60836) zein [Zea mays]
```

299111

Seq. ID LIB3152-015-P1-K1-F11

Method BLASTX NCBI GI g141616

BLAST score

51



```
BLAST score
  E value
                     3.0e-20
  Match length
                     98
                     61
  % identity
                    ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
  NCBI Description
                    >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
                     299112
  Seq. No.
                    LIB3152-015-P1-K1-H8
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                     q461498
  BLAST score
                     227
  E value
                     5.0e-19
  Match length
                     46
                     96
  % identity
                    ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
  NCBI Description
                     TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                     (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC
                     2.6.1.2) - proso millet >gi 296204 emb CAA49199 (X69421)
                     alanine aminotransferase [Panicum miliaceum]
                     299113
  Seq. No.
                     LIB3152-016-P1-K1-A1
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q4140644
                     324
  BLAST score
                     4.0e-30
  E value
                     90
  Match length
  % identity
                     76
                    (AF090447) 22-kDa zein protein 12 [Zea mays]
  NCBI Description
                     299114
  Seq. No.
                     LIB3152-016-P1-K1-A11
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     q4140643
  BLAST score
                     43
  E value
                     4.0e-15
  Match length
                     175
                     82
  % identity
                     Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
  NCBI Description
                     complete sequence
                     299115
  Seq. No.
  Seq. ID
                     LIB3152-016-P1-K1-A7
  Method
                     BLASTX
  NCBI GI
                     g3694807
  BLAST score
                     223
  E value
                     1.0e-18
                     55
  Match length
  % identity
                     84
  NCBI Description (AF055898) alanine aminotransferase [Zea mays]
                     299116
  Seq. No.
  Seq. ID
                     LIB3152-016-P1-K1-C11
                     BLASTN
  Method
  NCBI GI
                     g168685
```

```
E value
Match length
                  182
                  86
% identity
                  Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA
NCBI Description
                  299117
Seq. No.
Seq. ID
                  LIB3152-016-P1-K1-E3
Method
                  BLASTX
                  q4263695
NCBI GI
                  162
BLAST score
E value
                  4.0e-11
Match length
                  119
% identity
                  30
NCBI Description
                   (AC006223) putative myosin II heavy chain [Arabidopsis
                  thaliana]
                  299118
Seq. No.
                  LIB3152-016-P1-K1-E9
Seq. ID
Method
                  BLASTX
                  g22220
NCBI GI
                  252
BLAST score
                  1.0e-21
E value
Match length
                  110
% identity
                  51
                  (X55723) 22 kD zein [Zea mays]
NCBI Description
                   299119
Seq. No.
                  LIB3152-016-P1-K1-G2
Seq. ID
```

 Seq. No.
 299119

 Seq. ID
 LIB3152-016

 Method
 BLASTX

 NCBI GI
 g141600

 BLAST score
 168

 E value
 7.0e-12

Match length 61 % identity 57

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)

>gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 299120

Seq. ID LIB3152-016-P1-K1-G8

Method BLASTX
NCBI GI g22216
BLAST score 280
E value 4.0e-25
Match length 96
% identity 65

NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 299121

Seq. ID LIB3152-016-P1-K1-H1

Method BLASTN
NCBI GI g22516
BLAST score 261
E value 1.0e-145
Match length 360
% identity 94

NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

```
Seq. No.
                   299122
Seq. ID
                   LIB3152-017-P1-K1-A3
Method
                   BLASTN
NCBI GI
                   g22326
BLAST score
                   120
E value
                   6.0e-61
Match length
                   160
                   94
% identity
NCBI Description Z.mays gene for Hageman factor inhibitor
Seq. No.
                   299123
Seq. ID
                   LIB3152-017-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   q141603
BLAST score
                   416
                   6.0e-41
E value
Match length
                   92
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
Seq. No.
                   299124
                   LIB3152-017-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g121472
BLAST score
                   223
E value
                   9.0e-23
Match length
                   75
                   76
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                   mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
Seq. No.
                   299125
Seq. ID
                   LIB3152-017-P1-K1-C10
Method
                   BLASTX
                   g22220
NCBI GI
BLAST score
                   178
E valuè
                   2.0e-13
Match length
                   71
% identity
                   55
NCBI Description
                  (X55723) 22 kD zein [Zea mays]
                   299126
Seq. No.
Seq. ID
                   LIB3152-017-P1-K1-C5
Method
                   BLASTX
                   g533086
NCBI GI
BLAST score
                   171
```

42045

NCBI Description (U07605) precursor delta-9-stearoyl-acyl carrier protein

3.0e-12

46 74

E value Match length

% identity

Match length

% identity

105 70

NCBI Description (M60836) zein [Zea mays]



desaturase [Thunbergia alata]

```
299127
Seq. No.
                   LIB3152-017-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141603
BLAST score
                   244
                   2.0e-31
E value
                   99
Match length
                   80
% identity
NCBI Description
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                   >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi 22529 emb_CAA24723 (V01476) zein [Zea mays]
Seq. No.
                   299128
                   LIB3152-017-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q141614
BLAST score
                   174
                   1.0e-17
E value
                   89
Match length
                   63
% identity
NCBI Description
                   ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
                   >gi_82662_pir__B22831 22K zein precursor (clone M1) - maize
                   >gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea
mays] >gi_224510_prf__1107201D zein M1 [Zea mays]
Seq. No.
                   299129
Seq. ID
                   LIB3152-017-P1-K1-F3
Method
                   BLASTN
NCBI GI
                   g303854
BLAST score
                   82
E value
                   1.0e-38
Match length
                   114
                   93
% identity
NCBI Description Rice mRNA for ribosomal protein L7A, complete cds
                   299130
Seq. No.
Seq. ID
                   LIB3152-017-P1-K1-F5
Method
                   BLASTX
                   q224508
NCBI GI
BLAST score
                   302
                   1.0e-27
E value
Match length
                   109
% identity
                   67
NCBI Description zein A20 [Zea mays]
Seq. No.
                   299131
Seq. ID
                   LIB3152-017-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   q168699
BLAST score
                   256
E value
                   3.0e-27
```



```
Seq. No.
                  299132
Seq. ID
                  LIB3152-017-P1-K1-G7
Method
                  BLASTN
                  g168704
NCBI GI
BLAST score
                  57
                  1.0e-23
E value
                  119
Match length
% identity
                  92
NCBI Description Zea mays zein protein gene, complete cds
                  299133
Seq. No.
                  LIB3152-017-P1-K1-H11
Seq. ID
Method
                  BLASTX
                  g2832246
NCBI GI
BLAST score
                  308
                  3.0e-28
E value
                  110
Match length
                  60
% identity
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]
                  299134
Seq. No.
                  LIB3152-017-P1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2828011
BLAST score
                  41
E value
                  6.0e-14
Match length
                  61
                  92
% identity
NCBI Description Zea mays starch synthase I precursor (Ss1) mRNA, nuclear
                  gene encoding plastid protein, complete cds
                  299135
Seq. No.
                  LIB3152-017-P1-K1-H7
Seq. ID
Method
                  BLASTN
                  g2832242
NCBI GI
BLAST score
                  70
E value
                  3.0e-31
Match length
                  142
% identity
                  14
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                   299136
Seq. No.
                  LIB3152-017-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g141614
BLAST score
                  290
E value
                   8.0e-30
Match length
                   110
% identity
                   39
```

ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1) NCBI Description

>gi_82662_pir__B22831_22K_zein_precursor (clone M1) - maize
>gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea
mays] >gi_224510_prf__1107201D_zein_M1 [Zea mays]

Seq. No. 299137

Seq. ID LIB3152-018-P1-K1-A11

Method BLASTX



```
g141603
NCBI GI
BLAST score
                   290
E value
                   4.0e-26
Match length
                   116
                   58
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                   299138
Seq. No.
                   LIB3152-018-P1-K1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168681
BLAST score
                   92
                   3.0e-44
E value
                   124
Match length
                   94
% identity
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                   >gi 270686 gb I03333 Sequence 8 from Patent US
Seq. No.
                   299139
                   LIB3152-018-P1-K1-F6
Seq. ID
                   BLASTX
Method
                   g224508
NCBI GI
BLAST score
                   188
E value
                   1.0e-28
Match length
                   89
                   88
% identity
NCBI Description zein A20 [Zea mays]
                   299140
Seq. No.
                   LIB3152-019-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q141617
BLAST score
                   236
                   7.0e-20
E value
Match length
                   44
                   95
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
                   >gi_22515_emb_CAA37595
                                           (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
Seq. No.
                   299141
Seq. ID
                   LIB3152-019-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g141605
BLAST score
                   144
E value
                   5.0e-13
                   76
Match length
% identity
                   58
```

NCBI Description

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)

>gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 299142

```
LIB3152-019-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076791
BLAST score
                  251
                  1.0e-37
E value
                  122
Match length
% identity
                  calcium-binding protein - maize >gi_2119370_pir__S58170
NCBI Description
                  Calreticulin precursor - maize >gi_577612_emb_CAA86728_
                   (Z46772) calcium-binding protein [Zea mays]
                  >gi_927572_emb_CAA61939_ (X89813) Calreticulin precursor
                   [Zea mays] >gi 1587033 prf 2205314A calreticulin [Zea
                  mays]
                  299143
Seq. No.
                  LIB3152-019-P1-K1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168673
BLAST score
                  121
                  1.0e-61
E value
                  136
Match length
                  98
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
Seq. No.
                  299144
                  LIB3152-019-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  g141600
NCBI GI
BLAST score
                   171
E value
                   3.0e-12
Match length
                   84
                   50
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                   >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
Seq. No.
                   299145
                   LIB3152-019-P1-K1-H6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q168652
BLAST score
                   42
                   2.0e-14
E value
Match length
                   86
                   87
% identity
                  Maize amyloplast-specific transit protein (waxy; wx+
NCBI Description
                   locus), complete cds
Seq. No.
                   299146
                   LIB3152-020-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q82660
```

Method BLASTX
NCBI GI g82660
BLAST score 361
E value 2.0e-34
Match length 128
% identity 60

NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment) >gi 809117 emb CAA24720_ (V01473) zein [Zea mays]

BLAST score

% identity

E value Match length 173 2.0e-12

54 72

```
299147
Seq. No.
Seq. ID
                  LIB3152-020-P1-K1-B12
                  BLASTX
Method
                  g629861
NCBI GI
                  159
BLAST score
                  6.0e-11
E value
                  47
Match length
% identity
                  68
                  zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
                  299148
Seq. No.
Seq. ID
                  LIB3152-020-P1-K1-C2
Method
                  BLASTX
                  g3122071
NCBI GI
BLAST score
                  326
                  5.0e-42
E value
                  122
Match length
                  73
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_2130148_pir__S66339 translation elongation factor eEF-1
                  alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408)
                  alpha subunit of tlanslation elongation factor 1 [Zea mays]
                  299149
Seq. No.
                  LIB3152-020-P1-K1-D12
Seq. ID
                  BLASTX
Method
                  g168695
NCBI GI
BLAST score
                  231
                  1.0e-19
E value
Match length
                  63
                  70
% identity
NCBI Description
                  (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
                  zein gamma [Zea mays]
                  299150
Seq. No.
                  LIB3152-020-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q508545
                  222
BLAST score
                  3.0e-18
E value
                  99
Match length
% identity
                  56
NCBI Description (L34340) zein [Zea mays]
                  299151
Seq. No.
                  LIB3152-020-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2130065
```

42050

NCBI Description alpha-globulin precursor - rice >gi_1783206_dbj_BAA09308_ (D50643) 26 kDa globulin [Oryza sativa]



```
Seq. No.
Seq. ID
                  LIB3152-020-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  g2253277
BLAST score
                  41
                  9.0e-14
E value
Match length
                  92
                  86
% identity
                  Oryza sativa bZIP transcriptional activator RF2a (rf2a)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  299153
Seq. ID
                  LIB3152-020-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  a141603
                  304
BLAST score
                  7.0e-28
E value
Match length
                  72
% identity
                  88
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                  299154
Seq. ID
                  LIB3152-020-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q141615
BLAST score
                  222
E value
                  3.0e-18
Match length
                  64
                  73
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
NCBI Description
                  >gi 22536_emb_CAA24727 (V01480) zein protein 3 [Zea mays]
Seq. No.
                  299155
Seq. ID
                  LIB3152-021-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q121472
BLAST score
                  154
                  1.0e-10
E value
Match length
                  57
% identity
                  58
                  GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                  >gi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) -
                  maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
                  mays] >gi 1684\overline{8}5 (M\overline{16066}) glutelin-2 [Zea mays]
                  299156
Seq. No.
Seq. ID
                  LIB3152-021-P1-K1-A9
                  BLASTX
Method
                  g141597
NCBI GI
BLAST score
                  231
```

42051

2.0e-19

58 81

E value Match length

% identity





NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize >gi 22545_emb_CAA24728_ (V01481) reading frame zein [2] [Zea mays] 299157 Seq. No. Seq. ID LIB3152-021-P1-K1-B10 BLASTN Method g22514 NCBI GI 185 BLAST score E value 1.0e-100 Match length 253 % identity 93 NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2) Seq. No. 299158 LIB3152-021-P1-K1-B11 Seq. ID Method BLASTN g22514 NCBI GI 136 BLAST score E value 1.0e-70 Match length 192 % identity 93 NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2) 299159 Seq. No. LIB3152-021-P1-K1-C11 Seq. ID Method BLASTN NCBI GI g22326 135 BLAST score 5.0e-70 E value 167 Match length % identity 95 NCBI Description Z.mays gene for Hageman factor inhibitor Seq. No. 299160 Seq. ID LIB3152-021-P1-K1-C12 Method BLASTN NCBI GI q463151 BLAST score 180 E value 8.0e-97 Match length 264 % identity 92 NCBI Description Zea mays high sulfur zein gene, complete cds Seq. No. 299161 Seq. ID LIB3152-021-P1-K1-C2 Method BLASTX

NCBI GI g141616 BLAST score 191 1.0e-14 E value Match length 42 % identity 86

ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3) NCBI Description >gi_168662 (M12147) 15 kDa zein protein [Zea mays]

299162 Seq. No.

Seq. ID

299167

LIB3152-021-P1-K1-H10



```
LIB3152-021-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141598
BLAST score
                  297
                  5.0e-27
E value
                  98
Match length
                  66
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
NCBI Description
                  >gi_72313_pir__ZIZM99 19K zein precursor (clone ZG99) -
                  maize >gi_22519_emb_CAA24717_ (V01470) zein [Zea mays]
                  >gi_22534_emb_CAA24726_ (V01479) zein [Zea mays]
Seq. No.
                  299163
                  LIB3152-021-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q508545
BLAST score
                  243
                  1.0e-20
E value
Match length
                  124
% identity
                  50
NCBI Description (L34340) zein [Zea mays]
                  299164
Seq. No.
                  LIB3152-021-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82654
BLAST score
                  170
                  1.0e-12
E value
Match length
                  55
                  64
% identity
NCBI Description 10K zein precursor - maize >gi 22541 emb CAA30409 (X07535)
                  10kDa zein (AA 1 - 150) [Zea mays]
Seq. No.
                  299165
                  LIB3152-021-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629861
BLAST score
                  239
                  3.0e-20
E value
Match length
                  102
% identity
                  53
                  zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  299166
Seq. ID
                  LIB3152-021-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q1177320
BLAST score
                  345
E value
                  1.0e-32
Match length
                  98
% identity
                  64
                  (X89891) EFA27 for EF hand, abscisic acid, 27kD [Oryza
NCBI Description
                  sativa]
```

```
Method
NCBI GI
                  q22544
BLAST score
                  76
E value
                  1.0e-34
                  277
Match length
% identity
                  82
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
Seq. No.
                  299168
Seq. ID
                  LIB3152-021-P1-K1-H2
```

Method BLASTX
NCBI GI g1177320
BLAST score 226
E value 1.0e-18
Match length 93
% identity 49

NCBI Description (X89891) EFA27 for EF hand, abscisic acid, 27kD [Oryza

sativa]

 Seq. No.
 299169

 Seq. ID
 LIB3152-021-P1-K1-H9

 Method
 BLASTN

 NCBI GI
 g248336

 BLAST score
 44

 E. value
 6.0e-16

E value 6.0e-16
Match length 116
% identity 84

NCBI Description polyubiquitin [maize, Genomic, 3841 nt]

Seq. No. 299170

Seq. ID LIB3152-022-P1-K1-A8

Method BLASTX
NCBI GI g168697
BLAST score 321
E value 9.0e-30
Match length 78
% identity 87

NCBI Description (M60835) zein [Zea mays]

Seq. No. 299171

Seq. ID LIB3152-022-P1-K1-D1

Method BLASTX
NCBI GI g2564066
BLAST score 184
E value 8.0e-14
Match length 69
% identity 59

NCBI Description (D45900) LEDI-3 protein [Lithospermum erythrorhizon]

Seq. No. 299172

Seq. ID LIB3152-022-P1-K1-D7

Method BLASTX
NCBI GI g224513
BLAST score 207
E value 5.0e-35
Match length 107
% identity 79



```
NCBI Description zein M6 [Zea mays]
Seq. No.
                  299173
Seq. ID
                  LIB3152-022-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g141603
BLAST score
                  251
                  1.0e-21
E value
                  87
Match length
                  67
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                  >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                  299174
Seq. No.
Seq. ID
                  LIB3152-022-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q2244866
                  165
BLAST score
E value
                  1.0e-13
Match length
                  59
                   68
% identity
NCBI Description
                 (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  299175
Seq. ID
                  LIB3152-023-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  a2832242
BLAST score
                   78
                  3.0e-36
E value
Match length
                  162
% identity
                  12
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                   299176
Seq. ID
                   LIB3152-023-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2245020
BLAST score
                   381
                   5.0e-37
E value
Match length
                   93
% identity
                   76
NCBI Description (Z97341) growth regulator homolog [Arabidopsis thaliana]
                   299177
Seq. No.
                  LIB3152-023-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q72307
BLAST score
                   290
                   4.0e-26
E value
Match length
                   104
% identity
                   61
                  22K zein precursor (clone pZ22.3) - maize >gi 168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
```

Seq. ID LIB3152-023-P1-K1-C8



```
BLASTN
Method
NCBI GI
                   q22099
BLAST score
                   41
                   4.0e-14
E value
Match length
                   69
                   90
% identity
NCBI Description Z.mays 27kDa zein locus DNA
                   299179
Seq. No.
                   LIB3152-023-P1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g121472
BLAST score
                   219
E value
                   7.0e-18
Match length
                   61
                   70
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                   [Zea mays] >gi_\overline{2}251\overline{7}emb_CAA\overline{3}7594_ (X53514) zein Zc2 [Zea
                   mays] >gi 1684\overline{8}5 (M1\overline{6}066) glutelin-2 [Zea mays]
                   299180
Seq. No.
Seq. ID
                   LIB3152-023-P1-K1-E12
                   BLASTN
Method
                   g22544
NCBI GI
                   171
BLAST score
E value
                   2.0e-91
Match length
                   251
% identity
                   92
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                   299181
Seq. No.
                   LIB3152-023-P1-K1-F9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1419369
BLAST score
                   114
E value
                   2.0e-57
Match length
                   224
% identity
                    97
NCBI Description Z.mays ZmABP3 mRNA for actin depolymerizing factor
                    299182
Seq. No.
Seq. ID
                   LIB3152-023-P1-K1-G6
Method
                   BLASTX
NCBI GI
                    q141614
                    147
BLAST score
E value
                    2.0e-09
                    52
Match length
% identity
```

ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1) NCBI Description

>gi_82662_pir__B22831_22K_zein_precursor (clone M1) - maize >gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea mays] >gi_224510_prf__1107201D_zein_M1 [Zea mays]

Seq. No. 299183

Method

NCBI GI

BLAST score

BLASTX

341

g168701



```
LIB3152-024-P1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168704
                  38
BLAST score
                  3.0e-12
E value
                  102
Match length
                  84
% identity
NCBI Description Zea mays zein protein gene, complete cds
                  299184
Seq. No.
                  LIB3152-024-P1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22514
BLAST score
                  55
                  2.0e-22
E value
Match length
                  91
                  90
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                  299185
Seq. No.
                  LIB3152-024-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g168701
BLAST score
                  323
                  4.0e-30
E value
Match length
                  95
                  73
% identity
NCBI Description (M60837) zein [Zea mays]
                  299186
Seq. No.
                  LIB3152-024-P1-K1-C6
Seq. ID
Method
                  BLASTX
                  g141603
NCBI GI
BLAST score
                  266
                   2.0e-23
E value
Match length
                  78
% identity
                  76
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                   299187
Seq. ID
                  LIB3152-024-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  q4140643
BLAST score
                   58
E value
                   4.0e-24
Match length
                   94
% identity
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                   complete sequence
                   299188
Seq. No.
                  LIB3152-024-P1-K1-F10
Seq. ID
```



```
E value 2.0e-32
Match length 81
% identity 85
```

NCBI Description (M60837) zein [Zea mays]

Seq. No. 299189

Seq. ID LIB3152-024-P1-K1-G9

Method BLASTX
NCBI GI g224509
BLAST score 186
E value 4.0e-14
Match length 95
% identity 52

NCBI Description zein E19 [Zea mays]

Seq. No. 299190

Seq. ID LIB3152-026-P1-K1-B3

Method BLASTN
NCBI GI g22514
BLAST score 53
E value 4.0e-21
Match length 121
% identity 88

NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299191

Seq. ID LIB3152-026-P1-K1-C1

Method BLASTX
NCBI GI g224507
BLAST score 207
E value 1.0e-16
Match length 59
% identity 73

NCBI Description zein Al [Zea mays]

Seq. No. 299192

Seq. ID LIB3152-026-P1-K1-C8

Method BLASTN
NCBI GI g168484
BLAST score 108
E value 9.0e-54
Match length 164
% identity 92

NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 299193

Seq. ID LIB3152-026-P1-K1-D11

Method BLASTX
NCBI GI g508545
BLAST score 263
E value 8.0e-25
Match length 111
% identity 65

NCBI Description (L34340) zein [Zea mays]

Seq. No. 299194

Seq. ID LIB3152-026-P1-K1-D2



```
Method
                  BLASTX
                  g629861
NCBI GI
BLAST score
                  368
                  2.0e-35
E value
                  119
Match length
                  65
% identity
                  zein Zd1, 19K - maize >gi 535020 emb_CAA47639_ (X67203)
NCBI Description
                  zein Zdl (19 kDa zein) [Zea mays]
                  299195
Seq. No.
                  LIB3152-026-P1-K1-E7
Seq. ID
                  BLASTN
Method
                  g4140643
NCBI GI
BLAST score
                  100
                  4.0e-49
E value
                  207
Match length
                  47
% identity
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                  complete sequence
                  299196
Seq. No.
                  LIB3152-026-P1-K1-F5
Seq. ID
                  BLASTX
Method
                  g141616
NCBI GI
BLAST score
                  186
                  5.0e-16
E value
                  76
Match length
% identity
                  64
                  ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                  >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
                  299197
Seq. No.
                  LIB3152-027-P1-K2-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g141603
                  207
BLAST score
                   2.0e-16
E value
Match length
                  70
% identity
                   67
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                   299198
Seq. ID
                  LIB3152-027-P1-K2-A7
Method
                  BLASTX
                   q141597
NCBI GI
                   267
BLAST score
E value
                   2.0e-23
Match length
                   105
% identity
                   57
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
```

```
LIB3152-027-P1-K2-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22326
BLAST score
                  43
                  7.0e-15
E value
Match length
                  59
% identity
                  93
NCBI Description Z.mays gene for Hageman factor inhibitor
                  299200
Seq. No.
Seq. ID
                  LIB3152-027-P1-K2-C10
Method
                  BLASTX
NCBI GI
                  q168701
BLAST score
                  275
                  1.0e-24
E value
                  72
Match length
% identity
                  81
NCBI Description
                  (M60837) zein [Zea mays]
                  299201
Seq. No.
Seq. ID
                  LIB3152-027-P1-K2-D2
Method
                  BLASTN
NCBI GI
                  g168665
BLAST score
                  324
                  0.0e + 00
E value
                  344
Match length
                  99
% identity
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                  299202
Seq. No.
Seq. ID
                  LIB3152-027-P1-K2-D5
Method
                  BLASTX
NCBI GI
                  g141605
BLAST score
                  251
E value
                  1.0e-21
Match length
                  66
                  77
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >qi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
                  299203
Seq. No.
Seq. ID
                  LIB3152-027-P1-K2-E7
Method
                  BLASTX
NCBI GI
                  g141613
BLAST score
                  291
                  1.0e-26
E value
Match length
                  81
                  80
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                  >qi 72305 pir ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize > gi 225\overline{32} emb CAA24725 (V01478) zein [Zea mays]
```

Seq. ID LIB3152-027-P1-K2-H7

Method BLASTX NCBI GI g4416301

```
BLAST score
                    1.0e-36
E value
Match length
                    116
% identity
                    70
NCBI Description
                   (AF105716) gag protein [Zea mays]
Seq. No.
                    299205
                    LIB3152-028-P1-K1-A1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g141607
BLAST score
                    152
E value
                    5.0e-10
Match length
                    104
                    38
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
NCBI Description
                    >gi_22521_emb_CAA24718_ (V01471) zein [Zea mays] >gi 168672
                    (J01244) zein 19 kd protein (partial) [Zea mays]
                    299206
Seq. No.
Seq. ID
                    LIB3152-028-P1-K1-B4
Method
                    BLASTN
                    q508544
NCBI GI
BLAST score
                    63
E value
                    4.0e-27
Match length
                    182
% identity
                    90
NCBI Description Zea mays 24-kD alpha-zein gene (floury2), complete cds
Seq. No.
                    299207
Seq. ID
                    LIB3152-028-P1-K1-D6
Method
                    BLASTX
NCBI GI
                    g141617
BLAST score
                    246
E value
                    5.0e-21
Match length
                    47
% identity
                    89
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                    >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                    >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                    299208
Seq. No.
Seq. ID
                    LIB3152-028-P1-K1-E5
Method
                    BLASTX
NCBI GI
                    g266398
BLAST score
                    275
                    1.0e-24
E value
```

82 Match length % identity 61

TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR NCBI Description INHIBITOR) (CHFI) >gi 68849 pir TIZM1 trypsin/factor XIIa

inhibitor precursor - maize >gi 22327_emb CAA37998_

(X54064) corn Hageman factor inhibitor [Zea mays]

299209 Seq. No.

Seq. ID LIB3152-028-P1-K1-G10

E value

4.0e-14



```
Method
NCBI GI
                  q260042
BLAST score
                  332
                  4.0e-31
E value
Match length
                  80
                  82
% identity
                  (S48563) endosperm ADP-glucose pyrophosphorylase subunit
NCBI Description
                  homolog=Sh2 [maize, Peptide Partial, 542 aa] [Zea mays]
                  299210
Seq. No.
                  LIB3152-028-P1-K1-H5
Seq. ID
Method
                  BLASTX
                  g100846
NCBI GI
BLAST score
                  263
                  5.0e-23
E value
Match length
                  95
                  65
% identity
                  22K zein precursor (clone gZ22.8H3) - maize
NCBI Description
                  >gi 22179 emb CAA43399 (X61085) 22 kD alpha-zein [Zea
                  mays]
                  299211
Seq. No.
                  LIB3152-029-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q22220
BLAST score
                  216
                  2.0e-17
E value
Match length
                  97
                  54
% identity
NCBI Description (X55723) 22 kD zein [Zea mays]
                  299212
Seq. No.
                  LIB3152-029-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4185308
BLAST score
                   262
E value
                   7.0e-23
Match length
                   77
% identity
                   70
                  (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
NCBI Description
                   299213
Seq. No.
                  LIB3152-029-P1-K1-C8
Seq. ID
Method
                  BLASTX
                   g224509
NCBI GI
BLAST score
                   165
E value
                   5.0e-12
Match length
                   58
% identity
                   62
NCBI Description zein E19 [Zea mays]
                   299214
Seq. No.
                   LIB3152-029-P1-K1-D1
Seq. ID
                   BLASTX
Method
                   g100938
NCBI GI
BLAST score
                   187
```



Match length % identity 62 zein precursor - maize >gi 22442 emb CAA32513 (X14335) NCBI Description zein precursor (AA -21 to 90) [Zea mays] 299215 Seq. No. Seq. ID LIB3152-029-P1-K1-E1 Method BLASTX q72307 NCBI GI 260 BLAST score E value 4.0e-26 Match length 90 % identity 79 22K zein precursor (clone pZ22.3) - maize >gi 168686 NCBI Description

(J01246) 26.99 kd zein protein [Zea mays]

299216 Seq. No.

Seq. ID LIB3152-029-P1-K1-F1

Method BLASTX NCBI GI q141608 186 BLAST score 2.0e-26 E value Match length 112 % identity 65

ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943_pir_ S15655 NCBI Description zein, 19K - maize >gi_22446_emb_CAA3765 $\overline{1}$ _ (X53 $\overline{5}$ 82) $\overline{1}$ 9 kDa

zein [Zea mays]

Seq. No. 299217

LIB3152-029-P1-K1-F11 Seq. ID

BLASTX Method NCBI GI g141597 BLAST score 236 E value 6.0e-20 Match length 68 % identity 72

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) NCBI Description

>gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize >gi 22545 emb CAA24728 (V01481) reading frame zein [2]

[Zea mays]

299218 Seq. No.

LIB3152-029-P1-K1-F4 Seq. ID

Method BLASTX NCBI GI g2832247 BLAST score 367 E value 3.0e-35 Match length 95 % identity 83

(AF031569) 22-kDa alpha zein 10 [Zea mays] NCBI Description

299219 Seq. No.

Seq. ID LIB3152-029-P1-K1-F8

BLASTX Method g2832246 NCBI GI BLAST score 254 5.0e-22 E value



Match length 55 % identity 95

NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 299220

Seq. ID LIB3152-030-P1-K1-C6

Method BLASTX
NCBI GI g224507
BLAST score 249
E value 2.0e-21
Match length 94
% identity 60

NCBI Description zein Al [Zea mays]

Seq. No. 299221

Seq. ID LIB3152-030-P1-K1-D2

Method BLASTN
NCBI GI g168673
BLAST score 90
E value 5.0e-43
Match length 90
% identity 100

NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 299222

Seq. ID LIB3152-030-P1-K1-F8

Method BLASTX
NCBI GI g2832247
BLAST score 192
E value 1.0e-14
Match length 98
% identity 48

NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 299223

Seq. ID LIB3152-031-P1-K1-B2

Method BLASTX
NCBI GI g82696
BLAST score 382
E value 6.0e-37
Match length 82
% identity 90

NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_

(X61121) glycine-rich protein [Zea mays]

Seq. No. 299224

Seq. ID LIB3152-031-P1-K1-B3

Method BLASTN
NCBI GI g168681
BLAST score 86
E value 7.0e-41
Match length 138
% identity 91

NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.

>gi_270686_gb_I03333_ Sequence 8 from Patent US

Seq. No. 299225



```
LIB3152-031-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141605
                  435
BLAST score
                  3.0e-43
E value
                  103
Match length
% identity
                  88
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  299226
Seq. ID
                  LIB3152-031-P1-K1-F12
                  BLASTX
Method
                  a168695
NCBI GI
                  162
BLAST score
                  3.0e-11
E value
Match length
                   43
% identity
                   63
                   (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                  zein gamma [Zea mays]
                  299227
Seq. No.
Seq. ID
                  LIB3152-031-P1-K1-F9
Method
                  BLASTX
NCBI GI
                   g322870
BLAST score
                   532
                   2.0e-61
E value
Match length
                   120
                   99
% identity
                  glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
NCBI Description
                  maize (fragment)
Seq. No.
                   299228
Seq. ID
                   LIB3152-031-P1-K1-G6
Method
                   BLASTN
NCBI GI
                   q168484
BLAST score
                   295
E value
                   1.0e-165
Match length
                   359
                   96
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
Seq. No.
                   299229
                   LIB3152-031-P1-K1-H11
Seq. ID
Method
                   BLASTX
                   g508545
NCBI GI
BLAST score
                   245
                   2.0e-29
E value
Match length
                   98
                   77
% identity
NCBI Description
                  (L34340) zein [Zea mays]
Seq. No.
                   299230
                   LIB3152-031-P1-K1-H4
Seq. ID
                   BLASTX
Method
NCBI GI
```

42065

g168695

NCBI Description

partial



```
BLAST score
                  4.0e-17
E value
Match length
                  37
                  100
% identity
                  (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                  zein gamma [Zea mays]
                  299231
Seq. No.
                  LIB3152-031-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2739333
BLAST score
                  359
E value
                  1.0e-34
                  79
Match length
                  24
% identity
NCBI Description (U74318) polyubiquitin [Schizophyllum commune]
                  299232
Seq. No.
                  LIB3152-032-P1-K1-B12
Seq. ID
                  BLASTX
Method
                  q168691
NCBI GI
                  168
BLAST score
E value
                  6.0e-12
Match length
                  97
                  49
% identity
NCBI Description (M29628) zein [Zea mays]
Seq. No.
                  299233
Seq. ID
                  LIB3152-032-P1-K1-C10
Method
                  BLASTN
NCBI GI
                   q2832242
BLAST score
                  275
                   1.0e-153
E value
Match length
                   351
                   10
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                   299234
Seq. No.
                   LIB3152-032-P1-K1-D3
Seq. ID
                   BLASTN
Method
                   g168675
NCBI GI
BLAST score
                   164
                   3.0e-87
E value
Match length
                   352
                   87
% identity
NCBI Description Maize mutant zein (zE19) gene, complete cds
                   299235
Seq. No.
                   LIB3152-032-P1-K1-F11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2995383
                   80
BLAST score
                   3.0e-37
E value
Match length
                   128
                   92
% identity
```

42066

Zea mays mays mRNA for cytochrome P450 monooxygenase,



```
Seq. No.
                    299236
Seq. ID
                    LIB3152-032-P1-K1-H9
Method
                    BLASTX
                    g100940
NCBI GI
                    264
BLAST score
E value
                    3.0e-23
                    97
Match length
                    63
% identity
NCBI Description zein zA1 - maize
                    299237
Seq. No.
Seq. ID
                    LIB3152-033-P1-K1-A3
                    BLASTX
Method
                    q224508
NCBI GI
                    220
BLAST score
                    7.0e-18
E value
Match length
                    47
% identity
                    98
NCBI Description zein A20 [Zea mays]
                    299238
Seq. No.
                    LIB3152-033-P1-K1-C12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q141617
                    189
BLAST score
                    8.0e-22
E value
                    52
Match length
                    98
% identity
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                    >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                    >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
Seq. No.
                    299239
                    LIB3152-033-P1-K1-C4
Seq. ID
Method
                    BLASTX
NCBI GI
                    q168699
BLAST score
                    318
                    5.0e-43
E value
Match length
                    106
% identity
                    92
NCBI Description (M60836) zein [Zea mays]
                    299240
Seq. No.
                    LIB3152-033-P1-K1-E4
Seq. ID
Method
                    BLASTN
                    g22537
NCBI GI
                    <del>7</del>9
BLAST score
                    8.0e-37
E value
                    111
Match length
% identity
                    61
NCBI Description Maize mRNA for zein polypeptide (clone M6)
```

299241

LIB3152-033-P1-K1-F1

Seq. No.

Seq. ID

```
Method
NCBI GI
                   a168704
BLAST score
                   208
                   1.0e-113
E value
                   215
Match length
                   100
% identity
NCBI Description Zea mays zein protein gene, complete cds
                   299242
Seq. No.
                   LIB3152-033-P1-K1-G1
Seq. ID
Method
                   BLASTX
                   g141617
NCBI GI
BLAST score
                   240
                   3.0e-20
E value
                   58
Match length
                   78
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
                   >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M\overline{1}6460) 16-kDa zein protein [Zea mays]
                   299243
Seq. No.
                   LIB3152-033-P1-K1-G10
Seq. ID
Method
                   BLASTN
                    g22514
NCBI GI
BLAST score
                    132
                    2.0e-68
E value
                    180
Match length
% identity
                    94
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                    299244
Seq. No.
Seq. ID
                    LIB3152-033-P1-K1-G12
                    BLASTX
Method
NCBI GI
                    q2393775
BLAST score
                    435
                    4.0e-43
E value
                    115
Match length
% identity
                    73
                   (U82230) prolamin box binding factor [Zea mays]
NCBI Description
                    299245
Seq. No.
                    LIB3152-033-P1-K1-H2
Seq. ID
Method
                    BLASTN
NCBI GI
                    g168679
BLAST score
                    87
E value
                    2.0e-41
Match length
                    118
                    95
% identity
                    Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
NCBI Description
                    >qi 270687 qb I03334 Sequence 9 from Patent US
```

299246 Seq. No.

LIB3152-033-P1-K1-H8 Seq. ID

BLASTX Method g4185308 NCBI GI



```
BLAST score
                   1.0e-22
E value
                   68
Match length
                   79
% identity
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
                   299247
Seq. No.
                   LIB3152-034-P1-K1-A2
Seq. ID
                   BLASTX
Method
                   g168701
NCBI GI
                   256
BLAST score
                   3.0e-22
E value
                   84
Match length
                   69
% identity
NCBI Description (M60837) zein [Zea mays]
                   299248
Seq. No.
                   LIB3152-034-P1-K1-A5
Seq. ID
                   BLASTX
Method
                   g508545
NCBI GI
BLAST score
                   261
                   2.0e-25
E value
                   135
Match length
                    64
% identity
NCBI Description
                   (L34340) zein [Zea mays]
                   299249
Seq. No.
                   LIB3152-034-P1-K1-A6
Seq. ID
                   BLASTX
Method
                    g141603
NCBI GI
                    251
BLAST score
                    1.0e-28
E value
                    92
Match length
                    89
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                    >gi 72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                    >qi 22529 emb CAA24723 (V01476) zein [Zea mays]
                    299250
Seq. No.
Seq. ID
                    LIB3152-034-P1-K1-B12
                    BLASTX
Method
                    q121472
NCBI GI
                    276
BLAST score
                    2.0e-24
E value
Match length
                    104
 % identity
                    GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) -
                    maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
```

mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

299251 Seq. No.

LIB3152-034-P1-K1-B3 Seq. ID

Method BLASTN NCBI GI g22514

```
BLAST score
                  8.0e-63
E value
Match length
                  183
                  92
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                  299252
Seq. No.
                  LIB3152-034-P1-K1-C6
Seq. ID
                  BLASTX
Method
                  g141608
NCBI GI
                  230
BLAST score
                  2.0e-19
E value
                  62
Match length
                  77
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943_pir__S15655
NCBI Description
                  zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                  zein [Zea mays]
                  299253
Seq. No.
                  LIB3152-034-P1-K1-C7
Seq. ID
                  BLASTX
Method
                   g168701
NCBI GI
BLAST score
                   303
                   1.0e-27
E value
                   73
Match length
                   86
% identity
NCBI Description (M60837) zein [Zea mays]
                   299254
Seq. No.
                   LIB3152-034-P1-K1-D11
Seq. ID
                   BLASTN
Method
                   g168665
NCBI GI
                   238
BLAST score
                   1.0e-131
E value
                   266
Match length
                   97
% identity
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                   299255
Seq. No.
                   LIB3152-034-P1-K1-D7
Seq. ID
                   BLASTX
Method
                   q22216
NCBI GI
BLAST score
                   246
                   6.0e-25
E value
                   100
Match length
% identity
                   69
NCBI Description (X55722) 22kD zein [Zea mays]
                   299256
Seq. No.
                   LIB3152-034-P1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2832243
                   226
BLAST score
                   6.0e-19
E value
```

NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

70

71

Match length % identity



77

Match length % identity

NCBI Description

```
299257
Seq. No.
                  LIB3152-034-P1-K1-D9
Seq. ID
Method
                  BLASTX
                  g100938
NCBI GI
                  216
BLAST score
                  1.0e-17
E value
Match length
                  76
% identity
                  zein precursor - maize >gi 22442 emb CAA32513 (X14335)
NCBI Description
                  zein precursor (AA -21 to 90) [Zea mays]
                  299258
Seq. No.
                  LIB3152-034-P1-K1-E8
Seq. ID
                  BLASTX
Method
                  g118926
NCBI GI
                  274
BLAST score
                  2.0e-24
E value
                  102
Match length
                  50
% identity
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                  >gi_320600_pir__E45509 desiccation-related protein (clone
                  PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
                  dessication-related protein [Craterostigma plantagineum]
                  >gi_227781_prf__1710351E abscisic acid responsive protein E
                   [Craterostigma plantagineum]
                   299259
Seq. No.
                  LIB3152-034-P1-K1-F4
Seq. ID
Method
                  BLASTX
                   g508545
NCBI GI
BLAST score
                   232
                   6.0e-25
E value
Match length
                   104
% identity
                   63
NCBI Description
                  (L34340) zein [Zea mays]
                   299260
Seq. No.
                   LIB3152-034-P1-K1-F6
Seq. ID
Method
                   BLASTN
                   q1276923
NCBI GI
                   39
BLAST score
                   7.0e-13
E value
                   171
Match length
% identity
NCBI Description Zea perennis USDA Ames 21881 ITS1, 5.8S ribosomal RNA, ITS2
                   299261
Seq. No.
                   LIB3152-034-P1-K1-G1
Seq. ID
Method
                   BLASTX
                   q4140644
NCBI GI
BLAST score
                   366
E value
                   5.0e-35
```

(AF090447) 22-kDa zein protein 12 [Zea mays]

Method

NCBI GI

BLASTX

g1351303



```
299262
Seq. No.
                  LIB3152-034-P1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g224507
                  198
BLAST score
                  3.0e-20
E value
                  98
Match length
                  63
% identity
NCBI Description zein Al [Zea mays]
                  299263
Seq. No.
                  LIB3152-034-P1-K1-H7
Seq. ID
                  BLASTX
Method
                  g141607
NCBI GI
BLAST score
                  286
                  8.0e-26
E value
                  66
Match length
                  89
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
NCBI Description
                  >gi_22521_emb_CAA24718_ (V01471) zein [Zea mays] >gi_168672
                   (J01244) zein 19 kd protein (partial) [Zea mays]
                  299264
Seq. No.
                  LIB3152-035-P1-K1-A8
Seq. ID
                  BLASTN
Method
                  g22544
NCBI GI
BLAST score
                   62
                  1.0e-26
E value
                   206
Match length
                  78
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                  299265
Seq. No.
                  LIB3152-035-P1-K1-C7
Seq. ID
                  BLASTX
Method
                   g72307
NCBI GI
                   373
BLAST score
E value
                   8.0e-36
                   115
Match length
                   70
% identity
                  22K zein precursor (clone pZ22.3) - maize >gi 168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   299266
Seq. No.
                   LIB3152-035-P1-K1-C9
Seq. ID
                   BLASTN
Method
                   g22516
NCBI GI
BLAST score
                   50
                   2.0e-19
E value
Match length
                   142
% identity
                   82
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.
                   299267
                   LIB3152-035-P1-K1-D12
Seq. ID
```

BLAST score

E value

434

6.0e-43



```
BLAST score
                  4.0e-17
E value
Match length
                  91
% identity
                  47
                  INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS)
NCBI Description
                  >gi_619732 (U18770) indole-3-glycerol phosphate synthase
                   [Arabidopsis thaliana]
                  299268
Seq. No.
                  LIB3152-035-P1-K1-E5
Seq. ID
                  BLASTN
Method
                  g3342031
NCBI GI
BLAST score
                  53
                  2.0e-21
E value
Match length
                   65
% identity
                   97
                  Oryza sativa 18S small subunit ribosomal RNA gene, complete
NCBI Description
                   sequence
                   299269
Seq. No.
                   LIB3152-035-P1-K1-E7
Seq. ID
Method
                   BLASTX
                   g629861
NCBI GI
BLAST score
                   205
                   1.0e-28
E value
Match length
                   101
% identity
                   66
                   zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
NCBI Description
                   zein Zdl (19 kDa zein) [Zea mays]
                   299270
Seq. No.
                   LIB3152-036-P1-K1-A1
Seq. ID
                   BLASTN
Method
                   g4140643
NCBI GI
                   190
BLAST score
                   1.0e-103
E value
                   206
Match length
                   25
% identity
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   299271
Seq. No.
                   LIB3152-036-P1-K1-A12
Seq. ID
                   BLASTN
Method
                   g22326
NCBI GI
BLAST score
                   67
                   2.0e-29
E value
                   115
Match length
% identity
NCBI Description Z.mays gene for Hageman factor inhibitor
                   299272
Seq. No.
                   LIB3152-036-P1-K1-B4
Seq. ID
                   BLASTX
Method
                   g168701
NCBI GI
```



```
Match length
                   78
% identity .
NCBI Description (M60837) zein [Zea mays]
                   299273
Seq. No.
                   LIB3152-036-P1-K1-E5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g22216
                   177
BLAST score
                   2.0e-13
E value
                   59
Match length
                   64
% identity
NCBI Description (X55722) 22kD zein [Zea mays]
                   299274
Seq. No.
                   LIB3152-036-P1-K1-E7
Seq. ID
                   BLASTX
Method
                   g22216
NCBI GI
BLAST score
                   149
                   5.0e-10
E value
                   85
Match length
                   55
% identity
NCBI Description (X55722) 22kD zein [Zea mays]
                   299275
Seq. No.
                   LIB3152-036-P1-K1-H9
Seq. ID
                   BLASTX
Method
                   g141615
NCBI GI
                   252
BLAST score
                   7.0e-22
E value
Match length
                   78
                   68
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
                   >gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]
                   299276
Seq. No.
                   LIB3152-039-P1-K1-D4
Seq. ID
                   BLASTN
Method
                   g22447
NCBI GI
                   217
BLAST score
                   1.0e-119
E value
                   225
Match length
                    99
% identity
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein
                    299277
Seq. No.
                   LIB3152-039-P1-K1-D7
Seq. ID
                    BLASTX
Method
NCBI GI
                    q141617
                    239
BLAST score
E value
                    3.0e-20
                    107
Match length
                    50
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                    >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
```

>gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]

Seq. No.

Seq. ID



299278



```
>gi 168666 (M16460) 16-kDa zein protein [Zea mays]
```

```
Seq. No.
                  LIB3152-039-P1-K1-F2
Seq. ID
                  BLASTN
Method
                  g168685
NCBI GI
BLAST score
                  117
                  4.0e-59
E value
                  181
Match length
                   94
% identity
NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA
Seq. No.
                   299279
                  LIB3152-039-P1-K1-H4
Seq. ID
Method
                  BLASTN
                   q168484
NCBI GI
                   109
BLAST score
E value
                   2.0e-54
Match length
                   113
                   99
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   299280
Seq. No.
                   LIB3152-040-P1-K1-A10
Seq. ID
                   BLASTX
Method
                   g2832247
NCBI GI
                   235
BLAST score
                   1.0e-19
E value
Match length
                   104
                   52
% identity
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
                   299281
Seq. No.
                   LIB3152-040-P1-K1-C3
Seq. ID
Method
                   BLASTX
                   q141603
NCBI GI
BLAST score
                   483
                   8.0e-49
E value
Match length
                   118
% identity
                   86
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                   >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                   299282
Seq. No.
                   LIB3152-040-P1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q67155
BLAST score
                   345
                   8.0e-33
E value
                   88
Match length
                   84
% identity
                   pyruvate, orthophosphate dikinase (EC 2.7.9.1) precursor -
NCBI Description
                   maize
                   299283
```

42075

LIB3152-040-P1-K1-D8

```
BLASTX
Method
                   g2832246
NCBI GI
BLAST score
                   226
                   8.0e-19
E value
Match length
                   58
                   84
% identity
                   (AF031569) 22-kDa alpha zein 8 [Zea mays]
NCBI Description
                   299284
Seq. No.
                   LIB3152-040-P1-K1-E9
Seq. ID
                   BLASTX
Method
                   g3643809
NCBI GI
                   144
BLAST score
                   4.0e-09
E value
Match length
                   79
% identity
                   42
                   (AF062346) zinc finger protein 216 splice variant 1 [Homo
NCBI Description
                   sapiens] >gi_3643811 (AF062347) zinc finger protein 216
                   splice variant 2 [Homo sapiens] >gi_3668066 (AF062072) zinc
                   finger protein 216 [Homo sapiens]
                   299285
Seq. No.
                   LIB3152-040-P1-K1-F11
Seq. ID
                   BLASTX
Method
                   g141614
NCBI GI
BLAST score
                   205
                   3.0e-16
E value
Match length
                   78
% identity
                   60
                   ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
NCBI Description
                   >gi_82662_pir__B22831 22K zein precursor (clone M1) - maize
                   >gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea
                   mays] >gi224\overline{5}10_prf\overline{1}107201D zein M1 [Zea mays]
                   299286
Seq. No.
                   LIB3152-040-P1-K1-G2
 Seq. ID
                   BLASTN
Method
NCBI GI
                   g22445
                    52
BLAST score
                    1.0e-20
 E value
                    80
Match length
                    91
 % identity
 NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein
                    299287
 Seq. No.
                    LIB3152-040-P1-K1-G3
 Seq. ID
                    BLASTX
 Method
```

Method BLASTX
NCBI GI g141602
BLAST score 149
E value 4.0e-10
Match length 35
% identity 80

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)

>gi 82658_pir A22831 19K zein precursor (clone M6) - maize
>gi 22538_emb_CAA26294_ (X02450) zein precursor [Zea mays]

Seq. No. 299288



```
LIB3152-041-P1-K1-A8
Seq. ID
Method
                  BLASTX
                  q141605
NCBI GI
BLAST score
                  142
                  7.0e-18
E value
                  64
Match length
                  71
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
                  299289
Seq. No.
                  LIB3152-041-P1-K1-B12
Seq. ID
Method
                  BLASTX
                  g22216
NCBI GI
                  230
BLAST score
                   3.0e-19
E value
                   98
Match length
                   53
% identity
                  (X55722) 22kD zein [Zea mays]
NCBI Description
                   299290
Seq. No.
                   LIB3152-041-P1-K1-B2
Seq. ID
                   BLASTX
Method
                   g1742187
NCBI GI
BLAST score
                   177
                   6.0e-13
E value
                   101
Match length
                   41
% identity
                   (D90771) ORF_ID:o260#14; similar to [SwissProt Accession
NCBI Description
                   Number P11666 [Escherichia coli] >gi_1742198_dbj_BAA14933_
                   (D90772) ORF_ID:o260#14; similar to [SwissProt Accession
                   Number P1166\overline{6} [Escherichia coli] >gi_1787591 (AE000231)
                   orf, hypothetical protein [Escherichia coli]
                   299291
Seq. No.
                   LIB3152-041-P1-K1-C5
Seq. ID
Method
                   BLASTX
                   a168701
NCBI GI
BLAST score
                   387
                   2.0e-37
E value
                   111
Match length
% identity
                   77
                  (M60837) zein [Zea mays]
NCBI Description
                   299292
 Seq. No.
                   LIB3152-041-P1-K1-D2
 Seq. ID
                   BLASTX
Method
NCBI GI
                   q224507
                   161
BLAST score
E value
                   5.0e-11
                   123
Match length
```

34 % identity

NCBI Description zein A1 [Zea mays]

299293 Seq. No.

LIB3152-041-P1-K1-F12 Seq. ID

NCBI Description



```
Method
NCBI GI
                     a3063449
BLAST score
                     247
                     4.0e-21
E value
                     56
Match length
                     84
% identity
NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana]
                     299294
Seq. No.
                     LIB3152-041-P1-K1-F2
Seq. ID
Method
                     BLASTX
NCBI GI
                     g3024552
BLAST score
                     237
                     5.0e-20
E value
                     89
Match length
                     64
% identity
                    RAS-RELATED PROTEIN RGP2 (GTP-BINDING REGULATORY PROTEIN
NCBI Description
                     RGP2) >gi_419797_pir__S30273 GTP-binding protein rgp2 -
                     rice >gi 218204 dbj BAA02437 (D13152) GTP binding protein [Oryza sativa] >gi 446772 prf 1912297A rgp2 gene [Oryza
                     sativa]
                     299295
Seq. No.
                     LIB3152-041-P1-K1-G6
Seq. ID
                     BLASTX
Method
NCBI GI
                     q72307
                     213
BLAST score
                     3.0e-17
E value
                     65
Match length
                     69
% identity
                     22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                     (J01246) 26.99 kd zein protein [Zea mays]
                     299296
Seq. No.
                     LIB3152-041-P1-K1-H3
Seq. ID
Method
                     BLASTX
NCBI GI
                     q141617
                     265
BLAST score
E value
                     3.0e-23
Match length
                     48
 % identity
                     ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                     >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
                     >gi_1^{-1}6866\overline{6} (M\overline{1}6460) 16-kDa zein protein [Zea mays]
                      299297
 Seq. No.
                     LIB3152-041-P1-K1-H7
 Seq. ID
 Method
                     BLASTX
 NCBI GI
                      q141617
                      238
 BLAST score
                      4.0e-20
 E value
 Match length
                      81
 % identity
                      59
                     ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
```

42078

>qi 100941 pir S12140 zein Zc1 - maize

>gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays] >gi_168666 (M16460) 16-kDa zein protein [Zea mays]

299298 Seq. No.

LIB3152-042-P1-K1-A1 Seq. ID BLASTX Method

g2832246 NCBI GI 177 BLAST score 7.0e-13 E value 93 Match length 46 % identity

(AF031569) 22-kDa alpha zein 8 [Zea mays] NCBI Description

299299 Seq. No.

LIB3152-042-P1-K1-A10 Seq. ID

BLASTX Method g72307 NCBI GI 216 BLAST score 5.0e-18 E value Match length 51

86 % identity 22K zein precursor (clone pZ22.3) - maize >gi 168686 NCBI Description

(J01246) 26.99 kd zein protein [Zea mays]

299300 Seq. No.

LIB3152-042-P1-K1-B1 Seq. ID

BLASTX Method g141617 NCBI GI 222 BLAST score 3.0e-18 E value 45 Match length 89 % identity

ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) NCBI Description

>gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize

>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays] >qi $^{-}$ 16866 $^{-}$ (M $^{-}$ 16460) 16 $^{-}$ kDa zein protein [Zea mays]

299301 Seq. No.

LIB3152-042-P1-K1-B12 Seq. ID

BLASTX Method g1703108 NCBI GI 418 BLAST score 3.0e-41E value 104 Match length 76 % identity

NCBI Description

ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis

thaliana]

299302 Seq. No.

Seq. ID LIB3152-042-P1-K1-B5

Method BLASTN g22544 NCBI GI



```
BLAST score
                  4.0e-34
E value
Match length
                  243
                  84
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                  299303
Seq. No.
                  LIB3152-042-P1-K1-D3
Seq. ID
                  BLASTX
Method
                  g141597
NCBI GI
                  163
BLAST score
                  3.0e-11
E value
                  63
Match length
% identity
                  60
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                  [Zea mays]
                  299304
Seq. No.
                  LIB3152-042-P1-K1-D6
Seq. ID
                  BLASTX
Method
                  g72307
NCBI GI
BLAST score
                  185
                   6.0e-14
E value
Match length
                   51
                   76
% identity
                  22K zein precursor (clone pZ22.3) - maize >gi 168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   299305
Seq. No.
                   LIB3152-042-P1-K1-F6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168704
                   216
BLAST score
E value
                   1.0e-118
Match length
                   252
% identity
NCBI Description Zea mays zein protein gene, complete cds
                   299306
Seq. No.
                   LIB3152-042-P1-K1-H12
Seq. ID
                   BLASTN
Method
                   g22516
NCBI GI
BLAST score
                   189
                   1.0e-102
E value
                   258
Match length
                   95
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   299307
Seq. No.
                   LIB3152-042-P1-K1-H4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168700
BLAST score
                   154
```

3.0e-81

210

E value Match length



```
% identity
NCBI Description Z.mays zein mRNA, complete cds
                  299308
Seq. No.
                  LIB3152-043-P1-K1-B1
Seq. ID
                  BLASTX
Method
                  g168701
NCBI GI
BLAST score
                  238
                  3.0e-20
E value
                  68
Match length
                  72
% identity
NCBI Description (M60837) zein [Zea mays]
                  299309
Seq. No.
                  LIB3152-043-P1-K1-C8
Seq. ID
                  BLASTN
Method
                  g22518
NCBI GI
                  62
BLAST score
                  2.0e-26
E value
                  134
Match length
                  89
% identity
NCBI Description Zea mays gene encoding a zein gene (clone lambda-ZG99)
                  299310
Seq. No.
                  LIB3152-043-P1-K1-D12
Seq. ID
                  BLASTN
Method
                  g168681
NCBI GI
                  165
BLAST score
                   6.0e-88
E value
                   237
Match length
                   77
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
                   >gi 270686_gb I03333_ Sequence 8 from Patent US
                   299311
Seq. No.
                   LIB3152-043-P1-K1-D3
Seq. ID
                   BLASTN
Method
                   q168679
NCBI GI
                   100
BLAST score
                   5.0e-49
E value
                   302
Match length
                   88
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
                   >gi_270687_gb_I03334_ Sequence 9 from Patent US
                   299312
Seq. No.
 Seq. ID
                   LIB3152-043-P1-K1-D4
                   BLASTN
Method
NCBI GI
                   g16072
BLAST score
                   163
                   8.0e-87
E value
                   219
Match length
 % identity
                   94
NCBI Description Acetabularia mediterranea zein gene
```

299313

LIB3152-043-P1-K1-D5

Seq. No.

Seq. ID



```
BLASTN
Method
                  q4185305
NCBI GI
                  45
BLAST score
                  2.0e-16
E value
                  77
Match length
                  90
% identity
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
                  299314
Seq. No.
                  LIB3152-043-P1-K1-E2
Seq. ID
Method
                  BLASTX
                  g419803
NCBI GI
                  454
BLAST score
                  2.0e-45
E value
                  118
Match length
                  80
% identity
                  zein protein - maize >gi 168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
                  299315
Seq. No.
                  LIB3152-043-P1-K1-G12
Seq. ID
Method
                  BLASTN
                  g535019
NCBI GI
                  55
BLAST score
                   3.0e-22
E value
Match length
                   91
                   46
% identity
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
                   299316
Seq. No.
                  LIB3152-043-P1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g511870
BLAST score
                   206
                   3.0e-16
E value
Match length
                   36
                   100
% identity
                  (M23537) zein protein [Zea mays]
NCBI Description
                   299317
Seq. No.
Seq. ID
                   LIB3152-043-P1-K1-G7
Method
                   BLASTN
NCBI GI
                   q4185305
BLAST score
                   118
                   9.0e-60
E value
Match length
                   238
```

88 % identity

Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 NCBI Description

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

299318 Seq. No.

LIB3152-043-P1-K1-H6 Seq. ID

Method NCBI GI



```
BLASTN
Method
NCBI GI
                    q22540
BLAST score
                    54
                    4.0e-22
E value
                    66
Match length
                    95
% identity
NCBI Description Maize mRNA for 10kDa zein
                    299319
Seq. No.
                    LIB3152-044-P1-K1-A5
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2832247
BLAST score
                    213
                    6.0e-24
E value
                    85
Match length
                    71
% identity
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
                    299320
Seq. No.
                    LIB3152-044-P1-K1-B5
Seq. ID
Method
                    BLASTX
NCBI GI
                    g121472
BLAST score
                    210
E value
                    3.0e-17
Match length
                    67
% identity
                    58
                    GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                     (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                    maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
Seq. No.
                    299321
                    LIB3152-044-P1-K1-B7
Seq. ID
Method
                    BLASTN
NCBI GI
                    q508544
                    90
BLAST score
E value
                    5.0e-43
Match length
                    94
                     99
% identity
                    Zea mays 24-kD alpha-zein gene (floury2), complete cds
NCBI Description
Seq. No.
                     299322
                    LIB3152-044-P1-K1-C11
Seq. ID
Method
                    BLASTX
NCBI GI
                     g16073
BLAST score
                     235
                     6.0e-20
E value
Match length
                     62
% identity
                     81
                    (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                     299323
Seq. No.
                    LIB3152-044-P1-K1-C5
Seq. ID
                    BLASTX
```

42083

g4539660



```
BLAST score
E value
                   3.0e-15
Match length
                   117
% identity
                   36
NCBI Description (AF061282) polyprotein [Sorghum bicolor]
                   299324
Seq. No.
                   LIB3152-044-P1-K1-D2
Seq. ID
                   BLASTX
Method
                   g629862
NCBI GI
                   148
BLAST score
                   2.0e-09
E value
                   78
Match length
% identity
                   51
NCBI Description zein Zd1, 19K - maize >gi_535021_emb_CAA47640_ (X67203)
                   zein Zd1 (19 kDa zein) [Zea mays]
                   299325
Seq. No.
                   LIB3152-044-P1-K1-D9
Seq. ID
                   BLASTN
Method
                   g168673
NCBI GI
                   52
BLAST score
                   8.0e-21
E value
                   136
Match length
% identity
                   85
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
                   299326
Seq. No.
                   LIB3152-044-P1-K1-E2
Seq. ID
Method
                   BLASTN
NCBI GI
                    g168681
BLAST score
                    104
E value
                    2.0e-51
Match length
                    216
% identity
                    87
                   Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                    >gi 270686 gb I03333 Sequence 8 from Patent US
                    299327
Seq. No.
                    LIB3152-044-P1-K1-F12
Seq. ID
Method
                    BLASTX
NCBI GI
                    g141617
BLAST score
                    286
                    1.0e-25
E value
Match length
                    113
                    54
% identity
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                    >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                    >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
```

Seq. No. 299328

Seq. ID LIB3152-044-P1-K1-F5

Method BLASTX
NCBI GI g4140644
BLAST score 342



```
3.0e-32
E value
Match length
                   77
% identity
                   (AF090447) 22-kDa zein protein 12 [Zea mays]
NCBI Description
                   299329
Seq. No.
                   LIB3152-044-P1-K1-G11
Seq. ID
Method
                   BLASTX
                   q141602
NCBI GI
                   202
BLAST score
                   2.0e-23
E value
                   84
Match length
                   66
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
NCBI Description
                   >gi_82658_pir__A22831 19K zein precursor (clone M6) - maize
                   >gi_22538_emb_CAA26294_ (X02450) zein precursor [Zea mays]
                   299330
Seq. No.
                   LIB3152-044-P1-K1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2642636
                   144
BLAST score
                   1.0e-09
E value
Match length
                   42
% identity
                   76
                   (AF032471) ADP-glucose pyrophosphorylase small subunit
NCBI Description
                   [Citrullus lanatus]
                   299331
Seq. No.
                   LIB3152-045-P1-K1-A12
Seq. ID
                   BLASTX
Method
                   q141608
NCBI GI
                   192
BLAST score
E value
                   3.0e-15
                   44
Match length
% identity
                   86
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82)\overline{1}9 kDa
                   zein [Zea mays]
                   299332
Seq. No.
                   LIB3152-045-P1-K1-C12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22514
BLAST score
                   233
                   1.0e-128
E value
Match length
                   289
                   95
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                   299333
Seq. No.
                   LIB3152-045-P1-K1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g508545
                   178
BLAST score
```

6.0e-13

107

E value

Match length

Match length

% identity

112

43



```
% identity
NCBI Description (L34340) zein [Zea mays]
                   299334
Seq. No.
                   LIB3152-045-P1-K1-H11
Seq. ID
                   BLASTN
Method
                   g22516
NCBI GI
BLAST score
                   62
                   2.0e-26
E value
                   174
Match length
                    84
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                    299335
Seq. No.
                   LIB3152-045-P1-K1-H2
Seq. ID
                   BLASTN
Method
                    g22524
NCBI GI
                    72
BLAST score
                    2.0e-32
E value
                    130
Match length
                    93
% identity
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)
                    299336
Seq. No.
                    LIB3152-046-P1-K1-A2
Seq. ID
                    BLASTN
Method
                    q168679
NCBI GI
                    73
BLAST score
                    5.0e-33
E value
                    97
Match length
                    94
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
                    >gi_270687_gb_I03334_ Sequence 9 from Patent US
                    299337
Seq. No.
                    LIB3152-046-P1-K1-E6
Seq. ID
Method
                    BLASTX
                    g121472
NCBI GI
BLAST score
                    185
                    7.0e-14
E value
                    101
Match length
                    39
 % identity
                    GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
 NCBI Description
                     (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                    maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
                    mays] > \overline{gi} \ 1684\overline{8}5 \ (M1\overline{6}066) \ glutelin-2 \ [Zea mays]
                     299338
 Seq. No.
                    LIB3152-046-P1-K1-F1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                     q72307
 BLAST score
                     194
                     6.0e-15
 E value
```





```
NCBI Description
                  22K zein precursor (clone pZ22.3) - maize >gi 168686
                  (J01246) 26.99 kd zein protein [Zea mays]
Seq. No.
                  299339
                  LIB3152-046-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q168701
                  289
BLAST score
                  1.0e-32
E value
```

% identity 75 NCBI Description (M60837) zein [Zea mays]

116

299340 Seq. No. LIB3152-047-P1-K1-A9 Seq. ID Method BLASTN NCBI GI g22524

BLAST score 277 1.0e-154 E value 325 Match length % identity 98

Match length

NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 299341

Seq. ID LIB3152-047-P1-K1-C2

Method BLASTN NCBI GI g22445 141 BLAST score E value 2.0e-73 149 Match length 99 % identity

NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 299342

Seq. ID LIB3152-047-P1-K1-C4

Method BLASTX NCBI GI g508545 BLAST score 176 E value 4.0e-27 Match length 106 % identity 73

NCBI Description (L34340) zein [Zea mays]

Seq. No. 299343

Seq. ID LIB3152-047-P1-K1-D2

Method BLASTX NCBI GI g72307 BLAST score 161 E value 3.0e-21 107 Match length % identity 65

22K zein precursor (clone pZ22.3) - maize >gi 168686 NCBI Description

(J01246) 26.99 kd zein protein [Zea mays]

299344 Seq. No.

Seq. ID LIB3152-047-P1-K1-E7

Method BLASTN



```
NCBI GI
BLAST score
                    94
                    1.0e-45
E value
Match length
                    193
                    93
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                    299345
Seq. No.
                    LIB3152-047-P1-K1-F6
Seq. ID
Method
                    BLASTN
NCBI GI
                    q22522
BLAST score
                    237
E value
                    1.0e-130
                    319
Match length
                    94
% identity
NCBI Description Zea mays gene encoding a zein (clone Z4)
Seq. No.
                    299346
                    LIB3152-048-P1-K1-A11
Seq. ID
Method
                    BLASTX
                    q141617
NCBI GI
                    394
BLAST score
E value
                    2.0e-38
Match length
                    110
% identity
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                    >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                    >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                    299347
Seq. No.
                    LIB3152-048-P1-K1-C3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2832246
                    287
BLAST score
                    1.0e-25
E value
                    96
Match length
% identity
                    65
                    (AF031569) 22-kDa alpha zein 8 [Zea mays]
NCBI Description
                    299348
Seq. No.
                    LIB3152-048-P1-K1-C4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2194132
                    179
BLAST score
                    4.0e-13
 E value
Match length
                    129
 % identity
                    36
                    (AC002062) No definition line found [Arabidopsis thaliana]
 NCBI Description
                    299349
 Seq. No.
                    LIB3152-048-P1-K1-D9
 Seq. ID
                    BLASTX
 Method
                    g100846
 NCBI GI
                     319
 BLAST score
```

1.0e-29

E value



```
89
Match length
                  75
% identity
                  22K zein precursor (clone gZ22.8H3) - maize
NCBI Description
                  >gi 22179 emb_CAA43399_ (X61085) 22 kD alpha-zein [Zea
                  mays]
                  299350
Seq. No.
                  LIB3152-048-P1-K1-F4
Seq. ID
                  BLASTX
Method
                  g4519539
NCBI GI
                  280
BLAST score
                  6.0e-25
E value
                  86
Match length
                  60
% identity
                  (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
NCBI Description
                  domestica]
                  299351
Seq. No.
                  LIB3152-048-P1-K1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168704
                  171
BLAST score
                   2.0e-91
E value
                   351
Match length
                   84
% identity
                  Zea mays zein protein gene, complete cds
NCBI Description
Seq. No.
                   299352
                   LIB3152-048-P1-K1-H12
Seq. ID
                   BLASTX
Method
                   g141605
NCBI GI
BLAST score
                   202
                   4.0e-16
E value
                   80
Match length
                   59
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
                   299353
Seq. No.
                   LIB3152-048-P1-K1-H4
Seq. ID
                   BLASTX
Method
                   g168695
NCBI GI
                   262
BLAST score
                   3.0e-23
E value
Match length
                   67
                   69
% identity
                   (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                   zein gamma [Zea mays]
Seq. No.
                   299354
                   LIB3152-048-P1-K1-H9
Seq. ID
```

Method BLASTX
NCBI GI g141603
BLAST score 452
E value 4.0e-45
Match length 95



```
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLOÑE A20)
NCBI Description
                  >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                  299355
Seq. No.
                  LIB3152-049-P1-K1-C1
Seq. ID
Method
                  BLASTN
                  g168694
NCBI GI
BLAST score
                  110
                  6.0e-55
E value
                  162
Match length
                  92
% identity
NCBI Description Maize gamma zein mRNA, partial cds
                  299356
Seq. No.
                  LIB3152-049-P1-K1-C2
Seq. ID
Method
                  BLASTX
                  q141607
NCBI GI
BLAST score
                  272
                  5.0e-24
E value
Match length
                  66
% identity
                  82
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
NCBI Description
                  >gi 22521 emb CAA24718 (V01471) zein [Zea mays] >gi_168672
                  (J01244) zein 19 kd protein (partial) [Zea mays]
                  299357
Seq. No.
                  LIB3152-049-P1-K1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168681
BLAST score
                  292
                  1.0e-163
E value
Match length
                  371
% identity
                  97
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                  >gi 270686 gb I03333 Sequence 8 from Patent US
                  299358
Seq. No.
Seq. ID
                  LIB3152-049-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  g22537
BLAST score
                  69
                  1.0e-30
E value
Match length
                  125
                  90
% identity
NCBI Description Maize mRNA for zein polypeptide (clone M6)
                  299359
Seq. No.
Seq. ID
                  LIB3152-049-P1-K1-H6
Method
                  BLASTN
```

NCBI GI g168480 BLAST score 78 7.0e-36 E value Match length 146 88 % identity

NCBI Description Maize embryo globulin S allele (7S-like) mRNA, complete cds



```
299360
Seq. No.
                  LIB3152-049-P1-K1-H9
Seq. ID
Method
                  BLASTX
                  g141597
NCBI GI
                  150
BLAST score
                   3.0e-10
E value
                   37
Match length
% identity
                   81
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   299361
Seq. No.
                   LIB3152-050-P1-K1-B3
Seq. ID
Method
                   BLASTX
                   g141617
NCBI GI
BLAST score
                   317
                   2.0e-29
E value
Match length
                   107
                   59
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
                   >gi_100945_pir___B29017 zein 2 - maize
                                           (X53515) zein Zc1 [Zea mays]
                   >gi 22515 emb CAA37595
                   >gi^{-}16866\overline{6} (M\overline{1}6460) 16-kDa zein protein [Zea mays]
                   299362
Seq. No.
                   LIB3152-050-P1-K1-D10
Seq. ID
                   BLASTN
Method
                   g2832242
NCBI GI
                   196
BLAST score
                   1.0e-106
E value
                   322
Match length
                   11
% identity
                   Zea mays 22-kDa alpha zein gene cluster, complete sequence
NCBI Description
                   299363
Seq. No.
                   LIB3152-050-P1-K1-E5
Seq. ID
                   BLASTN
Method
                   g535019
NCBI GI
                   73
BLAST score
                   3.0e-33
E value
                   85
Match length
                    48
% identity
                  Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
NCBI Description
                    299364
Seq. No.
                   LIB3152-050-P1-K1-F4
Seq. ID
Method
                    BLASTN
                    q22548
NCBI GI
                    194
BLAST score
                    1.0e-105
E value
                    194
Match length
                    100
 % identity
NCBI Description Maize chimeric zein/beta-phaseolin gene 3'end region
```

NCBI GI

g168701

```
Seq. No.
                  299365
Seq. ID
                  LIB3152-050-P1-K1-G5
                  BLASTN
Method
                  g535019
NCBI GI
BLAST score
                  52
                  1.0e-20
E value
Match length
                  76
% identity
                  46
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
Seq. No.
                  299366
                  LIB3152-050-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2911059
BLAST score
                  162
E value
                  3.0e-11
Match length
                  75
                  45
% identity
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                  299367
Seq. ID
                  LIB3152-050-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  g22514
BLAST score
                  116
E value
                  1.0e-58
Match length
                  228
% identity
                  89
NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)
                  299368
Seq. No.
                  LIB3152-051-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g168691
                  274
BLAST score
                  2.0e-24
E value
                  82
Match length
% identity
                  65
NCBI Description
                  (M29628) zein [Zea mays]
                  299369
Seq. No.
Seq. ID
                  LIB3152-051-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g141606
BLAST score
                  315
E value
                  4.0e-29
Match length
                  112
% identity
                  62
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
NCBI Description
                  >gi 72309 pir ZIZMD1 19K zein precursor (clone cZ19D1) -
                  maize >gi 168682 (M12144) 19 kDa zein protein [Zea mays]
Seq. No.
                  299370
Seq. ID
                  LIB3152-051-P1-K1-C11
Method
                  BLASTX
```



```
BLAST score
E value
                   9.0e-28
                  93
Match length
                  72
% identity
                  (M60837) zein [Zea mays]
NCBI Description
                  299371
Seq. No.
                  LIB3152-051-P1-K1-C12
Seq. ID
Method
                  BLASTX
                  g2832243
NCBI GI
BLAST score
                  184
                  2.0e-25
E value
Match length
                  98
% identity
                  73
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                  299372
Seq. No.
                  LIB3152-051-P1-K1-C2
Seq. ID
Method
                  BLASTN
                  g22549
NCBI GI
BLAST score
                  94
                  2.0e-45
E value
Match length
                  260
% identity
                  84
NCBI Description Maize gene for a 27kDa storage protein, zein
Seq. No.
                  299373
                  LIB3152-051-P1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                   118
                   7.0e-60
E value
Match length
                  226
% identity
                   12
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                   299374
Seq. ID
                   LIB3152-051-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q141597
BLAST score
                   258
                   2.0e-22
E value
Match length
                   96
% identity
                   62
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi 22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
Seq. No.
                   299375
                   LIB3152-051-P1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832243
BLAST score
                   198
E value
                   3.0e-15
Match length
                   104
```

54

% identity



```
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                  299376
Seq. No.
                  LIB3152-051-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141604
BLAST score
                  231
                  2.0e-19
E value
                  89
Match length
                  58
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
                  >gi 72310_pir__ZIZM91 19K zein precursor (clone cZ19C1) -
                  maize >qi 168678 (M12146) 19 kDa zein protein [Zea mays]
                  299377
Seq. No.
                  LIB3152-051-P1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q224513
                  145
BLAST score
                  2.0e-11
E value
                  74
Match length
                  61
% identity
NCBI Description
                  zein M6 [Zea mays]
                  299378
Seq. No.
                  LIB3152-053-P1-K1-A8
Seq. ID
Method
                  BLASTN
                  q168681
NCBI GI
BLAST score
                   39
                  5.0e-13
E value
                  115
Match length
                  83
% identity
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                  >gi 270686 gb I03333 Sequence 8 from Patent US
Seq. No.
                   299379
Seq. ID
                  LIB3152-053-P1-K1-B1
Method
                  BLASTX
NCBI GI
                   q22220
BLAST score
                   249
E value
                   1.0e-21
Match length
                   70
                   76
% identity
NCBI Description
                  (X55723) 22 kD zein [Zea mays]
                   299380
Seq. No.
Seq. ID
                   LIB3152-053-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   q141601
BLAST score
                   237
                   6.0e-20
E value
Match length
                   63
                   76
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                   >gi 82657 pir S03417 19K zein precursor (clone gZ19AB11) -
                   maize >gi 22543 emb CAA29340 (X05911) 19 kd alpha zein (AA
```

1 - 234) [Zea mays]

Method

NCBI GI BLAST score BLASTN g168661

96

```
o. 299
```

```
Seq. No.
                  299381
                  LIB3152-053-P1-K1-B9
Seq. ID
Method
                  BLASTN
                  a340933
NCBI GI
                  37
BLAST score
                  9.0e-12
E value
Match length
                  77
                  87
% identity
NCBI Description Zea mays 10-kDa zein gene, complete cds
                  299382
Seq. No.
Seq. ID
                  LIB3152-053-P1-K1-D12
Method
                  BLASTX
                  q168703
NCBI GI
                  205
BLAST score
                  1.0e-16
E value
Match length
                  55
% identity
                  76
NCBI Description (M86591) 22 kDa zein protein [Zea mays]
                  299383
Seq. No.
                  LIB3152-053-P1-K1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168484
BLAST score
                  115
E value
                  4.0e-58
Match length
                  166
                  94
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                  299384
Seq. No.
                  LIB3152-053-P1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                  159
E value
                  2.0e-84
Match length
                  191
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  299385
                  LIB3152-053-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3790102
BLAST score
                  276
E value
                  2.0e-26
Match length
                   110
% identity
                   57
NCBI Description
                  (AF095521) pyrophosphate-dependent phosphofructokinase
                  alpha subunit [Citrus X paradisi]
                  299386
Seq. No.
Seq. ID
                  LIB3152-053-P1-K1-G4
```

```
E value 2.0e-46
Match length 308
% identity 91
```

NCBI Description Maize 15 kDa zein mRNA, clone cZ15A3, complete cds

Seq. No. 299387

Seq. ID LIB3152-054-P1-K1-A10

Method BLASTN
NCBI GI g2393774
BLAST score 197
E value 1.0e-107
Match length 269
% identity 94

NCBI Description Zea mays endosperm-specific prolamin box binding factor

(PBF) mRNA, complete cds

Seq. No. 299388

Seq. ID LIB3152-054-P1-K1-B2

Method BLASTX
NCBI GI g629861
BLAST score 289
E value 4.0e-26
Match length 85
% identity 74

NCBI Description zein Zdl, 19K - maize >gi_535020_emb_CAA47639_ (X67203)

zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 299389

Seq. ID LIB3152-054-P1-K1-B6

Method BLASTN
NCBI GI g4140643
BLAST score 73
E value 4.0e-33
Match length 133
% identity 36

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 299390

Seq. ID LIB3152-054-P1-K1-C8

Method BLASTN
NCBI GI g22445
BLAST score 142
E value 4.0e-74
Match length 310
% identity 86

NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 299391

Seq. ID LIB3152-054-P1-K1-D9

Method BLASTN
NCBI GI g22516
BLAST score 72
E value 1.0e-32
Match length 128
% identity 89

NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

NCBI Description

mays]



```
299392
Seq. No.
                   LIB3152-054-P1-K1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g168699
BLAST score
                   564
E value
                   3.0e-58
Match length
                   123
% identity
NCBI Description (M60836) zein [Zea mays]
Seq. No.
                   299393
Seq. ID
                   LIB3152-054-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q141608
BLAST score
                   195
E value
                   3.0e-15
Match length
                   47
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82)\overline{1}9 kDa
                   zein [Zea mays]
Seq. No.
                   299394
                   LIB3152-054-P1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q531829
BLAST score
                   156
E value
                   5.0e-11
Match length
                   61
                   59
% identity
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
Seq. No.
                   299395
                   LIB3152-054-P1-K1-F2
Seq. ID
Method
                   BLASTX
                   q141608
NCBI GI
                   223
BLAST score
                   3.0e-18
E value
                   56
Match length
% identity
                   86
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                   zein [Zea mays]
                   299396
Seq. No.
                   LIB3152-054-P1-K1-F3
Seq. ID
                   BLASTX
Method
                   q419803
NCBI GI
                   275
BLAST score
                   1.0e-24
E value
                   89
Match length
                   57
% identity
```

zein protein - maize >gi_168705 (M72708) zein protein [Zea

Seq. ID

Method



```
Seq. No.
Seq. ID
                  LIB3152-054-P1-K1-G6
Method
                  BLASTN
                  q22514
NCBI GI
                  205
BLAST score
E value
                  1.0e-111
Match length
                  312
% identity
                  92
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                  299398
Seq. No.
                  LIB3152-054-P1-K1-G7
Seq. ID
Method
                  BLASTX
                  g141615
NCBI GI
BLAST score
                   171
                   2.0e-12
E value
Match length
                   56
                   71
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
                   >gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]
                   299399
Seq. No.
                   LIB3152-054-P1-K1-G9
Seq. ID
Method
                   BLASTX
                   g141605
NCBI GI
BLAST score
                   317
                   2.0e-29
E value
                   90
Match length
                   78
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize > gi_168\overline{68}0 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                   299400
                   LIB3152-054-P1-K1-H2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22540
BLAST score
                   137
E value
                   3.0e-71
Match length
                   156
                   98
% identity
NCBI Description Maize mRNA for 10kDa zein
                   299401
Seq. No.
                   LIB3152-054-P1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141616
BLAST score
                   380
                   9.0e-37
E value
Match length
                   84
% identity
                   81
                   ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                   >gi_168662 (M12147) 15 kDa zein protein [Zea mays]
                   299402
Seq. No.
```

42098

LIB3152-056-P1-K1-B3

BLASTN

```
q168675
NCBI GI
                  246
BLAST score
                  1.0e-136
E value
Match length
                  336
% identity
                  94
NCBI Description Maize mutant zein (zE19) gene, complete cds
                  299403
Seq. No.
                  LIB3152-056-P1-K1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168681
BLAST score
                  227
E value
                  1.0e-125
Match length
                  320
% identity
                  93
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                  >gi_270686_gb_I03333_ Sequence 8 from Patent US
Seq. No.
                  299404
Seq. ID
                  LIB3152-056-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  q22514
BLAST score
                  293
E value
                  1.0e-164
Match length
                  335
                  97
% identity
NCBI Description, Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.
                  299405
Seq. ID
                  LIB3152-056-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g168664
BLAST score
                  233
E value
                  2.0e-19
Match length
                  90
% identity
                  53
NCBI Description
                  (M13507) zein protein precursor [Zea mays]
Seq. No.
                  299406
Seq. ID
                  LIB3152-057-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  g22537
BLAST score
                  54
E value
                   6.0e-22
Match length
                  142
% identity
                  85
NCBI Description Maize mRNA for zein polypeptide (clone M6)
Seq. No.
                  299407
Seq. ID
                  LIB3152-057-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q2832246
BLAST score
                  224
                  7.0e-19
E value
Match length
                  102
% identity
                   61
```

NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

```
Seq. No.
                  299408
                  LIB3152-057-P1-K1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g662367
BLAST score
                  83
                  6.0e-39
E value
Match length
                  159
                  88
% identity
NCBI Description
                  Zea mays farnesyl pyrophosphate synthetase (fps) mRNA,
                  complete cds
Seq. No.
                  299409
Seq. ID
                  LIB3152-057-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q168699
BLAST score
                  223
                  2.0e-18
E value
Match length
                   68
                   68
% identity
NCBI Description
                  (M60836) zein [Zea mays]
Seq. No.
                   299410
Seq. ID
                  LIB3152-057-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  q535019
BLAST score
                   64
E value
                   2.0e-27
Match length
                  .96
                   37
% identity
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
Seq. No.
                   299411
Seq. ID
                  LIB3152-057-P1-K1-B10
Method
                  BLASTX
                   q141603
NCBI GI
BLAST score
                   144
                   6.0e-09
E value
Match length
                   52
                   73
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                   >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                   299412
Seq. No.
Seq. ID
                   LIB3152-057-P1-K1-B2
Method
                   BLASTX
                   g141605
NCBI GI
BLAST score
                   215
                   1.0e-17
E value
Match length
                   68
                   66
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
```

Seq. No. 299413

maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]



```
LIB3152-057-P1-K1-B3
Seq. ID
Method
                  BLASTX
                  q508545
NCBI GI
                  229
BLAST score
                  6.0e-19
E value
Match length
                  95
                  57
% identity
NCBI Description (L34340) zein [Zea mays]
                  299414
Seq. No.
                  LIB3152-057-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q224514
BLAST score
                  225
                  1.0e-18
E value
Match length
                  63
                  76
% identity
NCBI Description zein M8 [Zea mays]
                  299415
Seq. No.
                  LIB3152-057-P1-K1-B7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q629861
BLAST score
                  225
                  1.0e-18
E value
Match length
                  79
                  61
% identity
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
                  299416
Seq. No.
                  LIB3152-057-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168484
BLAST score
                  147
E value
                  5.0e-77
Match length
                  159
                  98
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                  299417
Seq. No.
                  LIB3152-057-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g168699
BLAST score
                  393
                  3.0e-38
E value
Match length
                  102
% identity
                  79
NCBI Description (M60836) zein [Zea mays]
                   299418
Seq. No.
Seq. ID
                  LIB3152-057-P1-K1-C4
                  BLASTX
Method
                  g168699
NCBI GI
                  185
BLAST score
```

3.0e-14

73

E value Match length



```
% identity
NCBI Description
                  (M60836) zein [Zea mays]
                  299419
Seq. No.
                  LIB3152-057-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q72307
BLAST score
                   336
                  2.0e-31
E value
Match length
                  113
% identity
                   65
NCBI Description
                  22K zein precursor (clone pZ22.3) - maize >gi_168686
                   (J01246) 26.99 kd zein protein [Zea mays]
                  299420
Seq. No.
                  LIB3152-057-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141603
BLAST score
                   235
                  8.0e-20
E value
Match length
                  81
% identity
                   68
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                  >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
Seq. No.
                   299421
                  LIB3152-057-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g168701
BLAST score
                   150
E value
                   6.0e-10
Match length
                   74
% identity
                   49
NCBI Description
                  (M60837) zein [Zea mays]
Seq. No.
                   299422
Seq. ID
                  LIB3152-057-P1-K1-C8
Method
                  BLASTX
NCBI GI
                   q82659
BLAST score
                   294
                   1.0e-26
E value
Match length
                   75
                  79
% identity
                  19K zein precursor (clone Z4) - maize
NCBI Description
                  >gi_4388702_emb_CAA24719_ (V01472) zein [Zea mays]
Seq. No.
                   299423
Seq. ID
                  LIB3152-057-P1-K1-D1
Method
                  BLASTN
NCBI GI
                   g22528
BLAST score
                   117
E value
                   3.0e-59
                  292
Match length
                  85
% identity
```

NCBI Description Zea mays mRNA encoding a zein (clone A20)

Method

NCBI GI

BLAST score

BLASTX

257

g141617



```
Seq. No.
Seq. ID
                  LIB3152-057-P1-K1-D10
                  BLASTX
Method
                  g168693
NCBI GI
BLAST score
                  359
E value
                  3.0e - 34
Match length
                  114
% identity
                  67
NCBI Description (M29627) zein [Zea mays]
                  299425
Seq. No.
Seq. ID
                  LIB3152-057-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  g2828011
BLAST score
                  46
E value
                  5.0e-17
Match length
                  102
% identity
                  86
                  Zea mays starch synthase I precursor (Ss1) mRNA, nuclear
NCBI Description
                  gene encoding plastid protein, complete cds
Seq. No.
                  299426
Seq. ID
                  LIB3152-057-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q141616
BLAST score
                  316
E value
                  4.0e-29
Match length
                  93
% identity
                  68
                  ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                  >gi_168662 (M12147) 15 kDa zein protein [Zea mays]
Seq. No.
                  299427
Seq. ID
                  LIB3152-057-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q168703
BLAST score
                  221
                  4.0e-18
E value
Match length
                  56
                  79
% identity
NCBI Description (M86591) 22 kDa zein protein [Zea mays]
Seq. No.
                  299428
Seq. ID
                  LIB3152-057-P1-K1-E12
                  BLASTX
Method
NCBI GI
                  g2832243
BLAST score
                  152
                  2.0e-10
E value
Match length
                  42
                  67
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.
                  299429
Seq. ID
                  LIB3152-057-P1-K1-E2
```



```
E value
Match length
                   108
                   52
% identity
NCBI Description
```

ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)

>gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]

>gi 168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299430

Seq. ID LIB3152-057-P1-K1-E3

Method BLASTN NCBI GI g168679 BLAST score 47 2.0e-17 E value Match length 127 % identity 84

NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.

>gi 270687 gb I03334 Sequence 9 from Patent US

Seq. No. 299431

Seq. ID LIB3152-057-P1-K1-E4

Method BLASTX NCBI GI g224508 BLAST score 273 E value 2.0e-24 Match length 79 76 % identity

NCBI Description zein A20 [Zea mays]

299432 Seq. No.

Seq. ID LIB3152-057-P1-K1-E5

Method BLASTX NCBI GI q22216 BLAST score 271 4.0e-24 E value 67 Match length 79 % identity

NCBI Description (X55722) 22kD zein [Zea mays]

299433 Seq. No.

Seq. ID LIB3152-057-P1-K1-F11

Method BLASTX NCBI GI g399414 BLAST score 159 E value 4.0e-11 Match length 39 85 % identity

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_322865_pir__JC1454 translation elongation factor eEF-1

alpha chain - wheat >gi_170776 (M90077) translation elongation factor 1 alpha-subunit [Triticum aestivum]

>gi_949878_emb_CAA90651_ (Z50789) elongation factor 1-alpha

[Hordeum vulgare]

Seq. No. 299434

Seq. ID LIB3152-057-P1-K1-F3

```
Method
                   BLASTX
NCBI GI
                  q16073
BLAST score
                  175
                   9.0e-13
E value
Match length
                   64
                   61
% identity
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
Seq. No.
                   299435
Seq. ID
                  LIB3152-057-P1-K1-F4
Method
                  BLASTX
NCBI GI
                   q2832243
BLAST score
                   167
                   1.0e-11
E value
                   90
Match length
                   44
% identity
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
                   299436
Seq. No.
Seq. ID
                  LIB3152-057-P1-K1-F7
Method
                  BLASTX
NCBI GI
                   q2832243
BLAST score
                   203
E value
                   4.0e-16
                   81
Match length
                   59
% identity
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
Seq. No.
                   299437
Seq. ID
                   LIB3152-057-P1-K1-F8
Method
                   BLASTN
NCBI GI
                   g2832242
BLAST score
                   38
                   3.0e-12
E value
Match length
                   173
% identity
                   81
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                   299438
                   LIB3152-057-P1-K1-H10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168673
BLAST score
                   50
E value
                   2.0e-19
                   70
Match length
% identity
                   93
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
                   299439
Seq. No.
Seq. ID
                   LIB3153-004-Q1-K1-E5
                   BLASTN
Method
                   q22516
NCBI GI
BLAST score
                   51
                   4.0e-20
E value
Match length
                   143
                   84
% identity
```

NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)



```
Seq. No.
                   299440
                   LIB3153-005-Q1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g70774
BLAST score
                   273
                   2.0e-24
E value
                   55
Match length
                   100
% identity
                   histone H4 (TH091) - wheat >gi_170747 (M12277) histone H4
NCBI Description
                   [Triticum aestivum]
Seq. No.
                   299441
Seq. ID
                   LIB3153-005-Q1-K1-E4
Method
                   BLASTX
                   q119355
NCBI GI
BLAST score
                   192
E value
                   3.0e-15
                   39
Match length
                   97
% identity
                   ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                    (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                   >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
                    [Zea mays]
                   299442
Seq. No.
Seq. ID
                   LIB3153-005-Q1-K1-E8
Method
                   BLASTN
NCBI GI
                   g459896
BLAST score
                   54
                   7.0e-22
E value
Match length
                   86
% identity
                   91
NCBI Description Zea mays triosephosphate isomerase 1 gene, exon
Seq. No.
                   299443
                   LIB3153-005-Q1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                    q1084481
BLAST score
                    262
                   2.0e-23
E value
                   57
Match length
% identity
                    89
NCBI Description heat shock protein 70 - Maize
Seq. No.
                    299444
                   LIB3153-005-Q1-K1-G8
Seq. ID
                   BLASTN
Method
NCBI GI
                    q168500
BLAST score
                    51
                    4.0e-20
E value
                    83
Match length
                    90
% identity
NCBI Description Maize (Zea mays) histone H4 gene (H4C14), complete cds
```

299445

Seq. No.



```
LIB3153-006-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q129916
                  204
BLAST score
                  2.0e-16
E value
Match length
                  51
% identity
                  82
                  PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY
NCBI Description
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                  >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
Seq. No.
                  299446
                  LIB3153-006-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  a3746060
BLAST score
                  215
E value
                  3.0e-17
Match length
                  72
                  58
% identity
NCBI Description
                  (AC005311) unknown protein [Arabidopsis thaliana]
                  299447
Seq. No.
Seq. ID
                  LIB3153-007-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  q141608
BLAST score
                  192
                  2.0e-19
E value
Match length
                  66
% identity
                  83
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
NCBI Description
                  zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                  zein [Zea mays]
Seq. No.
                  299448
                  LIB3153-008-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115371
BLAST score
                  275
                  8.0e-25
E value
Match length
                  76
% identity
                  75
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                  299449
Seq. No.
Seq. ID
                  LIB3153-009-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g119355
BLAST score
                  240
                  7.0e-21
E value
                  47
Match length
                  100
% identity
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                  >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
```

[Zea mays]

4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase



```
Seq. No.
                   299450
Seq. ID
                  LIB3153-009-Q1-K1-G11
Method
                   BLASTX
NCBI GI
                   q3445207
BLAST score
                   345
E value
                   9.0e-33
Match length
                   101
% identity
NCBI Description
                  (AC004786) unknown protein [Arabidopsis thaliana]
Seq. No.
                   299451
Seq. ID
                  LIB3153-010-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                   q3128177
BLAST score
                   230
E value
                   3.0e-19
Match length
                   94
                   52
% identity
NCBI Description
                  (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  299452
Seq. ID
                  LIB3153-010-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q3914368
BLAST score
                   313
E value
                   3.0e-29
Match length
                   69
% identity
                   77
NCBI Description
                  GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
                  >gi_167519 (M80571) glycerol-3-phosphate acyltransferase
                   [Cucumis sativus] >gi_444331_prf__1906380A glycerol
                  phosphate acyltransferase [Cucumis sativus]
Seq. No.
                   299453
Seq. ID
                  LIB3153-011-Q1-K1-A4
Method
                  BLASTN
NCBI GI
                  q474009
BLAST score
                  54
                   6.0e-22
E value
Match length
                  110
% identity
                  87
NCBI Description Rice mRNA, partial homologous to ribosomal protein S19 gene
Seq. No.
                  299454
Seq. ID
                  LIB3153-011-Q1-K1-C4
Method
                  BLASTX
                  g3128231
                  202
                  8.0e-16
Match length
                  134
                  12
```

NCBI GI BLAST score E value

% identity

(AC004077) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi_3337370 (AC004481) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 299455

Seq. No.

Seq. ID

Method

299460

BLASTN

LIB3153-013-Q1-K1-D7



```
LIB3153-011-Q1-K1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3150406
BLAST score
                  242
                  1.0e-20
E value
Match length
                  97
% identity
                  48
                   (AC004165) putative indole-3-acetate
NCBI Description
                  beta-glucosyltransferase [Arabidopsis thaliana]
                  299456
Seq. No.
Seq. ID
                  LIB3153-011-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1362009
BLAST score
                  390
                  6.0e-38
E value
Match length
                  85
% identity
                  50
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana
                  299457
Seq. No.
Seq. ID
                  LIB3153-011-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g2982259
BLAST score
                  327
E value
                   9.0e-31
Match length
                  74
% identity
                  82
                  (AF051212) probable 60s ribosomal protein L13a [Picea
NCBI Description
                  mariana]
                  299458
Seq. No.
Seq. ID
                  LIB3153-012-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  q1169476
BLAST score
                  566
                  2.0e-58
E value
Match length
                  116
% identity
                  93
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                  ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
Seq. No.
                  299459
Seq. ID
                  LIB3153-012-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  q3135274
BLAST score
                  323
                  5.0e-30
E value
Match length
                  102
                  59
% identity
                  (AC003058) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                  thaliana]
```



```
NÇBI GI
                  q3821780
BLAST score
E value
                  8.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  299461
Seq. No.
                  LIB3154-001-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169475
BLAST score
                  665
E value
                  8.0e-74
                  146
Match length
                  99
% identity
                  ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION
NCBI Description
                  FACTOR TU) (EF-TU) >gi 556301 (M22432) elongation factor Tu
                  [Mus musculus]
                  299462
Seq. No.
                  LIB3154-001-Q1-K1-A2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g163349
BLAST score
                  33
                  4.0e-09
E value
Match length
                  33
                  100
% identity
NCBI Description Bovine MHC class I BoLA gene, complete cds, clone BL3-6
                  299463
Seq. No.
                  LIB3154-001-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501654
BLAST score
                  701
E value
                  3.0e-74
Match length
                  152
% identity
                  88
NCBI Description VILLIN >gi 202366 (M98454) villin [Mus musculus]
                  299464
Seq. No.
                  LIB3154-001-Q1-K1-B10
Seq. ID
Method
                  BLASTX
                  g3068759
NCBI GI
BLAST score
                  232
                  2.0e-19
E value
Match length
                  50
% identity
                  92
NCBI Description (AF059185) Mi-2 [Xenopus laevis]
                  299465
Seq. No.
Seq. ID
                  LIB3154-001-Q1-K1-B11
Method
                  BLASTN
NCBI GI
                  g353
BLAST score
                  173
                  8.0e-93
E value
```

197

97

Match length % identity



NCBI Description Bovine mRNA encoding fibromodulin

299466 Seq. No. LIB3154-001-Q1-K1-B3 Seq. ID Method BLASTN q2981246 NCBI GI

BLAST score 40

4.0e-13 E value 52 Match length 94 % identity

Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC NCBI Description

library) contains Bmx gene, complete sequence [Homo

sapiens]

Seq. No.

299467 LIB3154-001-Q1-K1-B6 Seq. ID

Method BLASTN NCBI GI g163460 BLAST score 123 E value 4.0e-63 Match length 127 99 % identity

NCBI Description Bovine osteonectin mRNA, complete cds

Seq. No. 299468

LIB3154-001-Q1-K1-C10 Seq. ID

Method BLASTX NCBI GI q4506515 BLAST score 541 2.0e-55 E value Match length 115 91 % identity

regulator of G-protein signalling 1 NCBI Description

>gi_728728_sp_Q08116_RGS1_HUMAN REGULATOR OF G-PROTEIN SIGNALING 1 (RGS1) (EARLY RESPONSE PROTEIN 1R20) (B-CELL ACTIVATION PROTEIN BL34) >gi_631051_pir__S43436 B-cell activation protein 1r20 - human >gi_313215_emb_CAA51826_

(X73427) 1r20 [Homo sapiens]

Seq. No. 299469

Seq. ID LIB3154-001-Q1-K1-C11

Method BLASTX NCBI GI g4503483 BLAST score 650 2.0e-68 E value Match length 128 % identity

NCBI Description eukaryotic translation elongation factor 2

>gi 119172 sp P13639 EF2 HUMAN ELONGATION FACTOR 2 (EF-2) >gi_2144947_pir_EFHU2 translation elongation factor eEF-2
- human >gi_31106_emb_CAA35829_(X51466) elongation factor 2 [Homo sapiens] >gi_31108_emb_CAA77750_ (Z11692) human

elongation factor 2 [Homo sapiens]

Seq. No. 299470

Seq. ID LIB3154-001-Q1-K1-C12

BLASTX Method



```
NCBI GI
                  q3242231
BLAST score
                  155
                  3.0e-10
E value
                  33
Match length
                  88
% identity
                  (AJ006486) RNA binding protein [Mus musculus]
NCBI Description
                  299471
Seq. No.
                  LIB3154-001-Q1-K1-C3
Seq. ID
Method
                  BLASTN
                  g1276618
                  34
```

NCBI GI BLAST score E value 8.0e-10 Match length 98 84 % identity

Bos taurus clone 14 immunoqlobulin lambda light chain NCBI Description

variable region (Vlambdalb) mRNA, partial cds

Seq. No. 299472

LIB3154-001-Q1-K1-C5 Seq. ID

Method BLASTN NCBI GI q1848270 BLAST score 55 E value 5.0e-22 Match length 83 % identity 92

Human calcium and integrin binding protein CIB mRNA, NCBI Description

complete cds

299473 Seq. No.

LIB3154-001-Q1-K1-C6 Seq. ID

Method BLASTX NCBI GI g2460124 BLAST score 609 E value 1.0e-63 Match length 126 % identity

(AF017789) putative transcription factor CA150 [Homo NCBI Description

sapiens]

Seq. No. 299474

Seq. ID LIB3154-001-Q1-K1-D1

Method BLASTX NCBI GI g4557387 BLAST score 702 2.0e-74 E value Match length 147 % identity 82

complement component 7 precursor NCBI Description

>gi_116610_sp_P10643_CO7_HUMAN_COMPLEMENT_COMPONENT_C7 PRECURSOR >gi_87197_pir__A27340 complement_C7 precursor human >gi 179716 (J03507) complement protein C7 precursor

[Homo sapiens]

299475 Seq. No.

Seq. ID LIB3154-001-Q1-K1-D10

BLASTX Method

```
NCBI GI
                   q2494890
BLAST score
                   485
                   6.0e-49
E value
                   87
Match length
                   100
% identity
                   CORONIN-LIKE PROTEIN P57 >gi 2136796 pir__S65666 p57
NCBI Description
                   protein - bovine >gi_927647_dbj_BAA07939_ (D44496) bovine
                   p57 [Bos taurus]
                   299476
Seq. No.
                   LIB3154-001-Q1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1665859
                   470
BLAST score
                   2.0e-47
E value
                   92
Match length
                   93
% identity
NCBI Description (Y09205) MHC class I molecule [Bos taurus]
                   299477
Seq. No.
                   LIB3154-001-Q1-K1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3688100
BLAST score
                   85
                   6.0e-40
E value
Match length
                   417
                   87
% identity
                   Homo sapiens chromosome 17, clone hRPK.178 C 3, complete
NCBI Description
                   sequence [Homo sapiens]
                   299478
Seq. No.
                   LIB3154-001-Q1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3820482
BLAST score
                   260
E value
                   2.0e-22
Match length
                   55
                   93
% identity
                   (AF032922) syntaxin 4 binding protein UNC-18c [Homo
NCBI Description
                   sapiens]
                   299479
Seq. No.
Seq. ID
                   LIB3154-001-Q1-K1-D7
Method
                   BLASTX
NCBI GI
                   g123332
BLAST score
                   700
E value
                   4.0e-74
Match length
                   137
% identity
                   HYDROXYMETHYLGLUTARYL-COA SYNTHASE, CYTOPLASMIC (HMG-COA
NCBI Description
                   SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
                   >gi_90200_pir__A25332 hydroxymethylglutaryl-CoA synthase
(EC 4.1.3.5) - Chinese hamster >gi_387072 (L00334)
```

Seq. No. 299480

[Mesocricetus auratus]

3-hydroxy-3-methylglutaryl coenzyme A synthase (HMG CoA)



```
LIB3154-001-Q1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2134796
                  260
BLAST score
                  2.0e-22
E value
Match length
                  57
% identity
                  84
                  B cell activation protein BL34 - human
NCBI Description
                  >gi_299705_bbs_129951 (S59049) BL34=B cell activation gene
                  [human, Peptide, 196 aa] [Homo sapiens]
Seq. No.
                  299481
Seq. ID
                  LIB3154-001-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  q731046
BLAST score
                  605
E value
                  5.0e-63
Match length
                  126
% identity
                  89
                  PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN
NCBI Description
                  THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE)
                  (DEUBIQUITINATING ENZYME) (KIAA0055)
                  >gi 473945 dbj BAA06225 (D29956) This gene is similar to
                  tre oncogene (X63547). [Homo sapiens]
                  299482
Seq. No.
                  LIB3154-001-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g399012
BLAST score
                  618
                  2.0e-64
E value
Match length
                  121
% identity
                  100
                  ADP, ATP CARRIER PROTEIN, ISOFORM T2 (ADP/ATP TRANSLOCASE 3)
NCBI Description
                  (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
                  >gi 280900 pir B43646 ADP, ATP carrier protein T2 - bovine
                  >qi 529417 (M24103) translocase [Bos taurus]
                  299483
Seq. No.
Seq. ID
                  LIB3154-001-Q1-K1-E3
                  BLASTN
Method
NCBI GI
                  g2582198
BLAST score
                  45
                  4.0e-16
E value
Match length
                  57
                  95
% identity
                  Bos taurus locus UW76 polymorphic microsatellite
NCBI Description
                  299484
Seq. No.
                  LIB3154-001-Q1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g178996
```

NCBI GI g178996
BLAST score 99
E value 3.0e-48
Match length 195
% identity 89

NCBI Description Human arginine-rich nuclear protein mRNA, complete cds

% identity

95

```
299485
Seq. No.
                   LIB3154-001-Q1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2353754
BLAST score
                   315
                   6.0e-29
E value
Match length
                   125
                   51
% identity
NCBI Description (AF015504) immunoglobulin variable region [Bos taurus]
Seq. No.
                   299486
                   LIB3154-001-Q1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3914346
BLAST score
                   500
E value
                   1.0e-50
Match length
                   108
                   87
% identity
                   POLYMERIC-IMMUNOGLOBULIN RECEPTOR PRECURSOR (PLGR)
NCBI Description
                   [CONTAINS: SECRETORY COMPONENT] >gi 388280 (L04797)
                   polymeric immunoglobulin receptor [Bos taurus]
                   >gi 1095524 prf 2109248A polymeric Ig receptor [Bos
                   taurus]
Seq. No.
                   299487
Seq. ID
                   LIB3154-001-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   g120742
BLAST score
                   406
                   7.0e-41
E value
Match length
                   114
% identity
                   80
                   GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (PHOSPHOGLUCOSE
NCBI Description
                   ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI)
                   >gi_68446_pir__NUPG glucose-6-phosphate isomerase (EC
5.3.1.9) - pig >gi_2043_emb_CAA30295_ (X07382) muscle
                   phosphohexose isomerase (AA 1 - 558) [Sus scrofa]
                   299488
Seq. No.
                   LIB3154-001-Q1-K1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g432627
BLAST score
                   567
                   2.0e-60
E value
                   149
Match length
% identity
                   81
                   (X62917) anti-testosterone antibody [Bos taurus]
NCBI Description
                   299489
Seq. No.
Seq. ID
                   LIB3154-001-Q1-K1-F12
                   BLASTX
Method
                   g4240299
NCBI GI
BLAST score
                   723
                   8.0e-77
E value
Match length
                   149
```





NCBI Description (AB020712) KIAA0905 protein [Homo sapiens]

Seq. No. 299490

Seq. ID LIB3154-001-Q1-K1-F3

Method BLASTX
NCBI GI g3915129
BLAST score 652
E value 2.0e-68
Match length 150
% identity 86

NCBI Description TRANSMEMBRANE PROTEIN TMP21 PRECURSOR (INTEGRAL MEMBRANE

PROTEIN P23) >gi_1370279_emb_CAA66947_ (X98303) transmembrane protein [Oryctolagus cuniculus]

Seq. No. 299491

Seq. ID LIB3154-001-Q1-K1-F4

Method BLASTX
NCBI GI g2146954
BLAST score 411
E value 3.0e-40
Match length 151
% identity 60

NCBI Description hevin precursor - human >gi_758066_emb_CAA57650_ (X82157)

hevin [Homo sapiens]

Seq. No. 299492

Seq. ID LIB3154-001-Q1-K1-F7

Method BLASTN
NCBI GI g2864757
BLAST score 112
E value 5.0e-56
Match length 313
% identity 88

NCBI Description Bos taurus gene for MHC class I heavy chain, partial cds,

clone 303F.10g

Seq. No. 299493

Seq. ID LIB3154-001-Q1-K1-F9

Method BLASTN
NCBI GI g3360459
BLAST score 91
E value 1.0e-43
Match length 297
% identity 87

NCBI Description Homo sapiens clone 24733 mRNA sequence

Seq. No. 299494

Seq. ID LIB3154-001-Q1-K1-G1

Method BLASTX
NCBI GI g1905974
BLAST score 333
E value 4.0e-31
Match length 78
% identity 82

NCBI Description (U80628) thymidine kinase 2 isoform B [Homo sapiens]

Seq. No. 299495



```
LIB3154-001-Q1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1374680
BLAST score
                  315
E value
                  1.0e-177
Match length
                  315
% identity
                  100
NCBI Description Bovine mRNA for invariant chain, complete cds
Seq. No.
                  299496
Seq. ID
                  LIB3154-001-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  q1209255
BLAST score
                  351
                  3.0e - 33
E value
Match length
                  71
                  92
% identity
NCBI Description
                   (L20311) immunoglobulin J-chain [Bos taurus] >gi 1408167
                   (U02301) immunoglobulin J chain [Bos taurus]
                  299497
Seq. No.
                  LIB3154-001-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2429083
BLAST score
                  469
E value
                  5.0e-47
                  89
Match length
                  96
% identity
NCBI Description
                  (D89730) T16 [Rattus rattus]
Seq. No.
                  299498
Seq. ID
                  LIB3154-001-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1345649
BLAST score
                  253
E value
                  1.0e-27
Match length
                  89
% identity
                  71
NCBI Description
                  PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR
                  >qi 71411 pir CGHU4B collagen alpha 1(IV) chain precursor
                   - human >gi 180803 (M26576) alpha-1 type IV collagen [Homo
                   sapiens]
Seq. No.
                  299499
Seq. ID
                  LIB3154-001-Q1-K1-G7
                  BLASTX
Method
NCBI GI
                  g547902
BLAST score
                  185
E value
                  1.0e-13
                  50
Match length
                   68
% identity
```

PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 NCBI Description

> (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) >gi_422794_pir__JX0235 core protein MGC-24 - human >gi_219925_dbj_BAAO3130_ (D14043) MGC-24 precursor

[Homo sapiens]

```
Seq. No.
                   299500
Seq. ID
                   LIB3154-001-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   q2088714
BLAST score
                   269
E value
                   1.0e-23
Match length
                   147
                   37
% identity
                   (AF003139) strong similarity to NADPH oxidases; partial
NCBI Description
                   CDS, the gene begins in the neighboring clone
                   [Caenorhabditis elegans]
Seq. No.
                   299501
                  LIB3154-001-Q1-K1-H12
Seq. ID
                  BLASTN
```

299502

299503

299504

Method BLASTN
NCBI GI g181154
BLAST score 136
E value 2.0e-70
Match length 200

% identity

Seq. No.

Seq. No.

NCBI Description Human casein kinase II beta subunit mRNA, complete cds

Seq. ID LIB3154-001-Q1-K1-H5
Method BLASTX
NCBI GI g3831588
BLAST score 208
E value 4.0e-17
Match length 55
% identity 75

NCBI Description (AF064741) carboxylesterase [Sus scrofa]

NCBI Description Homo sapiens mRNA for KIAA0719 protein, complete cds

Seq. No. Seq. ID

LIB3154-001-Q1-K1-H8

Method BLASTX
NCBI GI g128905
BLAST score 211
E value 9.0e-17
Match length 45
% identity 100

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 9 KD SUBUNIT PRECURSOR

(COMPLEX I-9KD) (CI-9KD) >gi_108827_pir__S15107 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 10K chain - bovine

>gi_220_emb_CAA41775_ (X59048) NADH dehydrogenase

(ubiquinone) [Bos taurus]

Seq. No. 299505

% identity

NCBI Description

59



```
Seq. ID
                    LIB3154-002-Q1-K1-C1
Method
                    BLASTX
NCBI GI
                    g141601
BLAST score
                    343
E value
                    3.0e-32
Match length
                    137
% identity
                    58
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                    >gi_82657_pir__S03417 19K zein precursor (clone gZ19AB11) -
maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA
                    1 - 234) [Zea mays]
Seq. No.
                    299506
Seq. ID
                    LIB3154-003-Q1-K1-D1
Method
                    BLASTX
NCBI GI
                    q419803
BLAST score
                    204
E value
                    3.0e-16
Match length
                    95
% identity
                    44
NCBI Description
                    zein protein - maize >gi 168705 (M72708) zein protein [Zea
Seq. No.
                    299507
Seq. ID
                    LIB3154-003-Q1-K1-E2
Method
                    BLASTX
NCBI GI
                    q141612
BLAST score
                    165
E value
                    1.0e-11
Match length
                    62
% identity
                    60
                    ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)
NCBI Description
                    >gi 72306 pir ZIZMC2 22K zein precursor (clone cZ22C2) -
                    maize (fragment) >gi 168688 (M12141) 22 kDa zein protein
                    [Zea mays]
Seq. No.
                    299508
Seq. ID
                    LIB3154-003-Q1-K1-F8
Method
                    BLASTN
NCBI GI
                    g22531
BLAST score
                    147
                    5.0e-77
E value
                    350
Match length
                    86
% identity
                    Zea mays mRNA encoding a zein (clone pZ22.1)
NCBI Description
                    >gi_270688_gb_I03336_Sequence 10 from Patent US 4885357
>gi_270741_gb_I03273_Sequence 2 from Patent US
                    299509
Seq. No.
Seq. ID
                    LIB3154-004-Q1-K1-A9
                    BLASTX
Method
NCBI GI
                    g168699
BLAST score
                    192
E value
                    1.0e-14
Match length
                    85
```

42119

(M60836) zein [Zea mays]



```
Seq. No.
                   299510
Sea. ID
                   LIB3154-004-Q1-K1-B1
Method
                   BLASTN
NCBI GI
                   q22544
BLAST score
                   215
E value
                   1.0e-117
                   303
Match length
                   93
% identity
NCBI Description
Seq. No.
                   299511
```

Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. ID LIB3154-004-Q1-K1-B12 Method BLASTX a971143 NCBI GI 149 BLAST score 4.0e-10 E value Match length 55 % identity 60

(D63842) modified alpha peptide of E. coli NCBI Description beta-galactosidase [Cloning vector pKF298]

>gi_971155_dbj_BAA09909_ (D63846) modified alpha peptide of

E. coli beta-galactosidase [Cloning vector pKF18k]

>gi_3953639_dbj_BAA34741_ (AB019603) beta-galactosidase

alpha-peptide [Cloning vector pKF28wt]

>gi 3953643 dbj BAA34744 (AB019604) beta-galactosidase

alpha-peptide [Cloning vector pKF28ts1]

>gi_3953647_dbj_BAA34747_ (AB019605) beta-galactosidase

alpha-peptide [Cloning vector pKF28ts5]

Seq. No. 299512

Seq. ID LIB3154-004-Q1-K1-B7

Method BLASTN NCBI GI g2832242 BLAST score 35 3.0e-10 E value Match length 63 89 % identity

Zea mays 22-kDa alpha zein gene cluster, complete sequence NCBI Description

299513 Seq. No.

Seq. ID LIB3154-004-Q1-K1-D7

BLASTX Method NCBI GI q121472 BLAST score 167 1.0e-11 E value Match length 101 % identity 40

GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) NCBI Description

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>qi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) maize >qi 22289 emb CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea

mays] >gi $1684\overline{8}5$ (M1 $\overline{6}066$) glutelin-2 [Zea mays]

Seq. No. 299514

Seq. ID LIB3154-004-Q1-K1-E5

```
Method
                     q141614
NCBI GI
BLAST score
                     144
                     4.0e-09
E value
Match length
                     63
                     51
% identity
                     ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
NCBI Description
                    >gi_82662_pir__B22831 22K zein precursor (clone M1) - maize
>gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea
mays] >gi_224510_prf__1107201D zein M1 [Zea mays]
Seq. No.
                     299515
Seq. ID
                     LIB3154-004-Q1-K1-E9
Method
                     BLASTX
NCBI GI
                     q2832243
                     354
BLAST score
                     1.0e-33
E value
Match length
                     116
% identity
                     65
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.
                     299516
Seq. ID
                     LIB3154-004-Q1-K1-F4
Method
                     BLASTX
NCBI GI
                     q168699
BLAST score
                     306
                     5.0e-28
E value
Match length
                     83
% identity
                     80
NCBI Description (M60836) zein [Zea mays]
                     299517
Seq. No.
Seq. ID
                     LIB3154-004-Q1-K1-G1
Method
                     BLASTX
NCBI GI
                     g141608
BLAST score
                     274
                     1.0e-29
E value
                     107
Match length
% identity
                     71
                     ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943_pir__S15655
NCBI Description
                     zein, 19K - maize >gi 22446 emb CAA3765\overline{1} (X53\overline{5}82) 19 kDa
                     zein [Zea mays]
                     299518
Seq. No.
Seq. ID
                     LIB3154-005-Q1-K1-A1
                     BLASTN
Method
NCBI GI
                     g22514
BLAST score
                     58
                     5.0e-24
E value
                     190
Match length
                     83
% identity
```

NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299519

Seq. ID LIB3154-005-Q1-K1-A2

Method BLASTN NCBI GI g168690

```
BLAST score 91
E value 1.0e-43
Match length 91
% identity 100
```

NCBI Description Maize zein mRNA, complete cds, clone ZG124 Seq. No. 299520

 Seq. ID
 LIB3154-005-Q1-K1-A6

 Method
 BLASTX

 NCBI GI
 g82660

 BLAST score
 286

 E value
 1.0e-25

Match length 104 % identity 60

NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment) >gi 809117 emb CAA24720_ (V01473) zein [Zea mays]

Seq. No. 299521

Seq. ID LIB3154-005-Q1-K1-B11

Method BLASTX
NCBI GI g419803
BLAST score 226
E value 4.0e-19
Match length 62
% identity 69

NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea

mays]

Seq. No. 299522

Seq. ID LIB3154-005-Q1-K1-B6

Method BLASTX
NCBI GI g168664
BLAST score 209
E value 1.0e-16
Match length 110
% identity 47

NCBI Description (M13507) zein protein precursor [Zea mays]

Seq. No. 299523

Seq. ID LIB3154-005-Q1-K1-C5

Method BLASTX
NCBI GI g168699
BLAST score 468
E value 5.0e-47
Match length 132
% identity 77

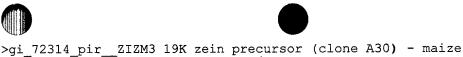
NCBI Description (M60836) zein [Zea mays]

Seq. No. 299524

Seq. ID LIB3154-005-Q1-K1-E8

Method BLASTX
NCBI GI g141597
BLAST score 396
E value 1.0e-38
Match length 105
% identity 78

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)



>qi 22545 emb CAA24728 (V01481) reading frame zein [2]

```
[Zea mays]
                  299525
Seq. No.
Seq. ID
                  LIB3154-005-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g100925
BLAST score
                  203
E value
                  3.0e-16
Match length
                  67
% identity
                  55
                  zein, 27K - maize (fragment) >gi 22550 emb CAA41175
NCBI Description
                   (X58197) 27kDa storage protein, zein [Zea mays]
                  299526
Seq. No.
Seq. ID
                  LIB3154-005-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2262105
                  186
BLAST score
                  6.0e-14
E value
                  74
Match length
% identity
                  49
NCBI Description
                  (AC002343) unknown protein [Arabidopsis thaliana]
                  299527
Seq. No.
                  LIB3154-005-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q168699
BLAST score
                  202
E value
                  9.0e-16
Match length
                  60
                  72
% identity
NCBI Description
                  (M60836) zein [Zea mays]
Seq. No.
                  299528
                  LIB3154-005-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q531829
BLAST score
                  185
E value
                   5.0e-14
Match length
                  81
% identity
                   51
NCBI Description
                   (U12390) beta-galactosidase alpha peptide [cloning vector
                  pSport1]
Seq. No.
                  299529
Seq. ID
                  LIB3154-005-Q1-K1-H9
Method
                  BLASTN
NCBI GI
                  g22537
BLAST score
                  127
```

Seq. No. 299530

E value Match length

% identity

2.0e-65

NCBI Description Maize mRNA for zein polypeptide (clone M6)

175 68



```
LIB3154-006-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                  g82660
NCBI GI
                  190
BLAST score
                   6.0e-18
E value
Match length
                   91
% identity
                   62
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi 809117 emb CAA24720_ (V01473) zein [Zea mays]
                  299531
Seq. No.
                  LIB3154-006-Q1-K1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                   q168704
                  87
BLAST score
                  3.0e-41
E value
Match length
                   161
% identity
                   91
NCBI Description Zea mays zein protein gene, complete cds
                   299532
Seq. No.
Seq. ID
                  LIB3154-006-Q1-K1-E5
Method
                  BLASTX
                   g224508
NCBI GI
BLAST score
                   360
                   2.0e-34
E value
Match length
                   103
                   75
% identity
NCBI Description zein A20 [Zea mays]
                   299533
Seq. No.
                   LIB3154-007-Q1-K1-C1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q168425
BLAST score
                   187
                   1.0e-101
E value
                   215
Match length
                   97
% identity
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds
                   299534
Seq. No.
Seq. ID
                   LIB3154-007-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   g141603
BLAST score
                   418
                   4.0e-41
E value
Match length
                   115
                   79
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >qi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                   >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                   299535
```

Seq. ID LIB3154-007-Q1-K1-D6

Method BLASTX NCBI GI g224508 BLAST score 338



```
E value
                   8.0e-32
Match length
                   81
% identity
```

NCBI Description zein A20 [Zea mays]

299536 Seq. No.

Seq. ID LIB3154-007-Q1-K1-E3

Method BLASTX NCBI GI q419803 196 BLAST score E value 2.0e-15 Match length 80 % identity 53

zein protein - maize >gi_168705 (M72708) zein protein [Zea NCBI Description

mays]

299537 Seq. No.

Seq. ID LIB3154-007-Q1-K1-E6

Method BLASTX g168691 NCBI GI BLAST score 273 3.0e-24E value Match length 99 % identity 58

NCBI Description (M29628) zein [Zea mays]

299538 Seq. No.

LIB3154-007-Q1-K1-E8 Seq. ID

Method BLASTX g121472 NCBI GI BLAST score 140 4.0e-18 E value 69 Match length % identity 68

GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) NCBI Description

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 299539

Seq. ID LIB3154-007-Q1-K1-E9

Method BLASTN NCBI GI g4140643 BLAST score 71 9.0e-32 E value Match length 231 % identity 58

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

299540 Seq. No.

Seq. ID LIB3154-007-Q1-K1-F6

Method BLASTX NCBI GI g141617 356 BLAST score



```
E value
                   106
Match length
% identity
                   62
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
                   >gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                   >gi^{-}16866\overline{6} (M\overline{1}6460) 16-kDa zein protein [Zea mays]
Seq. No.
                   299541
                   LIB3154-007-Q1-K1-G1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q22516
                   111
BLAST score
E value
                   1.0e-55
Match length
                   219
                   88
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   299542
Seq. No.
                   LIB3154-007-Q1-K1-G6
Seq. ID
                   BLASTN
Method
NCBI GI
                   q168665
BLAST score
                    162
                    5.0e-86
E value
                    346
Match length
                    87
% identity
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
Seq. No.
                    299543
                   LIB3154-008-Q1-K1-B12
Seq. ID
Method
                   BLASTN
NCBI GI
                    g168690
BLAST score
                    43
E value
                    4.0e-15
                    91
Match length
% identity
                    87
NCBI Description Maize zein mRNA, complete cds, clone ZG124
                    299544
Seq. No.
                    LIB3154-010-Q1-K1-A7
Seq. ID
                    BLASTN
Method
                    g535019
NCBI GI
                    43
BLAST score
                    6.0e-15
E value
                    53
Match length
                    48
% identity
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
                    299545
Seq. No.
Seq. ID
                    LIB3154-010-Q1-K1-B1
```

BLASTN Method NCBI GI g168673 156 BLAST score 2.0e-82 E value 189 Match length % identity 97



NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. LIB3154-010-Q1-K1-B6 Seq. ID BLASTX Method g141608 NCBI GI BLAST score 143 5.0e-09 E value 46 Match length 63 % identity

ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943_pir_ S15655 NCBI Description zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa

zein [Zea mays]

299547 Seq. No.

LIB3154-010-Q1-K1-C3 Seq. ID

Method BLASTX NCBI GI g2832243 203 BLAST score 7.0e-16 E value 40 Match length 100 % identity

NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

299548 Seq. No.

LIB3154-010-Q1-K1-F5 Seq. ID

BLASTX Method q1182065 NCBI GI BLAST score 198 3.0e-15 E value 53 Match length 77 % identity

NCBI Description (X55661) 22 kD zein [Zea mays]

299549 Seq. No.

LIB3154-010-Q1-K1-F6 Seq. ID

Method BLASTN NCBI GI q168690 BLAST score 54 2.0e-21 E value 62 Match length % identity 98

NCBI Description Maize zein mRNA, complete cds, clone ZG124

299550 Seq. No.

Seq. ID LIB3154-010-Q1-K1-G5

Method BLASTX NCBI GI q508545 BLAST score 168 7.0e-12 E value 49 Match length 73 % identity

NCBI Description (L34340) zein [Zea mays]

299551 Seq. No.

Seq. ID LIB3154-010-Q1-K1-H8

BLASTX Method

```
NCBI GI
BLAST score
                  192
E value
                  1.0e-14
Match length
                   49
                  76
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
Seq. No.
                   299552
Seq. ID
                  LIB3154-011-Q1-K1-C12
Method
                  BLASTN
NCBI GI
                  q1037129
BLAST score
                   308
                   1.0e-173
E value
                   392
Match length
% identity
                   95
                   (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
Seq. No.
                   299553
Seq. ID
                  LIB3154-011-Q1-K1-D4
Method
                  BLASTX
                   q82654
NCBI GI
BLAST score
                   161
                   2.0e-11
E value
Match length
                   53
% identity
                   60
                   10K zein precursor - maize >gi 22541 emb CAA30409_ (X07535)
NCBI Description
                   10kDa zein (AA 1 - 150) [Zea mays]
Seq. No.
                   299554
Seq. ID
                   LIB3154-011-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   q141608
                   251
BLAST score
                   2.0e-21
E value
Match length
                   103
% identity
                   54
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                   zein [Zea mays]
                   299555
Seq. No.
Seq. ID
                   LIB3154-011-Q1-K1-G7
Method
                   BLASTX
NCBI GI
                   g141601
```

BLAST score 168 7.0e-12 E value 66 Match length 62 % identity

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11) NCBI Description

>gi 82657 pir S03417 19K zein precursor (clone gZ19AB11) maize >gi 22543 emb CAA29340 (X05911) 19 kd alpha zein (AA

1 - 234) [Zea mays]

BLAST score

E value Match length 278 9.0e-25

108



```
Seq. No.
                  299556
Seq. ID
                  LIB3154-013-Q1-K1-A1
Method
                  BLASTN
NCBI GI
                  g22514
BLAST score
                   69
E value
                  1.0e-30
Match length
                  264
                  81
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.
                  299557
Seq. ID
                  LIB3154-013-Q1-K1-B12
Method
                  BLASTN
NCBI GI
                  q22514
BLAST score
                   67
E value
                  2.0e-29
Match length
                  255
% identity
                  82
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.
                  299558
Seq. ID
                  LIB3154-013-Q1-K1-B6
Method
                  BLASTN
NCBI GI
                  q1061304
BLAST score
                   54
E value
                  7.0e-22
Match length
                  142
                   85
% identity
NCBI Description
                  Z.mays ZSF4C5 gene for zein
                   299559
Seq. No.
Seq. ID
                  LIB3154-013-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                   g2832247
BLAST score
                   267
E value
                   2.0e-23
Match length
                   87
% identity
                   66
NCBI Description
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
                   299560
Seq. No.
Seq. ID
                  LIB3154-013-Q1-K1-C7
Method
                   BLASTN
NCBI GI
                   g22514
BLAST score
                   252
E value
                   1.0e-139
Match length
                   340
% identity
                   94
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                   299561
Seq. No.
Seq. ID
                  LIB3154-013-Q1-K1-E1
                  BLASTX
Method
NCBI GI
                   g419803
```



```
% identity
                  zein protein - maize >gi 168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
                  299562
Seq. No.
                  LIB3154-013-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4519539
BLAST score
                  207
                  2.0e-16
E value
Match length
                  86
% identity
                  52
NCBI Description
                  (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
                  domestica]
                  299563
Seq. No.
                  LIB3154-013-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141603
BLAST score
                  476
E value
                  6.0e-48
Match length
                  119
                  85
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                  >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
Seq. No.
                  299564
Seq. ID
                  LIB3154-014-Q1-K1-B2
Method
                  BLASTN
NCBI GI
                  g168652
BLAST score
                  114
                  2.0e-57
E value
Match length
                  261
% identity
                  90
                  Maize amyloplast-specific transit protein (waxy; wx+
NCBI Description
                  locus), complete cds
Seq. No.
                  299565
Seq. ID
                  LIB3154-014-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q567893
BLAST score
                  176
E value
                   6.0e-13
Match length
                  79
                  48
% identity
NCBI Description
                  (L37382) beta-galactosidase-complementation protein
                   [Cloning vector]
Seq. No.
                  299566
                  LIB3154-014-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g168701
```

Method BLASTX
NCBI GI g168701
BLAST score 167
E value 4.0e-12
Match length 66
% identity 59



```
NCBI Description (M60837) zein [Zea mays]
Seq. No.
                  299567
                  LIB3154-014-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q567893
BLAST score
                  157
                  1.0e-10
E value
Match length
                  77
                  45
% identity
NCBI Description (L37382) beta-galactosidase-complementation protein
                  [Cloning vector]
Seq. No.
                  299568
                  LIB3154-014-Q1-K1-D7
Seq. ID
                  BLASTX
Method
                  g168701
NCBI GI
                  464
BLAST score
E value
                  1.0e-46
Match length
                  111
                  87
% identity
NCBI Description (M60837) zein [Zea mays]
                  299569
Seq. No.
Seq. ID
                  LIB3154-014-Q1-K1-E10
Method
                  BLASTX
                  g168691
NCBI GI
                  240
BLAST score
                  1.0e-20
E value
Match length
                  86
% identity
                  62
NCBI Description (M29628) zein [Zea mays]
Seq. No.
                  299570
                  LIB3154-014-Q1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22447
                  101
BLAST score
                  9.0e-50
E value
Match length
                  116
                  97
% identity
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein
                  299571
Seq. No.
Seq. ID
                  LIB3154-014-Q1-K1-H1
Method
                  BLASTN
NCBI GI
                  q4185305
BLAST score
                  85
E value
                  4.0e-40
Match length
                  317
% identity
                  82
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
```

Seq. No. 299572

cds; and unknown genes



```
LIB3154-014-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q168664
BLAST score
                  308
                  2.0e-28
E value
                  78
Match length
% identity
                  78
                  (M13507) zein protein precursor [Zea mays]
NCBI Description
                  299573
Seq. No.
                  LIB3154-014-Q1-K1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168665
                  81
BLAST score
E value
                  5.0e-38
                  109
Match length
                  95
% identity
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                  299574
Seq. No.
                  LIB3156-001-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g72287
BLAST score
                  528
                  5.0e-54
E value
Match length
                  117
                  90
% identity
NCBI Description
                  beta-globulin A precursor (clone 94) - upland cotton
                   (fragment) >gi 167377 (M16905) legumin precursor [Gossypium
                  hirsutum]
Seq. No.
                  299575
                  LIB3156-001-Q1-K1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2642323
BLAST score
                  38
E value
                  3.0e-12
Match length
                  46
                  96
% identity
NCBI Description Zea mays profilin (PRO4) mRNA, complete cds
                  299576
Seq. No.
                  LIB3156-001-Q1-K1-A9
Seq. ID
Method
                  BLASTX
                  g1561774
NCBI GI
                  504
BLAST score
                  3.0e-51
E value
Match length
                  109
% identity
                  85
                  (U67426) malate dehydrogenase [Vitis vinifera]
NCBI Description
                  299577
Seq. No.
Seq. ID
                  LIB3156-001-Q1-K1-B12
                  BLASTX
Method
```

Method BLASTX
NCBI GI g4588906
BLAST score 167
E value 4.0e-12



Match length 65 % identity 58

NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]

Seq. No. 299578

Seq. ID LIB3156-001-Q1-K1-C10

Method BLASTX
NCBI GI g131015
BLAST score 469
E value 4.0e-47
Match length 112
% identity 73

NCBI Description PATHOGENESIS-RELATED PROTEIN R MAJOR FORM PRECURSOR

(THAUMATIN-LIKE PROTEIN E22) >gi_100385_pir__JH0230

pathogenesis-related protein R precursor - common tobacco >gi_19855_emb_CAA33293_ (X15224) thaumatin-like protein [Nicotiana tabacum] >gi_19980_emb_CAA31235_ (X12739) pathogenesis-related protein R (AA 1 - 226) [Nicotiana

tabacum]

Seq. No. 299579

Seq. ID LIB3156-001-Q1-K1-C11

Method BLASTX
NCBI GI g3850999
BLAST score 245
E value 8.0e-21
Match length 79
% identity 71

NCBI Description (AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1

[Zea mays]

Seq. No. 299580

Seq. ID LIB3156-001-Q1-K1-D10

Method BLASTX
NCBI GI g1350956
BLAST score 230
E value 2.0e-19
Match length 62
% identity 85

NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No. 299581

Seq. ID LIB3156-001-Q1-K1-D9

Method BLASTX
NCBI GI g2618721
BLAST score 155
E value 3.0e-10
Match length 70
% identity 46

NCBI Description (U49072) IAA16 [Arabidopsis thaliana]

Seq. No. 299582

Seq. ID LIB3156-001-Q1-K1-F9

Method BLASTX NCBI GI g1419370 BLAST score 302 E value 2.0e-27



Match length 70 % identity 84 NCBI Description (X97726) actin depolymerizing factor [Zea mays]

 Seq. No.
 299583

 Seq. ID
 LIB3156-001-Q1-K1-G9

 Method
 BLASTX

 NCBL CI
 62462927

NCBI GI g2462927 BLAST score 241 E value 2.0e-20 Match length 90 % identity 53

NCBI Description (Y10342) putative amidase [Arabidopsis thaliana]

Seq. No. 299584

Seq. ID LIB3156-001-Q1-K1-H12

Method BLASTX
NCBI GI g1107526
BLAST score 310
E value 1.0e-28
Match length 85
% identity 68

NCBI Description (X87931) SIEPIL protein [Beta vulgaris]

Seq. No. 299585

Seq. ID LIB3156-001-Q1-K1-H9

Method BLASTX
NCBI GI g2467088
BLAST score 181
E value 2.0e-13
Match length 65
% identity 60

NCBI Description (AJ001911) putative Ckc2 [Arabidopsis thaliana]

Seq. No. 299586

Seq. ID LIB3156-002-Q1-K1-A12

Method BLASTX
NCBI GI g2673918
BLAST score 194
E value 7.0e-15
Match length 46
% identity 78

NCBI Description (AC002561) unknwon protein [Arabidopsis thaliana]

Seq. No. 299587

Seq. ID LIB3156-002-Q1-K1-B6

Method BLASTN
NCBI GI g2208987
BLAST score 100
E value 4.0e-49
Match length 178
% identity 90

NCBI Description Z.mays mRNA for signal recognition particle subunit

Seq. No. 299588

Seq. ID LIB3156-002-Q1-K1-D4

Method BLASTX



```
NCBI GI
                   q1173194
BLAST score
                   322
                   8.0e-30
E value
                   88
Match length
% identity
                   68
                   30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13)
NCBI Description
                   >gi_2119093_pir__S59594 ribosomal protein S13 precursor,
                   chloroplast - Arabidopsis thaliana >gi_16767_emb_CAA79013
                   (Z17611) chloroplast 30S ribosomal protein ST3 [Arabidopsis
                   thaliana] >gi_662869_emb_CAA88028_(Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana]
                   >gi_1107483_emb_CAA63021_ (X91955) 30S ribosomal protein
                   S13 [Arabidopsis thaliana] >gi_1515107_emb_CAA60413_
                   (X86734) plastid ribosomal protein S13 [Arabidopsis
                   thaliana]
                   299589
Seq. No.
Seq. ID
                   LIB3156-002-Q1-K1-E10
Method
                   BLASTN
```

Seq. ID LIB3156-002-Q1-K1-E10
Method BLASTN
NCBI GI g603189
BLAST score 88
E value 6.0e-42
Match length 140
% identity 91

NCBI Description Zea mays translation initiation factor eIF-4A mRNA,

complete cds

 Seq. No.
 299590

 Seq. ID
 LIB3156-002-Q1-K1-F5

 Method
 BLASTN

 NCBI GI
 g1177368

 BLAST score
 246

 E. value
 1.0e-136

BLAST score 246 E value 1.0e-136 Match length 338 % identity 94

NCBI Description Z.mays mRNA for ribosomal protein L39

Seq. No. 299591

Seq. ID LIB3156-002-Q1-K1-H7

Method BLASTX
NCBI GI g2668742
BLAST score 335
E value 2.0e-31
Match length 86
% identity 79

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 299592

Seq. ID LIB3156-002-Q1-K2-A12

Method BLASTX
NCBI GI g2673918
BLAST score 157
E value 2.0e-10
Match length 46
% identity 65

NCBI Description (AC002561) unknwon protein [Arabidopsis thaliana]

```
299593
Seq. No.
Seq. ID
                  LIB3156-002-Q1-K2-B10
Method
                  BLASTX
                  q1172818
NCBI GI
BLAST score
                  218
                  1.0e-17
E value
Match length
                  45
% identity
                  91
                  40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal
NCBI Description
                  protein S16 [Oryza sativa] >gi_1096552_prf__2111468A
                  ribosomal protein S16 [Oryza sativa]
Seq. No.
                  299594
                  LIB3156-002-Q1-K2-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172818
BLAST score
                  203
E value
                  5.0e-16
Match length
                  45
                  87
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal
                  protein S16 [Oryza sativa] >gi_1096552_prf__2111468A
                  ribosomal protein S16 [Oryza sativa]
Seq. No.
                  299595
Seq. ID
                  LIB3156-002-Q1-K2-G8
Method
                  BLASTX
NCBI GI
                  g3080420
BLAST score
                  167
                  4.0e-12
E value
Match length
                  50
% identity
                  64
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  299596
Seq. ID
                  LIB3156-003-Q1-K1-D11
Method
                  BLASTN
                  g168577
NCBI GI
BLAST score
                  69
E value
                  2.0e-30
                  158
Match length
% identity
                  91
NCBI Description Maize phospholipid transfer protein mRNA, 3' end
                  299597
Seq. No.
                  LIB3156-003-Q1-K1-D5
Seq. ID
```

Method BLASTN
NCBI GI g4218534
BLAST score 37
E value 1.0e-11

Match length 61 % identity 90

NCBI Description Triticum sp. mRNA for GRAB1 protein

Seq. No. 299598

Seq. ID LIB3156-003-Q1-K1-E4

```
Method
NCBI GI
                  q2618699
                  191
BLAST score
                  1.0e-14
E value
Match length
                  101
% identity
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
                  299599
Seq. No.
                  LIB3156-003-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1040877
BLAST score
                  477
                  4.0e-48
E value
                  121
Match length
                  69
% identity
                  (U30460) expansin S2 precursor [Cucumis sativus]
NCBI Description
                  299600
Seq. No.
                  LIB3156-004-Q1-K1-B12
Seq. ID
                  BLASTX
Method
                  g1172813
NCBI GI
BLAST score
                  149
E value
                  5.0e-10
Match length
                  45
                   64
% identity
                  60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPRESSOR SG12)
NCBI Description
                  >gi 1076752_pir__S49596 ribosomal protein L10.e, cytosolic
                   - rice >gi_575357_emb_CAA57340_ (X81692) putative tumor
                   supressor [Oryza sativa]
                   299601
Seq. No.
                  LIB3156-004-Q1-K1-B4
Seq. ID
Method
                  BLASTX
                   g3395938
NCBI GI
BLAST score
                   241
                   2.0e-20
E value
```

103 Match length 29 % identity

(AF076924) polypyrimidine tract-binding protein homolog NCBI Description

[Arabidopsis thaliana]

299602 Seq. No.

Seq. ID LIB3156-004-Q1-K1-C1

Method BLASTX NCBI GI q4104056 BLAST score 520 E value 4.0e-53 Match length 113 81 % identity

(AF031194) S276 [Triticum aestivum] NCBI Description

299603 Seq. No.

LIB3156-004-Q1-K1-C10 Seq. ID

Method BLASTN NCBI GI g168436 BLAST score 82

```
E value
                  3.0e-38
Match length
                  142
                  89
% identity
NCBI Description Zea mays catalase (Cat3) gene, complete cds
Seq. No.
                  299604
Seq. ID
                  LIB3156-004-Q1-K1-C3
Method
                  BLASTX
                  g2344871
NCBI GI
                  225
BLAST score
E value
                  1.0e-18
Match length
                  92
% identity
                  (AJ001270) purple acid phosphatase precursor [Phaseolus
NCBI Description
                  vulgaris]
                  299605
Seq. No.
                  LIB3156-004-Q1-K1-C6
                  BLASTX
                  q1732511
```

Seq. ID LIB3156-004-Q1-K1-C6
Method BLASTX
NCBI GI g1732511
BLAST score 410
E value 4.0e-40
Match length 124
% identity 65

% identity 65
NCBI Description (U62742) Ran binding protein 1 homolog [Arabidopsis

thaliana]

 Seq. No.
 299606

 Seq. ID
 LIB3156-004-Q1-K1-C7

 Method
 BLASTX

 NCBI GI
 g2695711

 BLAST score
 160

BLAST score 160 E value 7.0e-11 Match length 62 % identity 50

NCBI Description (AJ001370) cytochome b5 [Olea europaea]

Seq. No. 299607

Seq. ID LIB3156-004-Q1-K1-C9

Method BLASTX
NCBI GI g3126965
BLAST score 206
E value 5.0e-17
Match length 118
% identity 45

NCBI Description (AF061806) basic chitinase [Elaeagnus umbellata]

Seq. No. 299608

Seq. ID LIB3156-004-Q1-K1-D6

Method BLASTX
NCBI GI g3913427
BLAST score 345
E value 1.0e-32
Match length 123
% identity 58

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi_1532073_emb_CAA69075_ (Y07767)





S-adenosylmethionine decarboxylase [Zea mays]

```
299609
Seq. No.
                   LIB3156-004-01-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g99894
BLAST score
                   274
                   3.0e-24
E value
Match length
                   120
                   55
% identity
NCBI Description chlorophyll a/b-binding protein 5 - soybean
Seq. No.
                   299610
Seq. ID
                   LIB3156-004-Q1-K1-H3
Method
                   BLASTN
NCBI GI
                   q22320
BLAST score
                   37
E value
                   2.0e-11
Match length
                   37
                   100
% identity
NCBI Description Maize H1 mRNA for H1 histone
Seq. No.
                   299611
Seq. ID
                   LIB3156-005-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   g2832632
BLAST score
                   320
                   1.0e-29
E value
                   126
Match length
% identity
                   52
NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   299612
Seq. ID
                   LIB3156-005-Q1-K1-B4
Method
                   BLASTX
NCBI GI
                   q266398
BLAST score
                   309
                   2.0e-28
E value
                   90
Match length
% identity
                   63
                   TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
NCBI Description
                   INHIBITOR) (CHFI) >gi_68849_pir__TIZM1 trypsin/factor XIIa
inhibitor precursor - maize >gi_22327_emb_CAA37998_
                    (X54064) corn Hageman factor inhibitor [Zea mays]
Seq. No.
                   299613
Seq. ID
                   LIB3156-005-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   g118104
BLAST score
                   439
E value
                   1.0e-43
Match length
                   110
% identity
                   78
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                    (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
```

maize >gi_168461 (M55021) cyclophilin [Zea mays]

>gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -

Seq. ID

Method





>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea máys]

```
299614
Seq. No.
Seq. ID
                  LIB3156-005-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1184776
BLAST score
                  164
E value
                  6.0e-12
Match length
                  39
% identity
                  82
NCBI Description
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                  GAPC4 [Zea mays]
Seq. No.
                  299615
Seq. ID
                  LIB3156-005-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2832247
BLAST score
                  149
E value
                  3.0e-14
Match length
                  78
% identity
                  65
NCBI Description
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.
                  299616
Seq. ID
                  LIB3156-005-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q498040
BLAST score
                  212
E value
                  6.0e-17
Match length
                  65
% identity
                  66
NCBI Description
                  (L33793) ORF [Senecio odorus]
Seq. No.
                  299617
Seq. ID
                  LIB3156-006-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2894568
BLAST score
                  167
E value
                  7.0e-12
Match length
                  69
% identity
                  43
                  (AL021890) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  299618
Seq. ID
                  LIB3156-006-Q1-K1-E9
Method
                  BLASTN
                  g452340
NCBI GI
BLAST score
                  255
E value
                  1.0e-141
                  275
Match length
% identity
                  99
                  Z.mays mRNA for type II light-harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  299619
Seq. No.
```

42140

LIB3156-007-Q1-K1-A7

BLASTN

```
NCBI GI
                   q758352
                   79
BLAST score
                   2.0e-36
E value
Match length
                   182
% identity
                   86
NCBI Description
                   Z.mays mRNA for cysteine synthase
                   299620
Seq. No.
                   LIB3156-007-Q1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g322752
BLAST score
                   311
E value
                   8.0e-29
Match length
                   97
% identity
                   58
                   auxin-independent growth promoter - Nicotiana tabacum
NCBI Description
                   >qi 559921 emb CAA56570 (X80301) axi 1 [Nicotiana tabacum]
                   299621
Seq. No.
Seq. ID
                   LIB3156-007-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   q1170508
BLAST score
                   139
E value
                   8.0e-09
                   50
Match length
                   58
% identity
                   EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8)
NCBI Description
                   >gi_2119931_pir__S60244 translation initiation factor
                   eIF-4A.8, anther-specific - common tobacco
                   >gi_475219_emb_CAA55639_ (X79004) translation initiation
factor (eIF-4A) [Nicotiana tabacum]
                   >gi_475221_emb_CAA55640 (X79005) translation initiation
                   factor (eIF-4A) [Nicotiana tabacum]
Seq. No.
                   299622
                   LIB3156-007-Q1-K1-F10
Seq. ID
Method
                   BLASTX
                   g2440160
NCBI GI
BLAST score
                   174
                   2.0e-12
E value
Match length
                   73
% identity
                   48
                   (Y14836) beta-galactosidase [Phagemid cloning vector
NCBI Description
                   pTZ19U]
Seq. No.
                   299623
Seq. ID
                   LIB3156-007-Q1-K1-F8
```

Method BLASTX
NCBI GI g1709619
BLAST score 220
E value 6.0e-21
Match length 92
% identity 64

NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /

DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE

(GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)

>gi 2146814 pir__S69181 protein disulfide isomerase (EC



5.3.4.1) precursor - maize >gi_625148 (L39014) protein disulfide isomerase [Zea mays]

Seq. No. 299624

Seq. ID LIB3156-007-Q1-K1-H10

Method BLASTX
NCBI GI g626042
BLAST score 178
E value 4.0e-13
Match length 51
% identity 65

NCBI Description beta-glucosidase, root meristem (EC 3.2.1.-) precursor -

maize >gi_435313_emb_CAA52293_ (X74217) beta-glucosidase

[Zea mays]

Seq. No. 299625

Seq. ID LIB3156-007-Q1-K1-H3

Method BLASTX
NCBI GI g3334222
BLAST score 164
E value 2.0e-12
Match length 61

% identity 69

NCBI Description 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)

>gi 2695710 emb CAA04245 (AJ000693)

4-hydroxyphenylpyruvate dioxygenase [Hordeum vulgare]

Seq. No. 299626

Seq. ID LIB3156-008-Q1-K1-B3

Method BLASTX
NCBI GI g1346882
BLAST score 381
E value 1.0e-36
Match length 105
% identity 69

NCBI Description PHYTOENE SYNTHASE PRECURSOR (MEL5) >gi_2129505_pir__S56668

geranylgeranyl-diphosphate geranylgeranyltransferase (EC 2.5.1.32) precursor - muskmelon >gi_870985_emb_CAA85775_

(Z37543) phytoene synthase [Cucumis melo]

Seq. No. 299627

Seq. ID LIB3156-008-Q1-K1-C3

Method BLASTX
NCBI GI g1173347
BLAST score 272
E value 6.0e-24
Match length 61
% identity 89

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

Seq. No. 299628

Seq. ID LIB3156-008-Q1-K1-D11

Method

NCBI GI BLAST score BLASTX g2384669

155



```
BLASTX
Method
NCBI GI
                   q3451075
                   247
BLAST score
                   5.0e-21
E value
Match length
                   132
                   36
% identity
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
                   299629
Seq. No.
                   LIB3156-008-Q1-K1-H12
Seq. ID
                   BLASTX
Method
                   g3128177
NCBI GI
BLAST score
                   218
E value
                   1.0e-17
                   107
Match length
                   47
 % identity
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
                   299630
 Seq. No.
                   LIB3156-009-Q1-K1-B6
 Seq. ID
                   BLASTX
Method
                   g133867
NCBI GI
                   197
BLAST score
                   3.0e-15
E value
Match length
                   98
                   44
 % identity
                   40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
 NCBI Description
                   protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                   ribosomal protein S11 [Zea mays]
 Seq. No.
                   299631
                   LIB3156-009-Q1-K1-B8
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    q133867
                    224
 BLAST score
                    2.0e-18
 E value
 Match length
                   ,95
                    56
 % identity
                   40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
 NCBI Description
                    protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                    ribosomal protein S11 [Zea mays]
                    299632
 Seq. No.
                    LIB3156-009-Q1-K1-C4
 Seq. ID
 Method
                    BLASTN
                    g236729
 NCBI GI
 BLAST score
                    40
 E value
                    4.0e-13
Match length
                    76
                    84
 % identity
 NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
 Seq. No.
                    299633
                    LIB3156-009-Q1-K1-C9
 Seq. ID
```



```
E value
Match length
                  45
% identity
                  (AF012656) putative potassium transporter AtKT1p
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  299634
                  LIB3156-009-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2146732
BLAST score
                  458
E value
                  8.0e-46
Match length
                  118
% identity
                  39
NCBI Description FK506-binding protein - Arabidopsis thaliana >gi_1373396
                  (U57838) rof1 [Arabidopsis thaliana]
Seq. No.
                  299635
                  LIB3156-009-Q1-K1-H11
Seq. ID
Method
                  BLASTX
                  q115833
NCBI GI
                  340
BLAST score
E value
                  2.0e-32
Match length
                  77
                  78
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
NCBI Description
                   (CAB-10A) (LHCP) >gi_100195_pir S11877 chlorophyll
                  a/b-binding protein Cab10A - tomato >gi_170394 (M32605)
                  a-binding protein [Lycopersicon esculentum]
                  299636
Seq. No.
                  LIB3156-010-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3036951
BLAST score
                  528
E value
                   6.0e-54
Match length
                  101
                   98
% identity
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   299637
Seq. No.
                  LIB3156-010-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g531829
                   214
BLAST score
                  3.0e-17
E value
                  79
Match length
                   53
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
```

Seq. No. 299638

Seq. ID LIB3156-010-Q1-K1-B7

Method BLASTX NCBI GI g134104 BLAST score 148



E value 7.0e-10
Match length 49
% identity 67
NCRI Description RUBISCO

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60

KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)

>gi 99800 pir PW0007 chaperonin 62.5K beta chain - rape plastid >gi 167117 (M35600) 60-kDa beta-polypeptide of

plastid chaperonin-60 precursor [Brassica napus]

Seq. No. 299639

Seq. ID LIB3156-010-Q1-K1-C8

Method BLASTX
NCBI GI 9730510
BLAST score 226
E value 1.0e-18
Match length 103
% identity 49

NCBI Description RAS-RELATED PROTEIN RIC1 >gi_542150_pir_S38740 GTP-binding

protein - rice >gi_432607_gb_AAB28535_ (S66160) ras-related GTP binding protein possessing GTPase activity=ric1 [Oryza sativa=rice, var. Yamahoushi, callus, Peptide, 202 aa]

[Oryza sativa]

Seq. No. 299640

Seq. ID LIB3156-010-Q1-K1-D9

Method BLASTX
NCBI GI g1550814
BLAST score 301
E value 1.0e-27
Match length 89
% identity 71

NCBI Description (Y07959) 60S acidic ribosomal protein P0 [Zea mays]

Seq. No. 299641

Seq. ID LIB3156-010-Q1-K1-E2

Method BLASTN
NCBI GI 94079799
BLAST score 34
E value 2.0e-09
Match length 62
% identity 89

NCBI Description Oryza sativa S-phase-specific ribosomal protein (RSPSP94)

mRNA, complete cds

Seq. No. 299642

Seq. ID LIB3156-011-Q1-K1-A2

Method BLASTX
NCBI GI g2497492
BLAST score 362
E value 1.0e-34
Match length 113
% identity 64

NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP

KINASE) >gi 1653646 dbj BAA18558 (D90915) uridine

monophosphate kinase [Synechocystis sp.]

Seq. No. 299643



```
Seq. ID
                  LIB3156-011-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g4539423
BLAST score
                  143
                  4.0e-09
E value
Match length
                  48
% identity
                  54
NCBI Description
                  (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
                  [Arabidopsis thaliana]
Seq. No.
                  299644
Seq. ID
                  LIB3156-011-Q1-K1-B4
Method
                  BLASTN
NCBI GI
                  q2828011
BLAST score
                  84
E value
                  2.0e-39
Match length
                  116
% identity
                  93
                  Zea mays starch synthase I precursor (Ss1) mRNA, nuclear
NCBI Description
                  gene encoding plastid protein, complete cds
Seq. No.
                  299645
Seq. ID
                  LIB3156-011-Q1-K1-B5
Method
                  BLASTN
NCBI GI
                  q3450841
BLAST score
                  47
E value
                  2.0e-17
Match length
                  59
% identity
                  95
NCBI Description
                  Oryza sativa mitogen activated protein kinase kinase (MEK1)
                  mRNA, complete cds
Seq. No.
                  299646
Seq. ID
                  LIB3156-011-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2130105
BLAST score
                  266
E value
                  1.0e-23
Match length
                  78
                  74
% identity
                  histone H2A type 2 (clone wcH2A-4) - wheat
NCBI Description
                  >gi 536892 dbj BAA07278 (D38089) protein H2A [Triticum
                  aestivum] >gi 536896 dbj BAA07280 (D38091) protein H2A
                  [Triticum aestivum]
                  299647
Seq. No.
Seq. ID
                  LIB3156-011-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g4151319
BLAST score
                  230
                  4.0e-19
E value
Match length
                  48
                  96
% identity
                  (AF089084) putative auxin efflux carrier protein; AtPIN1
NCBI Description
```

Seq. No. 299648

[Arabidopsis thaliana]



```
LIB3156-011-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                  q1172811
NCBI GI
BLAST score
                  242
                  8.0e-21
E value
Match length
                  65
                  71
% identity
                  60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)
NCBI Description
                  >gi 1076751_pir__S49575 ribosomal protein L10.e, cytosolic
                  - rice >gi_575355_emb_CAA57339_ (X81691) putative tumor
                  suppresser [Oryza sativa]
Seq. No.
                  299649
Seq. ID
                  LIB3156-011-Q1-K1-E2
Method
                  BLASTX
                  g1173218
NCBI GI
BLAST score
                  142
E value
                  2.0e-11
Match length
                  59
                  71
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
                  protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                  299650
                  LIB3156-011-Q1-K1-G6
Seq. ID
Method
                  BLASTX
                  g3335365
NCBI GI
BLAST score
                  170
E value
                  3.0e-12
Match length
                  91
% identity
                  43
                  (AC003028) high affinity calcium antiporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  299651
Seq. ID
                  LIB3156-012-Q1-K1-D11
Method
                  BLASTN
NCBI GI
                  q168514
BLAST score
                  46
                  9.0e-17
E value
Match length
                  66
% identity
                  92
NCBI Description Z.mays c1 locus myb homologue cDNA, exons 1-3
Seq. No.
                  299652
Seq. ID
                  LIB3156-012-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2623300
BLAST score
                  297
                  6.0e-27
E value
Match length
                  98
                  57
% identity
                  (AC002409) putative protein phosphatase 2C [Arabidopsis
NCBI Description
```

Seq. No. 299653

thaliana]



```
Seq. ID
                  LIB3156-013-Q1-K1-A9
Method
                  BLASTX
                  q2662310
NCBI GI
                  208
BLAST score
                  1.0e-16
E value
Match length
                  39
                  97
% identity
NCBI Description (AB009307) bpw1 [Hordeum vulgare]
                  299654
Seq. No.
                  LIB3156-013-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3152607
BLAST score
                  152
                  4.0e-10
E value
                  45
Match length
                  60
% identity
                  (AC004482) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                  299655
Seq. No.
                  LIB3156-013-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                  g3746964
NCBI GI
BLAST score
                  241
E value
                  9.0e-21
                  84
Match length
% identity
                   60
                  (AF092168) signal recognition particle 54 kDa subunit
NCBI Description
                  precursor [Arabidopsis thaliana]
                   299656
Seq. No.
                   LIB3156-013-Q1-K1-C9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2668744
BLAST score
                   265
E value
                   2.0e-23
Match length
                   75
                   67
% identity
                  (AF034946) ubiquitin conjugating enzyme [Zea mays]
NCBI Description
                   299657
Seq. No.
Seq. ID
                   LIB3156-013-Q1-K1-D6
Method
                   BLASTN
NCBI GI
                   g2582640
BLAST score
                   37
                   2.0e-11
E value
                   65
Match length
                   89
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   299658
Seq. No.
                   LIB3156-013-Q1-K1-E4
Seq. ID
Method
                   BLASTN
```

Method BLASTN
NCBI GI g236729
BLAST score 153
E value 1.0e-80



Match length 231 % identity 91

NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]

Seq. No. 299659

Seq. ID LIB3156-013-Q1-K1-G12

Method BLASTX
NCBI GI g1076758
BLAST score 269
E value 1.0e-23
Match length 108
% identity 57

NCBI Description heat-shock protein precursor - rye >gi_2130093_pir__S65776

heat-shock protein, 82K, precursor - rye

>gi 556673 emb_CAA82945_ (Z30243) heat-shock protein

[Secale cereale]

Seq. No. 299660

Seq. ID LIB3156-013-Q1-K1-G6

Method BLASTN
NCBI GI g22292
BLAST score 37
E value 1.0e-11
Match length 77
% identity 87

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 299661

Seq. ID LIB3156-014-Q1-K1-D4

Method BLASTX
NCBI GI g2499932
BLAST score 397
E value 1.0e-38
Match length 128
% identity 66

NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305

(U22442) adenine phosphoribosyltransferase form 1 [Triticum

aestivum]

Seq. No. 299662

Seq. ID LIB3156-014-Q1-K1-F3

Method BLASTN
NCBI GI g1532072
BLAST score 163
E value 2.0e-86
Match length 186
% identity 97

NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 299663

Seq. ID LIB3156-015-Q1-K1-A5

Method BLASTX
NCBI GI g1419090
BLAST score 231
E value 2.0e-19
Match length 111
% identity 49



(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

299664 Seq. No.

NCBI Description

LIB3156-015-Q1-K1-B10 Seq. ID

Method BLASTX NCBI GI g1044940 BLAST score 387 2.0e-37 E value 102 Match length 74 % identity

NCBI Description (X92422) fusion gene [Zea mays]

Seq. No. 299665

LIB3156-015-Q1-K1-D11 Seq. ID

Method BLASTX q3212539 NCBI GI 147 BLAST score E value 1.0e-09 64 Match length 50 % identity

Chain A, Structure Of Human Isovaleryl-Coa Dehydrogenase At NCBI Description

2.6 Angstroms Resolution: Structural Basis For Substrate Specificity >gi_3212540_pdb_1IVH_B Chain B, Structure Of Human Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity >gi_3212541_pdb_1IVH_C Chain C, Structure Of Human

Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution:

Structural Basis For Substrate Specificity

>gi_3212542_pdb_1IVH_D Chain D, Structure Of Human
Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution:

Structural Basis For Substrate Specificity

Seq. No. 299666

LIB3156-015-Q1-K1-E12 Seq. ID

Method BLASTN NCBI GI q4140643 68 BLAST score 8.0e-30 E value

Match length 120 % identity

Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description

complete sequence

Seq. No. 299667

Seq. ID LIB3156-015-Q1-K1-F6

Method BLASTX NCBI GI g112994 BLAST score 322 E value 7.0e-30 Match length 71 92 % identity

GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN NCBI Description

>gi_82685_pir__S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]

>gi 226091 prf 1410284A abscisic acid inducible gene [Zea



mays]

```
299668
Seq. No.
                  LIB3156-015-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4415916
BLAST score
                  447
E value
                  2.0e-44
Match length
                  149
                  58
% identity
                  (AC006282) putative pectin methylesterase [Arabidopsis
NCBI Description
                  thaliana]
                  299669
Seq. No.
                  LIB3156-015-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g554565
BLAST score
                  279
                  6.0e-25
E value
Match length
                  78
                  73
% identity
                  (M24889) glutathione S-transferase [Artificial gene]
NCBI Description
                  299670
Seq. No.
Seq. ID
                  LIB3156-015-Q1-K1-G6
                  BLASTX
Method
NCBI GI
                  g3860247
BLAST score
                  214
E value
                  1.0e-17
Match length
                  58
                  69
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                  299671
Seq. No.
                  LIB3156-015-Q1-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q175854
                  36
BLAST score
                  7.0e-11
E value
Match length
                  60
% identity
                  90
NCBI Description O.sativa 28S large subunit rRNA, 5' end
                  299672
Seq. No.
Seq. ID
                  LIB3156-016-Q1-K1-A7
Method
                  BLASTX
                  q115782
NCBI GI
BLAST score
                  163
E value
                  4.0e-18
Match length
                   63
% identity
                   64
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB) (LHCP) >gi 72747 pir CDWT chlorophyll a/b-binding
                  protein precursor - wheat >gi 170674 (M10144) chlorophyll
                  a/b-binding protein precursor [Triticum aestivum]
```

Seq. No. 299673



```
LIB3156-016-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1657621
BLAST score
                  148
E value
                  1.0e-13
Match length
                  96
% identity
                  50
                  (U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236)
NCBI Description
                  putative acyl-coA dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  299674
Seq. ID
                  LIB3156-016-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  q542179
BLAST score
                  494
E value
                  4.0e-50
Match length
                  115
% identity
                  83
                  alpha tubulin - maize >gi 629837 pir S39998 tubulin alpha
NCBI Description
                  chain - maize (fragment) >gi_393401_emb_CAA52158_ (X73980)
                  alpha tubulin [Zea mays]
Seq. No.
                  299675
Seq. ID
                  LIB3156-016-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3914430
BLAST score
                  400
E value
                  4.0e-39
Match length
                  87
% identity
                  86
                  PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
NCBI Description
                  CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                  >gi 2285800 dbj BAA21650 (D78172) 26S proteasome beta
                   subunit [Spinacia oleracea]
Seq. No.
                   299676
                  LIB3156-016-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1587206
BLAST score
                  237
E value
                  2.0e-26
Match length
                  122
% identity
                   60
NCBI Description
                  T complex protein [Cucumis sativus]
                  299677
Seq. No.
Seq. ID
                  LIB3156-016-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q4512616
BLAST score
                  343
                  2.0e-32
E value
                  83
Match length
```

% identity 80

NCBI Description (AC004793) Contains similarity to gi 1653332 extragenic suppressor (SuhB) from Synechocystis sp. gb D90912 and is a member of the Inositol monophophatase family PF 00459.

gb AA597395 comes from this gene. [Arabidopsis tha



299678

Seq. No.

```
Seq. ID
                  LIB3156-016-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  q2208962
                  211
BLAST score
E value
                  4.0e-17
                  66
Match length
% identity
NCBI Description (Y10118) signal recognition particle subunit 14 [Oryza
                  sativa]
Seq. No.
                  299679
                  LIB3156-016-Q1-K1-F11
Seq. ID
Method
                  BLASTX
                  g3355468
NCBI GI
                  244
BLAST score
E value
                  5.0e-21
Match length
                  91
                  59
% identity
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  299680
                  LIB3156-016-Q1-K1-H9
Seq. ID
Method
                  BLASTX
                  g1008904
NCBI GI
                  264
BLAST score
                  5.0e-44
E value
Match length
                  109
                  80
% identity
                  (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
NCBI Description
Seq. No.
                  299681
                  LIB3156-017-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4457221
BLAST score
                   143
E value
                   2.0e-09
Match length
                   50
                   58
% identity
                   (AF127797) putative bZIP DNA-binding protein [Capsicum
NCBI Description
                   chinense]
                   299682
Seq. No.
                   LIB3156-017-Q1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2766452
BLAST score
                   183
E value
                   1.0e-13
Match length
                   71
% identity
                   54
                  (AF029858) cytochrome P450 CYP71E1 [Sorghum bicolor]
NCBI Description
                   299683
Seq. No.
Seq. ID
                  LIB3156-017-Q1-K1-C10
Method
                   BLASTX
```



```
NCBI GI
                   q1931647
BLAST score
                   167
                   1.0e-11
E value
Match length
                   75
% identity
                   45
                   (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                   [Arabidopsis thaliana]
                   299684
Seq. No.
                   LIB3156-017-Q1-K1-C5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q167086
BLAST score
                   34
                   8.0e-10
E value
                   94
Match length
                   84
% identity
                   Hordeum vulgare photosystem I protein (PSI-L) mRNA,
NCBI Description
                   complete cds
                   299685
Seq. No.
                   LIB3156-017-Q1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3776005
BLAST score
                   154
                   1.0e-10
E value
                   45
Match length
% identity
                   67
                   (AJ010466) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   299686
Seq. No.
                   LIB3156-017-Q1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g113621
BLAST score
                   264
                   2.0e-23
E value
Match length
                   66
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                   >gi 68196 pir ADZM fructose-bisphosphate aldolase (EC
                   4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850 emb_CAA31366 (X12872) fructose
                   bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A
                   cytoplasmic aldolase [Zea mays]
                   299687
Seq. No.
                   LIB3156-017-Q1-K1-D6
Seq. ID
Method
                   BLASTX
                   g2764992
NCBI GI
BLAST score
                   166
                    3.0e-18
E value
                    97
Match length
```

55 % identity

NCBI Description (Y08609) plasma membrane polypeptide [Nicotiana tabacum]

Seq. No.

299688

LIB3156-017-Q1-K1-E12 Seq. ID

Method BLASTX

```
q2760334
NCBI GI
                  259
BLAST score
                  2.0e-22
E value
                  83
Match length
% identity
                  57
NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana]
Seq. No.
                  299689
                  LIB3156-017-Q1-K1-G11
Seq. ID
Method
                  BLASTN
```

NCBI GI g21892 BLAST score 94 1.0e-45 E value Match length 134 93 % identity

NCBI Description T.aestivum (clone pTAU1.3) U1 snRNA

299690 Seq. No. LIB3156-017-Q1-K1-H9 Seq. ID Method BLASTN q312178 NCBI GI 181 BLAST score E value 2.0e-97 219

Match length 96 % identity

NCBI Description Z.mays GapC2 gene

299691 Seq. No.

LIB3156-020-Q1-K1-A10 Seq. ID

Method BLASTX NCBI GI g4587549 225 BLAST score E value 6.0e-19 Match length 61 % identity 69

(AC006577) Similar to gb_U55861 RNA binding protein NCBI Description

nucleolysin (TIAR) from \overline{M} us musculus and contains several PF 00076 RNA recognition motif domains. ESTs gb_T21032 and

gb T44127 come from this gene. [Arabidopsis t

299692 Seq. No.

Seq. ID LIB3156-020-Q1-K1-A7

BLASTX Method g3687240 NCBI GI 323 BLAST score 5.0e-30 E value 121 Match length 50 % identity

NCBI Description (AC005169) extensin-like protein [Arabidopsis thaliana]

299693 Seq. No.

Seq. ID LIB3156-021-Q1-K1-D1

BLASTX Method NCBI GI g2842698 BLAST score 194 2.0e-15 E value Match length 48



% identity PROBABLE ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC) NCBI Description >gi 1644319 emb CAB03609.1 (Z81317) arp 2-3 complex 20kd subunit [Schizosaccharomyces pombe] 299694 Seq. No. Seq. ID LIB3156-021-Q1-K1-D4 Method BLASTN g18963 NCBI GI 231 BLAST score E value 1.0e-127 Match length 247 % identity 98 NCBI Description Z.mays mRNA for dehydrin (dhn3) 299695 Seq. No. LIB3156-021-Q1-K1-F6 Seq. ID Method BLASTX NCBI GI g3169182 BLAST score 191 2.0e-14 E value Match length 40 78 % identity NCBI Description (AC004401) unknown protein [Arabidopsis thaliana] Seq. No. 299696 LIB3156-021-Q1-K1-G2 Seq. ID Method BLASTX NCBI GI q4587550 267 BLAST score 2.0e-23 E value 70 Match length % identity (AC006577) EST gb R64848 comes from this gene. [Arabidopsis NCBI Description thaliana] Seq. No. 299697 Seq. ID LIB3156-021-Q1-K1-G3 Method BLASTX NCBI GI q1076758 BLAST score 431 E value 7.0e-43 Match length 99 86 % identity heat-shock protein precursor - rye >gi 2130093 pir S65776 NCBI Description heat-shock protein, 82K, precursor - rye >gi 556673 emb CAA82945 (Z30243) heat-shock protein [Secale cereale] 299698

Seq. No.

LIB3156-021-Q1-K1-G8 Seq. ID

Method BLASTX g4587550 NCBI GI BLAST score 437 2.0e-43 E value 133 Match length 65 % identity



NCBI Description (AC006577) EST gb_R64848 comes from this gene. [Arabidopsis thaliana]

Seq. No. 299699

Seq. ID LIB3157-002-Q1-K1-A8

Method BLASTN
NCBI GI g4140643
BLAST score 39
E value 1.0e-12

Match length 39 % identity 100

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 299700

Seq. ID LIB3157-002-Q1-K1-E6

Method BLASTN
NCBI GI g22204
BLAST score 35
E value 2.0e-10
Match length 59
% identity 90

NCBI Description Maize Bz-McC gene for UDPglucose flavonoid

glycosyl-transferase

Seq. No. 299701

Seq. ID LIB3157-002-Q1-K1-F3

Method BLASTX
NCBI GI g729470
BLAST score 517
E value 9.0e-53
Match length 123
% identity 77

NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR

(NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)

>gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2)
precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
(Z21493) mitochondrial formate dehydrogenase precursor

[Solanum tuberosum]

Seq. No. 299702

Seq. ID LIB3157-002-Q1-K1-F5

Method BLASTX
NCBI GI . g4263517
BLAST score 153
E value 3.0e-10
Match length 80
% identity 39

NCBI Description (AC004044) similar to PHZF, catalyzing the hydroxylation of

phenazine-1-carboxylic acid to

2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis

thaliana]

Seq. No. 299703

Seq. ID LIB3157-003-Q1-K1-A2

Method BLASTX NCBI GI g2137490

BLAST score 2.0e-16 E value Match length 98 % identity 48 NCBI Description lymphocyte specific helicase - mouse >gi 805296 (U25691) lymphocyte specific helicase [Mus musculus] Seq. No. 299704 Seq. ID LIB3157-003-Q1-K1-C2 Method BLASTN NCBI GI q2668741 BLAST score 253 E value 1.0e-140 Match length 253 100 % identity NCBI Description Zea mays glycine-rich RNA binding protein (GRP) mRNA, complete cds Seq. No. 299705 Seq. ID LIB3157-003-Q1-K1-H8 Method BLASTN NCBI GI q22237 BLAST score 192 1.0e-104 200 99

E value Match length % identity NCBI Description Maize mRNA for cytosolic GAPDH (GapC)

glyceraldehyde-3-phosphate dehydrogenase

Seq. No. 299706 Seq. ID LIB3157-004-Q1-K1-A11 Method BLASTN NCBI GI g22292 BLAST score 53 E value 4.0e-21 Match length 61 % identity 97

NCBI Description Z.mays mRNA for glycine-rich protein

299707 Seq. No. Seq. ID LIB3157-004-Q1-K1-A2 Method BLASTX NCBI GI g3894186 BLAST score 241 E value 2.0e-20 Match length 107

% identity NCBI Description (AC005662) putative embryo-abundant protein [Arabidopsis

thaliana]

Seq. No. 299708

Seq. ID LIB3157-004-Q1-K1-A6

50

Method BLASTN NCBI GI g2668747 BLAST score 119 2.0e-60 E value Match length 123



```
% identity
                  Zea mays ribosomal protein L17 (rpl17) mRNA, complete cds
NCBI Description
                  299709
Seq. No.
Seq. ID
                  LIB3157-004-Q1-K1-A9
Method
                  BLASTX
                  g2668742
NCBI GI
BLAST score
                  211
E value
                  6.0e-17
Match length
                  71
% identity
NCBI Description
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
                  299710
Seq. ID
                  LIB3157-004-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g3913430
BLAST score
                  223
E value
                  3.0e-18
Match length
                  94
                  48
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX
NCBI Description
                  PROTEIN 13) >gi_2407195 (AF017153) putative RNA helicase
                  and RNA dependent ATPase [Mus musculus]
Seq. No.
                  299711
Seq. ID
                  LIB3157-005-Q1-K1-A10
Method
                  BLASTN
NCBI GI
                  g22161
BLAST score
                  110
E value
                  6.0e-55
Match length
                  154
                  93
% identity
NCBI Description
                  Z.mays MANT1 mRNA for adenine nucleotide translocator (also
                  called ADP/ATP translocase)
Seq. No.
                  299712
Seq. ID
                  LIB3157-005-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  q730456
BLAST score
                  198
E value
                  1.0e-15
Match length
                  43
% identity
                  86
NCBI Description 40S RIBOSOMAL PROTEIN S19
Seq. No.
                  299713
Seq. ID
                  LIB3157-005-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  q4336747
```

BLAST score 166 2.0e-11 E value Match length 66 % identity 52

NCBI Description (AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No. 299714

Method

NCBI GI

BLASTN

g1870198



```
Seq. ID
                  LIB3157-005-Q1-K1-G3
Method
                  BLASTX
                  q531829
NCBI GI
                  209
BLAST score
                  1.0e-16
E value
Match length
                  66
                  62
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                  299715
Seq. No.
                  LIB3157-006-Q1-K1-F9
Seq. ID
Method
                  BLASTN
                  g2062691
NCBI GI
BLAST score
                  37
                  1.0e-11
E value
                  37
Match length
                  100
% identity
                  Human sodium phosphate transporter (NPT4) mRNA, complete
NCBI Description
                  299716
Seq. No.
                  LIB3157-007-Q1-K1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g463151
                  45
BLAST score
                  4.0e-16
E value
Match length
                  65
                  92
% identity
NCBI Description Zea mays high sulfur zein gene, complete cds
                  299717
Seq. No.
                  LIB3157-007-Q1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2921303
BLAST score
                   67
E value
                   2.0e-29
                   159
Match length
% identity
                   86
                  Zea mays herbicide safener binding protein (SBP1) mRNA,
NCBI Description
                   complete cds
                   299718
Seq. No.
                  LIB3157-007-Q1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3128168
BLAST score
                   190
                   2.0e-14
E value
Match length
                   59
                   58
% identity
                   (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   299719
Seq. ID
                   LIB3157-007-Q1-K1-H7
```



```
BLAST score
E value
                  6.0e-27
Match length
                  62
                  100
% identity
NCBI Description Z.mays mRNA for acyl carrier protein
                  299720
Seq. No.
                  LIB3157-008-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2160174
BLAST score
                  221
                  4.0e-18
E value
Match length
                  58
% identity
                  74
                  (AC000132) Identical to A. thaliana PUR2 (gb_X74766). ESTs
NCBI Description
                  gb ATTS3927,gb_N96446 come from this gene. [Arabidopsis
                  thaliana]
                  299721
Seq. No.
                  LIB3157-008-Q1-K1-G6
Seq. ID
Method
                  BLASTN
                  g1063665
NCBI GI
BLAST score
                   48
                  2.0e-18
E value
Match length
                  146
                   82
% identity
NCBI Description Zea mays unknown protein mRNA, complete cds
                   299722
Seq. No.
                   LIB3157-008-Q1-K1-H9
Seq. ID
Method
                   BLASTN
                   g3043528
NCBI GI
                   147
BLAST score
E value
                   6.0e-77
                   171
Match length
% identity
                   97
NCBI Description Zea mays mRNA for flavin containing polyamine oxidase (PAO)
                   299723
Seq. No.
Seq. ID
                   LIB3157-009-Q1-K1-B6
Method
                   BLASTN
NCBI GI
                   g949979
BLAST score
                   34
E value
                   9.0e-10
                   57
Match length
% identity
                   89
NCBI Description Z.mays Glossy2 locus DNA
                   299724
Seq. No.
                   LIB3157-009-Q1-K1-C11
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g2511531
BLAST score 172
E value 2.0e-12
Match length 40
% identity 85

NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]



```
>gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
[Eleusine indica]
```

Seq. No. 299725 Seq. ID LIB3157-009-Q1-K1-D9

Method BLASTN NCBI GI g2773153

BLAST score 61

E value 9.0e-26
Match length 157
% identity 85

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 299726

Seq. ID LIB3157-009-Q1-K1-G10

Method BLASTN
NCBI GI g1177368
BLAST score 170
E value 1.0e-90
Match length 294
% identity 90

NCBI Description Z.mays mRNA for ribosomal protein L39

Seq. No. 299727

Seq. ID LIB3157-009-Q1-K1-G11

Method BLASTX
NCBI GI g3928093
BLAST score 191
E value 2.0e-14
Match length 48
% identity 77

NCBI Description (AC005770) IVR-like protein [Arabidopsis thaliana]

Seq. No. 299728

Seq. ID LIB3157-012-Q1-K1-A3

Method BLASTN
NCBI GI g531828
BLAST score 47
E value 2.0e-17
Match length 79
% identity 90

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 299729

Seq. ID LIB3157-012-Q1-K1-G6

Method BLASTX
NCBI GI g531829
BLAST score 163
E value 2.0e-11
Match length 63
% identity 51

NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector

pSport1]

Seq. No. 299730

Seq. ID LIB3157-013-Q1-K1-A12



```
Method
NCBI GI
                  q1498052
                  105
BLAST score
                  5.0e-52
E value
                  197
Match length
                  88
% identity
                  Zea mays ribosomal protein S8 mRNA, complete cds
NCBI Description
                  299731
Seq. No.
                  LIB3157-013-Q1-K1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168577
BLAST score
                  68
                  6.0e-30
E value
                  109
Match length
                  99
% identity
NCBI Description Maize phospholipid transfer protein mRNA, 3' end
                  299732
Seq. No.
                  LIB3157-014-Q1-K1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1532072
BLAST score
                   73
                  7.0e-33
E value
Match length
                   236
% identity
                   83
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase
Seq. No.
                   299733
                  LIB3157-014-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   q1706738
NCBI GI
                   273
BLAST score
E value
                   4.0e-24
                   119
Match length
% identity
                   44
NCBI Description FLAVONOL 3-SULFOTRANSFERASE (F3-ST) >gi 498645 (U10275)
                   flavonol 3-sulfotransferase [Flaveria bidentis]
Seq. No.
                   299734
                   LIB3157-014-Q1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g531829
BLAST score
                   200
E value
                   1.0e-15
Match length
                   69
                   57
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
Seq. No.
                   299735
                   LIB3157-014-Q1-K1-G12
Seq. ID
Method
                   BLASTX
                   g3789942
NCBI GI
BLAST score
                   144
```

42163

1.0e-14

68

E value

Match length



```
% identity
NCBI Description
                  (AF093505) polyubiquitin [Saccharum hybrid cultivar
                  H32-8560]
                  299736
Seq. No.
                  LIB3157-015-Q1-K1-D5
Seq. ID
Method
                  BLASTX
                  g971137
NCBI GI
BLAST score
                  145
                  4.0e-09
E value
                  58
Match length
% identity
                  48
NCBI Description
                  (D63840) modified alpha peptide of E. coli
                  beta-galactosidase [Cloning vector pKF296]
                  >gi_971149_dbj_BAA09905_ (D63844) modified alpha peptide of
                  E. coli beta-galactosidase [Cloning vector pKF16k]
                  299737
Seq. No.
                  LIB3157-015-Q1-K1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  37
                  2.0e-11
E value
Match length
                  37
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  299738
Seq. No.
                  LIB3157-016-Q1-K1-C12
Seq. ID
Method
                  BLASTN
                  g498774
NCBI GI
BLAST score
                  77
                  2.0e-35
E value
Match length
                  263
                  82
% identity
NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein
Seq. No.
                  299739
                  LIB3157-016-Q1-K1-C3
Seq. ID
Method
                  BLASTN
                  q3420038
NCBI GI
                  60
BLAST score
                  1.0e-25
E value
                  123
Match length
% identity
                  44
                  Zea mays gypsy/Ty3-type retrotransposon Tekay, complete
NCBI Description
                  sequence
Seq. No.
                  299740
                  LIB3157-016-Q1-K1-F7
Seq. ID
Method
                  BLASTN
```

NCBI GI q1870200 BLAST score 59 E value 6.0e-25 Match length 75 % identity 95

NCBI Description Z.mays cyp71c2 gene



```
Seq. No.
                  299741
                  LIB3157-016-Q1-K1-G2
Seq. ID
Method
                  BLASTX
                  q1079321
NCBI GI
                  155
BLAST score
E value
                  2.0e-13
                  83
Match length
                  51
% identity
                  XPMC2 protein - African clawed frog >gi_595380 (U10185)
NCBI Description
                  XPMC2 protein [Xenopus laevis]
Seq. No.
                  299742
                  LIB3157-017-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1711381
BLAST score
                  137
                  1.0e-08
E value
Match length
                  53
                   57
% identity
                  PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)
NCBI Description
                  >gi_1256204_dbj_BAA12206_ (D84061) phosphoserine
                   aminotransferase [Spinacia oleracea]
Seq. No.
                  299743
                  LIB3157-017-Q1-K1-C6
Seq. ID
Method
                  BLASTX
                  g567893
NCBI GI
BLAST score
                   177
                   8.0e-13
E value
Match length
                   73
                   52
% identity
                  (L37382) beta-galactosidase-complementation protein
NCBI Description
                   [Cloning vector]
Seq. No.
                   299744
Seq. ID
                   LIB3157-017-Q1-K1-D10
Method
                   BLASTN
                   g342631
NCBI GI
BLAST score
                   104
E value
                   2.0e-51
Match length
                   239
% identity
NCBI Description Maize mitochondrial F-1-ATPase subunit-2 mRNA, complete cds
                   299745
Seq. No.
Seq. ID
                   LIB3157-017-Q1-K1-D5
Method
                   BLASTN
NCBI GI
                   q433038
BLAST score
                   95
E value
                   6.0e - 46
Match length
                   202
% identity
                   88
```

NCBI Description Zea mays W-22 clone cDNA7 retroelement PREM-1-containing

mRNA

Seq. No. 299746

% identity

89



```
LIB3157-017-Q1-K1-D8
Seq. ID
Method
                  BLASTN
                  g22223
NCBI GI
                  55
BLAST score
                  3.0e-22
E value
Match length
                  59
                  98
% identity
NCBI Description Maize cab-1 gene for chlorophyll a/b-binding protein
                  299747
Seq. No.
                  LIB3157-017-Q1-K1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22332
BLAST score
                  76
                  7.0e-35
E value
                  120
Match length
                  91
% identity
NCBI Description Z.mays HRGP gene
                  299748
Seq. No.
                  LIB3157-018-Q1-K1-B11
Seq. ID
                  BLASTN
Method
                  g1498052
NCBI GI
BLAST score
                  160
E value
                  8.0e-85
Match length
                  229
% identity
                  92
NCBI Description Zea mays ribosomal protein S8 mRNA, complete cds
Seq. No.
                  299749
                  LIB3157-018-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2323410
BLAST score
                  186
                  5.0e-14
E value
Match length
                  56
% identity
                  61
NCBI Description (AF015913) Skb1Hs [Homo sapiens]
Seq. No.
                  299750
Seq. ID
                  LIB3157-018-Q1-K1-E11
Method
                  BLASTN
NCBI GI
                  q531828
BLAST score
                  42
E value
                  1.0e-14
Match length
                  82
                  88
% identity
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  299751
Seq. ID
                  LIB3157-018-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q168422
BLAST score
                  211
E value
                  5.0e-17
Match length
                  46
```





```
(J04550) auxin-binding protein precursor [Zea mays]
NCBI Description
                   299752
Seq. No.
                  LIB3157-018-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  q2267597
NCBI GI
BLAST score
                   259
                  1.0e-24
E value
                  83
Match length
                  70
% identity
NCBI Description
                  (AF009413) 10 kDa chaperonin [Oryza sativa]
Seq. No.
                   299753
                  LIB3157-019-Q1-K1-A10
Seq. ID
Method
                  BLASTX
                   q3894187
NCBI GI
BLAST score
                   218
E value
                   1.0e-17
                   83
Match length
                   63
% identity
                  (AC005662) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   299754
Seq. ID
                  LIB3157-019-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                   g2864618
BLAST score
                   149
                   1.0e-09
E value
Match length
                   67
% identity
                   46
NCBI Description
                  (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                   299755
                   LIB3157-019-Q1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160180
BLAST score
                   261
                   1.0e-22
E value
Match length
                   76
% identity
                   63
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   299756
Seq. No.
Seq. ID
                   LIB3157-019-Q1-K1-G1
                   BLASTN
Method
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   9.0e-11
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   299757
```

Seq. No.

Seq. ID LIB3157-019-Q1-K1-H1

BLASTX Method g4235430 NCBI GI BLAST score 187



E value 3.0e-14
Match length 50
% identity 72
NCRI Description (AF09845)

NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No. 299758

Seq. ID LIB3157-020-Q1-K1-A4

Method BLASTN
NCBI GI g22091
BLAST score 108
E value 4.0e-54
Match length 173
% identity 91

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 299759

Seq. ID LIB3157-020-Q1-K1-A7

Method BLASTN
NCBI GI g444046
BLAST score 48
E value 4.0e-18
Match length 48
% identity 100

NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor

Seq. No. 299760

Seq. ID LIB3157-020-Q1-K1-C11

Method BLASTN
NCBI GI g22324
BLAST score 120
E value 5.0e-61
Match length 192
% identity 91

NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No. 299761

Seq. ID LIB3157-020-Q1-K1-G1

Method BLASTN
NCBI GI g168500
BLAST score 86
E value 7.0e-41
Match length 110
% identity 95

NCBI Description Maize (Zea mays) histone H4 gene (H4C14), complete cds

Seq. No. 299762

Seq. ID LIB3157-021-Q1-K1-B10

Method BLASTN
NCBI GI g3822035
BLAST score 146
E value 2.0e-76
Match length 201
% identity 94

NCBI Description Zea mays endo-1,3-1,4-beta-D-glucanase mRNA, complete cds

Seq. No. 299763

Seq. ID LIB3157-021-Q1-K1-C4



```
Method
NCBI GI
                   q1001834
BLAST score
                   538
E value
                   4.0e-55
Match length
                   143
                   69
% identity
NCBI Description
                  (D64005) hypothetical protein [Synechocystis sp.]
                   299764
Seq. No.
                  LIB3157-021-Q1-K1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                   q168468
BLAST score
                   42
                   3.0e-14
E value
                   42
Match length
                   100
% identity
NCBI Description Maize ferredoxin I (Fd) isoprotein mRNA, pFD1
                   299765
Seq. No.
                  LIB3157-021-Q1-K1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                   g22251
BLAST score
                   55
E value
                   5.0e-22
Match length
                   55
% identity
                   100
                  Z.mays mRNA that delineates a novel subset of cortical
NCBI Description
                   cells
Seq. No.
                   299766
                  LIB3157-021-Q1-K1-G1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1244652
BLAST score
                   81
E value
                   1.0e-37
Match length
                   141
% identity
                   89
                  Zea mays copia-type retroelement PREM-2 gag gene, complete
NCBI Description
                   cds
Seq. No.
                   299767
Seq. ID
                   LIB3158-001-Q1-K1-C6
Method
                   BLASTX
NCBI GI
                   g1170937
BLAST score
                   203
                   4.0e-16
E value
Match length
                   51
% identity
                   76
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >qi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   299768
Seq. No.
```

BLASTX NCBI GI g3024018

LIB3158-001-Q1-K1-D2

Seq. ID

Method



```
BLAST score
E value
                   1.0e-27
Match length
                   71
% identity
                   85
                   INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation
                   initiation factor 5A [Zea mays]
                   299769
Seq. No.
Seq. ID
                   LIB3158-001-Q1-K1-E2
Method
                   BLASTX
NCBI GI
                   g1747294
BLAST score
                   184
E value
                   3.0e-14
                   47
Match length
                   79
% identity
NCBI Description
                  (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
Seq. No.
                   299770
                   LIB3158-001-Q1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q480669
BLAST score
                   289
                   3.0e-26
E value
Match length
                   103
% identity
                   62
                   NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Jerusalem
NCBI Description
                   artichoke (fragment) >gi_1359894_emb_CAA81210_ (Z26251)
                   NADPH-ferrihemoprotein reductase [Helianthus tuberosus]
Seq. No.
                   299771
Seq. ID
                   LIB3158-001-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   q693916
BLAST score
                   372
E value
                   5.0e-36
Match length
                   85
% identity
                   85
NCBI Description
                   (U21111) chlorophyll a/b binding protein [Solanum
                   tuberosum]
                   299772
Seq. No.
Seq. ID
                   LIB3158-003-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   g2662343
BLAST score
                   196
                   2.0e-15
E value
```

Match length 80 % identity 51

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 299773

Seq. ID LIB3158-003-Q1-K1-C11

Method BLASTN NCBI GI g169818 BLAST score 76



```
E value
                  1.0e-34
Match length
                  76
                  100
% identity
NCBI Description Rice 25S ribosomal RNA gene
                  299774
Seq. No.
                  LIB3158-003-Q1-K1-D2
Seq. ID
Method
                  BLASTN
                  g2921303
NCBI GI
                  98
BLAST score
                  4.0e-48
E value
                  170
Match length
                  89
% identity
                  Zea mays herbicide safener binding protein (SBP1) mRNA,
NCBI Description
                  complete cds
                  299775
Seq. No.
                  LIB3158-003-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                  g548604
NCBI GI
BLAST score
                  164
                  2.0e-11
E value
                  34
Match length
                  88
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                  >gi_1076728_pir__S51813 photosystem-I PSI-F chain precursor
                   - barley >gi 469560 (U08135) photosystem-I PSI-F subunit
                  precursor [Hordeum vulgare]
                  299776
Seq. No.
                  LIB3158-003-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3068714
                   201
BLAST score
E value
                   2.0e-30
Match length
                  114
% identity
                   61
                  (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                   299777
Seq. No.
                   LIB3158-003-Q1-K1-G5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1850902
BLAST score
                   93
E value
                   5.0e-45
                   121
Match length
                   95
% identity
NCBI Description Z.mays cyp71c4 gene
                   299778
Seq. No.
```

Seq. ID LIB3158-003-Q1-K1-G6

Method BLASTX
NCBI GI g3258575
BLAST score 320
E value 6.0e-30
Match length 93



```
% identity
                  (U89959) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  299779
Seq. No.
                  LIB3158-003-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3603353
BLAST score
                  218
E value
                  8.0e-18
Match length
                  109
% identity
                  (AF074843) peroxisomal targeting signal type 1 receptor
NCBI Description
                   [Arabidopsis thaliana]
                  299780
Seq. No.
                  LIB3158-004-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454799
BLAST score
                  158
                  3.0e-11
E value
                  38
Match length
                  87
% identity
                  (AF079782) translation initiation factor 4A2 [Zea mays]
NCBI Description
Seq. No.
                  299781
                  LIB3158-004-Q1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q435312
BLAST score
                  73
                  2.0e-33
E value
                  81
Match length
                   98
% identity
NCBI Description Z.mays mRNA for beta-D-glucosidase
Seq. No.
                   299782
                  LIB3158-005-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                   g4539459
NCBI GI
BLAST score
                   152
                   3.0e-10
E value
                   59
Match length
% identity
                   54
                  (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
                   299783
Seq. No.
Seq. ID
                   LIB3158-005-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   q82734
BLAST score
                   645
                   9.0e-68
E value
                   136
Match length
                   29
% identity
                  ubiquitin precursor - maize (fragment)
NCBI Description
                   >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
```

42172

299784

LIB3158-005-Q1-K1-A5

Seq. No.

Seq. ID



```
Method
                  BLASTN
NCBI GI
                  g1060934
BLAST score
                  55
                  2.0e-22
E value
Match length
                  63
                  97
% identity
NCBI Description Maize mRNA for mLIP15 (DNA-binding factor), complete cds
                  299785
Seq. No.
Seq. ID
                  LIB3158-005-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q3176669
BLAST score
                  162
                  3.0e-11
E value
Match length
                  57
                   42
% identity
NCBI Description (AC004393) End is cut off. [Arabidopsis thaliana]
                   299786
Seq. No.
Seq. ID
                  LIB3158-005-Q1-K1-H12
Method
                  BLASTN
                  q3108052
NCBI GI
BLAST score
                   47
E value
                   2.0e-17
                   59
Match length
                   95
% identity
                  Zea mays myo-inositol 1-phosphate synthase mRNA, complete
NCBI Description
                   299787
Seq. No.
Seq. ID
                   LIB3158-006-Q1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2285792
BLAST score
                   168
E value
                   9.0e-12
Match length
                   43
% identity
                   70
                   (AB004568) cyanase [Arabidopsis thaliana]
NCBI Description
                   >qi 3287503 dbj BAA31224 (AB015748) cyanase [Arabidopsis
                   thaliana]
                   299788
Seq. No.
Seq. ID
                   LIB3158-006-Q1-K1-D4
Method
                   BLASTX
                   g531829
NCBI GI
                   163
BLAST score
E value
                   2.0e-11
Match length
                   64
% identity
                   55
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
                   299789
Seq. No.
```

Seq. ID LIB3158-006-Q1-K1-E5

Method BLASTN g4140643 NCBI GI BLAST score 109



E value 2.0e-54 Match length 237 % identity 87

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 299790

Seq. ID LIB3158-006-Q1-K1-F5

Method BLASTX
NCBI GI g1666228
BLAST score 293
E value 2.0e-34
Match length 83
% identity 92

NCBI Description (U76190) actin [Pisum sativum] >gi_1666230 (U76191) actin

[Pisum sativum] >gi 1724137 (U81046) actin [Pisum sativum]

>gi 1724139 (U81047) actin [Pisum sativum]

Seq. No. 299791

Seq. ID LIB3158-008-Q1-K1-B6

Method BLASTX
NCBI GI g3450889
BLAST score 167
E value 4.0e-12
Match length 70
% identity 53

NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 299792

Seq. ID LIB3158-008-Q1-K1-B7

Method BLASTX
NCBI GI g1705678
BLAST score 258
E value 1.0e-22
Match length 84
% identity 68

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING

PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No. 299793

Seq. ID LIB3158-008-Q1-K1-E4

Method BLASTN
NCBI GI g2921303
BLAST score 75
E value 2.0e-34
Match length 159
% identity 87

NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA,

complete cds

Seq. No. 299794

Seq. ID LIB3158-008-Q1-K1-F4

Method BLASTX
NCBI GI g4585901
BLAST score 148
E value 4.0e-17



```
Match length
% identity
                   43
                  (AC007133) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  299795
Seq. No.
Seq. ID
                  LIB3158-008-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  q1362615
BLAST score
                  149
                  1.0e-17
E value
Match length
                  100
% identity
                   50
                  iswi protein - fruit fly (Drosophila melanogaster)
NCBI Description
                  >gi 439197 (L27127) ISWI protein [Drosophila melanogaster]
                   299796
Seq. No.
                  LIB3158-008-Q1-K1-H11
Seq. ID
Method
                  BLASTX
                   g541800
NCBI GI
                   238
BLAST score
                   3.0e-20
E value
Match length
% identity
                   64
                  protein kinase (EC 2.7.1.37) cdc2-Pa - Norway spruce
NCBI Description
                  >gi 454980 emb_CAA54746_ (X77680) cdc2Pa [Picea abies]
Seq. No.
                   299797
                   LIB3158-010-Q1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129613
BLAST score
                   414
                   1.0e-40
E value
Match length
                   141
% identity
                   59
NCBI Description homeotic protein BEL1 - Arabidopsis thaliana >gi_1122533
                   (U39944) BELL1 [Arabidopsis thaliana]
Seq. No.
                   299798
Seq. ID
                   LIB3158-010-Q1-K1-E2
Method
                   BLASTX
NCBI GI
                   g2370232
BLAST score
                   152
                   3.0e-10
E value
Match length
                   44
% identity
                   64
                  (AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]
NCBI Description
Seq. No.
                   299799
                   LIB3158-010-Q1-K1-E4
Seq. ID
```

Method BLASTN NCBI GI q3043528 BLAST score 41 1.0e-13 E value 77

Match length 88 % identity

Zea mays mRNA for flavin containing polyamine oxidase (PAO) NCBI Description



```
Seq. No.
                  299800
                  LIB3158-010-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245378
BLAST score
                  143
E value
                  3.0e-13
Match length
                  80
                  53
% identity
                  (U83245) auxin response factor 1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  299801
Seq. ID
                  LIB3158-011-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  q4580394
BLAST score
                  214
                  2.0e-17
E value
                  62
Match length
% identity
                   60
                   (AC007171) putative fatty acid elongase [Arabidopsis
NCBI Description
                  thaliana]
                   299802
Seq. No.
Seq. ID
                  LIB3158-011-Q1-K1-C4
Method
                  BLASTX
                  q3688328
NCBI GI
                   192
BLAST score
                   3.0e-15
E value
                   64
Match length
% identity
                   66
                  (AJ228325) reverse transcriptase [Ginkgo biloba]
NCBI Description
Seq. No.
                   299803
Seq. ID
                   LIB3158-012-Q1-K1-A6
Method
                   BLASTX
NCBI GI
                   q4090884
BLAST score
                   188
E value
                   3.0e-14
Match length
                   62
% identity
                   63
                   (AF025333) vesicle-associated membrane protein 7B;
NCBI Description
                   synaptobrevin 7B [Arabidopsis thaliana]
                   299804
Seq. No.
Seq. ID
                   LIB3158-012-Q1-K1-A7
                   BLASTN
Method
                   g559535
NCBI GI
BLAST score
                   46
                   9.0e-17
E value
                   146
Match length
% identity
                   83
NCBI Description Z.mays mRNA for metallothionein
                   299805
Seq. No.
Seq. ID
                   LIB3158-012-Q1-K1-B3
```

42176

BLASTX

405

g1498388

Method

NCBI GI BLAST score



```
E value
Match length
                  104
% identity
                  86
                  (U60510) actin [Zea mays]
NCBI Description
Seq. No.
                  299806
Seq. ID
                  LIB3158-012-Q1-K1-H10
Method
                  BLASTX
                  g629843
NCBI GI
                  353
BLAST score
E value
                  1.0e-33
Match length
                  99
% identity
                  74
                  heat shock protein hsp70-4 - maize (fragment)
NCBI Description
                  >gi_498773_emb_CAA55183_ (X78414) heat shock protein 70 kDa
                  [Zea mays]
                  299807
Seq. No.
                  LIB3158-012-Q1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22121
                  35
BLAST score
                  2.0e-10
E value
Match length
                  111
% identity
                  83
NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1F)
                  299808
Seq. No.
                  LIB3158-014-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                  q119355
NCBI GI
                  158
BLAST score
                   5.0e-11
E value
Match length
                   59
                   58
% identity
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                   >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
                   4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
                   [Zea mays]
                   299809
Seq. No.
                   LIB3158-014-Q1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3377797
BLAST score
                   175
                   4.0e-14
E value
Match length
                   71
```

% identity

(AF075597) Similar to 60S ribosome protein L19; coded for NCBI Description

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

299810 Seq. No.

LIB3158-014-Q1-K1-A3 Seq. ID

% identity

56



```
BLASTX
Method
                  q2880047
NCBI GI
                  182
BLAST score
                  3.0e-16
E value
                  118
Match length
% identity
NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]
                  299811
Seq. No.
                  LIB3158-014-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                  g531829
NCBI GI
                  144
BLAST score
                  4.0e-09
E value
                  62
Match length
                  48
% identity
NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector
                  pSport1]
                   299812
Seq. No.
                  LIB3158-014-Q1-K1-C8
Seq. ID
                   BLASTN
Method
                   g500854
NCBI GI
BLAST score
                   36
                   6.0e-11
E value
                   96
Match length
                   84
% identity
NCBI Description Maize dissociation element DNA
                   299813
Seq. No.
                   LIB3158-014-Q1-K1-E8
Seq. ID
                   BLASTN
Method
                   g473602
NCBI GI
                   71
BLAST score
                   7.0e-32
E value
                   151
Match length
                   87
% identity
NCBI Description Zea mays W-22 histone H2A mRNA, complete cds
                   299814
Seq. No.
                   LIB3158-014-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g728630
NCBI GI
                   170
BLAST score
E value
                   5.0e-12
                   59
Match length
                   61
% identity
                  (X85103) orf [Oryza sativa]
NCBI Description
                   299815
 Seq. No.
                   LIB3158-014-Q1-K1-G9
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q1518540
 BLAST score
                   268
                   1.0e-23
 E value
Match length
                   103
```



[Glyci

```
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
                  299816
Seq. No.
                  LIB3158-015-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g2149640
NCBI GI
                  230
BLAST score
                  1.0e-19
E value
Match length
                  63
                  65
% identity
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
                  299817
Seq. No.
                  LIB3158-015-Q1-K1-C5
Seq. ID
Method
                  BLASTX
                  g2996096
NCBI GI
                  545
BLAST score
                  3.0e-56
E value
                  107
Match length
                  98
% identity
NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
                  299818
Seq. No.
                  LIB3158-015-Q1-K1-D1
Seq. ID
Method
                  BLASTX
                  g1173456
NCBI GI
BLAST score
                  140
                  4.0e-09
E value
                  44
Match length
                  55
% identity
                  SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN
NCBI Description
                  D3) (SM-D3) > gi_600750 (U15009) Sm D3 [Homo sapiens]
                  299819
Seq. No.
                  LIB3158-016-Q1-K1-A7
Seq. ID
                  BLASTX
Method
                   g1710841
NCBI GI
BLAST score
                   150
                   5.0e-10
E value
Match length
                   43
                   70
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905)
                   S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
                   299820
Seq. No.
                   LIB3158-016-Q1-K1-D2
Seq. ID
Method
                   BLASTX
                   g2995953
NCBI GI
BLAST score
                   266
                   3.0e-23
E value
Match length
                   72
                   69
% identity
NCBI Description (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]
```

Seq. No. 299821



```
LIB3158-016-01-K1-E4
Seq. ID
Method
                   BLASTX
                   g2190992
NCBI GI
BLAST score
                   202
                   3.0e-16
E value
                   83
Match length
% identity
                  (AF004358) glutathione S-transferase TSI-1 [Aegilops
NCBI Description
                   tauschii]
                   299822
Seq. No.
                   LIB3158-016-Q1-K1-F12
Seq. ID
Method
                   BLASTX
                   g417482
NCBI GI
                   139
BLAST score
                   8.0e-09
E value
Match length
                   41
                   63
% identity
                   PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX
NCBI Description
                   FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS
                   PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir__JQ2254 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta
                   chain - garden pea >gi_169049 (L08664) farnesyl-protein
                   transferase beta-subunīt [Pisum sativum]
Seq. No.
                   299823
                   LIB3158-017-Q1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1532168
                   189
BLAST score
                   1.0e-14
E value
                   60
Match length
                   75
% identity
                   (U63815) localized according to blastn similarity to EST
NCBI Description
                   sequences; therefore, the coding span corresponds only to
                   an area of similarity since the initation codon and stop
                   codon could not be precisely determined [Arabidopsis
                   thaliana]
Seq. No.
                   299824
Seq. ID
                   LIB3158-017-Q1-K1-B11
Method
                   BLASTX
NCBI GI
                   q1076644
BLAST score
                   161
E value
                   1.0e-11
                   72
Match length
                   49
% identity
                   sucrose transport protein - common tobacco
NCBI Description
                   >gi 575351 emb_CAA57727_ (X82276) sucrose transporter
                   [Nicotiana tabacum]
```

299825 Seq. No.

Seq. ID LIB3158-017-Q1-K1-B12

Method BLASTX NCBI GI g1061040 BLAST score 350 1.0e-33 E value



Match length % identity

(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] NCBI Description

>gi 1587694 prf 2207220A sterol C-methyltransferase

[Arabidopsis thaliana]

Seq. No.

299826

Seq. ID

LIB3158-017-Q1-K1-B4

Method NCBI GI BLASTX g1532165

BLAST score E value

264 4.0e-23

Match length % identity

80 60

NCBI Description

(U63815) similar to dehydrogenase encoded by GenBank Accession Number S39508; localized according to blastn similarity to EST sequences; therefore, the coding span

corresponds only to an area of similarity since the

initation codon and stop

Seq. No.

299827

Seq. ID

LIB3158-017-Q1-K1-C10

Method NCBI GI BLASTX g416758 247

BLAST score E value Match length

3.0e-21 86

58

% identity

SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130) NCBI Description

carboxypeptidase Y-like protein [Arabidopsis thaliana] >qi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis

thaliana]

Seq. No.

299828

Seq. ID

LIB3158-017-Q1-K1-D12

Method BLASTX NCBI GI g2827715 BLAST score 432 E value 6.0e-43107

Match length % identity

26 (AL021684) receptor protein kinase - like protein NCBI Description

[Arabidopsis thaliana]

Seq. No.

299829

Seq. ID

LIB3158-017-Q1-K1-F11

Method BLASTX NCBI GI q2829924 BLAST score 177 E value 2.0e-13 Match length 72

% identity NCBI Description

(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.

299830

53

Seq. ID

LIB3158-017-Q1-K1-F3

Method

BLASTN



```
g13923
NCBI GI
                  60
BLAST score
                  1.0e-25
E value
                  100
Match length
                  91
% identity
NCBI Description Maize mitochondrial gene for 18S rRNA
                  299831
Seq. No.
                  LIB3158-017-Q1-K1-F9
Seq. ID
                  BLASTX
Method
                  g1150932
NCBI GI
                   305
BLAST score
                   3.0e-28
E value
                   89
Match length
% identity
                   70
```

(X88864) cyclin [Medicago sativa] NCBI Description

299832

LIB3158-017-Q1-K1-G12 Seq. ID BLASTX Method g4206210 NCBI GI 151 BLAST score 2.0e-10 E value 43 Match length 65

Seq. No.

% identity (AF071527) putative calcium channel [Arabidopsis thaliana] NCBI Description

>gi 4263043 gb AAD15312 (AC005142) putative calcium

channel [Arabidopsis thaliana]

299833 Seq. No.

LIB3158-017-Q1-K1-G9 Seq. ID

BLASTX Method g1053047 NCBI GI 416 BLAST score 3.0e-41E value 83 Match length 100 % identity

(U38425) histone H3 [Glycine max] >gi 1053049 (U38426) NCBI Description histone H3 [Glycine max] >gi_1053051 (U38427) histone H3

[Glycine max]

299834 Seq. No.

LIB3158-017-Q1-K1-H10 Seq. ID

BLASTX Method NCBI GI q3452497 442 BLAST score 3.0e-44E value 87 Match length % identity

(Y17796) ketol-acid reductoisomerase [Pisum sativum] NCBI Description

299835 Seq. No.

LIB3158-017-Q1-K1-H11 Seq. ID

Method BLASTX NCBI GI q4580460 396 BLAST score 6.0e-39 E value

BLAST score

Match length

% identity

E value

71

133

87

9.0e-32



```
Match length
% identity
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                  thaliana]
                  299836
Seq. No.
                  LIB3158-018-Q1-K1-D4
Seq. ID
Method
                  BLASTX
                  g3378652
NCBI GI
BLAST score
                  602
                  1.0e-62
E value
                  119
Match length
                  99
% identity
                  (AJ005039) CaM-1 [Nicotiana plumbaginifolia]
NCBI Description
                  >gi 3378654_emb_CAA06307_ (AJ005040) CaM-2 [Nicotiana
                  plumbaginifolia]
                  299837
Seq. No.
                  LIB3158-018-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                  g629858
NCBI GI
                  219
BLAST score
                  9.0e-18
E value
Match length
                   38
% identity
                  100
NCBI Description protein kinase C inhibitor - maize
                  299838
Seq. No.
                  LIB3158-018-Q1-K1-F1
Seq. ID
Method
                  BLASTX
                   g4587614
NCBI GI
                   256
BLAST score
E value
                   4.0e-22
Match length
                   82
                   52
% identity
                  (AC006951) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   299839
Seq. No.
                   LIB3158-018-Q1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4582445
                   175
BLAST score
                   1.0e-12
E value
                   49
Match length
% identity
                   65
                   (AC007071) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4589952 gb AAD26470.1 AC007169_2 (AC007169) unknown
                   protein [Arabidopsis thaliana]
Seq. No.
                   299840
                   LIB3158-018-Q1-K1-G5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q22435
```

Match length

% identity

262

84



```
NCBI Description Z.mays PK1 gene for receptor-like protein kinase
                   299841
Seq. No.
                   LIB3158-018-Q1-K1-H3
Seq. ID
Method
                   BLASTX
                   g119355
NCBI GI
                   365
BLAST score
                   6.0e-35
E value
                   128
Match length
                   64
% identity
                   ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                    (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                   >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
                    4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
                    [Zea mays]
                   299842
Seq. No.
                   LIB3159-001-Q1-K1-A9
Seq. ID
                   BLASTN
Method
                   g4140643
NCBI GI
                   107
BLAST score
                   2.0e-53
E value
                    215
Match length
                    33
% identity
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                    complete sequence
                    299843
Seq. No.
                    LIB3159-001-Q1-K1-C10
Seq. ID
                    BLASTN
Method
                    q16072
NCBI GI
BLAST score
                    47
                    2.0e-17
E value
                    202
Match length
% identity
                    81
NCBI Description Acetabularia mediterranea zein gene
                    299844
Seq. No.
                    LIB3159-001-Q1-K1-C9
Seq. ID
Method
                    BLASTX
                    a141606
NCBI GI
                    154
BLAST score
E value
                    2.0e-10
                    74
Match length
                    50
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
NCBI Description
                    >gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) -
                    \overline{\text{maize}} > \overline{\text{gi}} \cdot 168\overline{68}2 \text{ (M12144)} 19 \text{ kDa zein protein [Zea mays]}
                    299845
Seq. No.
Seq. ID
                    LIB3159-001-Q1-K1-E9
                    BLASTN
Method
NCBI GI
                    q22514
BLAST score
                    87
                    2.0e-41
E value
```



NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299846

Seq. ID LIB3159-001-Q1-K1-F11

Method BLASTX
NCBI GI g2832246
BLAST score 232
E value 2.0e-19
Match length 61
% identity 77

NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 299847

Seq. ID LIB3159-001-Q1-K1-H10

Method BLASTN
NCBI GI g168687
BLAST score 35
E value 4.0e-10
Match length 51
% identity 92

NCBI Description Maize 22 kDa zein mRNA, clone cZ22C2, partial cds

Seq. No. 299848

Seq. ID LIB3159-002-Q1-K1-C4

Method BLASTX
NCBI GI g2501353
BLAST score 182
E value 6.0e-14
Match length 72
% identity 56

NCBI Description TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir__S54300

transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) >gi_664901_emb_CAA86607_ (Z46646) transketolase

[Craterostigma plantagineum]

Seq. No. 299849

Seq. ID LIB3159-002-Q1-K1-D3

Method BLASTX
NCBI GI g2149640
BLAST score 159
E value 4.0e-11
Match length 66
% identity 61

NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No. 299850

Seq. ID LIB3159-002-Q1-K1-D4

Method BLASTX
NCBI GI g3024018
BLAST score 374
E value 2.0e-36
Match length 77

% identity 95
NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]



```
299851
Seq. No.
                  LIB3159-002-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  q1903359
NCBI GI
                  145
BLAST score
                  4.0e-09
E value
Match length
                  83
% identity
NCBI Description (AC000104) F19P19.21 [Arabidopsis thaliana]
                  299852
Seq. No.
Seq. ID
                  LIB3159-002-Q1-K1-F10
                  BLASTX
Method
                  q4567273
NCBI GI
                  291
BLAST score
                  4.0e-26
E value
Match length
                  119
% identity
                  55
NCBI Description (AC006841) putative vacuolar proton ATPase subunit
                   [Arabidopsis thaliana]
                  299853
Seq. No.
                  LIB3159-002-Q1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22312
BLAST score
                  37
                  2.0e-11
E value
                  123
Match length
                  89
% identity
NCBI Description Maize ABA-inducible gene for glycine-rich protein ( ABA =
                  abscisic acid)
                   299854
Seq. No.
                  LIB3159-002-Q1-K1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                   q22292
                   103
BLAST score
                   9.0e-51
E value
Match length
                   191
% identity
                   96
NCBI Description Z.mays mRNA for glycine-rich protein
                   299855
Seq. No.
                   LIB3159-002-Q1-K1-H8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168575
BLAST score
                   99
                   1.0e-48
E value
Match length
                   164
% identity
                   90
                  Maize phospholipid transfer protein mRNA, complete cds. of
NCBI Description
                   clone 9C2
```

42186

299856

BLASTX

LIB3159-003-Q1-K1-A6

Seq. No.

Seq. ID

Method



```
q4096786
NCBI GI
                    188
BLAST score
                    2.0e-14
E value
Match length
                    60
                    68
% identity
NCBI Description
                   (U39958) NADP-malic enzyme [Zea mays]
                    299857
Seq. No.
                    LIB3159-003-Q1-K1-B12
Seq. ID
Method
                    BLASTX
                    g3885884
NCBI GI
                    424
BLAST score
                    8.0e-42
E value
Match length
                    97
                    86
% identity
                    (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
                    299858
Seq. No.
                    LIB3159-004-Q1-K1-D1
Seq. ID
                    BLASTX
Method
                    g464707
NCBI GI
                    450
BLAST score
                    7.0e-45
E value
                    111
Match length
% identity
                    76
                    40S RIBOSOMAL PROTEIN S18 >gi_480908_pir _S37496 ribosomal
NCBI Description
                    protein S18.A - Arabidopsis thaliana
                    >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                     [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
                    S18 ribosomal protein [Arabidopsis thaliana]
                    >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                     [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)
                    S18 ribosomal protein [Arabidopsis thaliana]
                    >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
                    thaliana. ESTs qb T21121, gb Z17755, gb R64776 and
                    qb R30430 come from this gene. [Arabidopsis thaliana]
                    >qi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal
                    protein [Arabidopsis thaliana]
                    299859
Seq. No.
                    LIB3159-005-Q1-K1-A4
Seq. ID
                    BLASTX
Method
```

Method BLASTX
NCBI GI g2288999
BLAST score 320
E value 5.0e-34
Match length 90
% identity 78

NCBI Description (AC002335) electron transfer flavoprotein ubiquinone

oxidoreductase isolog [Arabidopsis thaliana]

Seq. No. 299860

Seq. ID LIB3159-005-Q1-K1-B1

Method BLASTX
NCBI GI g3033380
BLAST score 206



```
3.0e-16
E value
Match length
% identity
                  (AC004238) putative coatomer epsilon subunit [Arabidopsis
NCBI Description
                  thaliana]
                  299861
Seq. No.
                  LIB3159-005-Q1-K1-F3
Seq. ID
Method
                  BLASTX
                  q4056480
NCBI GI
BLAST score
                  159
                  7.0e-11
E value
Match length
                  41
% identity
                  73
                  (AC005896) putative adenylate kinase [Arabidopsis thaliana]
NCBI Description
                  299862
Seq. No.
                  LIB3159-005-Q1-K1-F4
Seq. ID
Method
                  BLASTN
                  g22227
NCBI GI
BLAST score
                  165
                  7.0e-88
E value
                  251
Match length
                  95
% identity
NCBI Description Z.mays CAB48 gene for chlorophyll a/b binding protein
                  299863
Seq. No.
                  LIB3159-007-Q1-K1-E12
Seq. ID
Method
                  BLASTN
                  g22646
NCBI GI
                   66
BLAST score
E value
                  1.0e-28
                  158
Match length
% identity
                   94
NCBI Description Z.mays MFS18 mRNA
Seq. No.
                   299864
                   LIB3159-007-Q1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2921512
BLAST score
                   215
E value
                   2.0e-17
                   92
Match length
                   54
% identity
                  (AF037460) GF14 protein [Fritillaria agrestis]
NCBI Description
                   299865
Seq. No.
                   LIB3159-007-Q1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2894379
BLAST score
                   206
                   2.0e-16
E value
                   85
Match length
                   53
% identity
                  (Y14573) ring finger protein [Hordeum vulgare]
NCBI Description
```

42188

299866

Seq. No.



```
LIB3159-007-Q1-K1-F6
Seq. ID
Method
                   BLASTX
                   q3096949
NCBI GI
                   245
BLAST score
                   5.0e-21
E value
Match length
% identity
                   (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana] >gi 3894399 (AF067798) cyclic
                   nucleotide-gated cation channel [Arabidopsis thaliana]
                   299867
Seq. No.
Seq. ID
                   LIB3159-007-Q1-K1-F8
                   BLASTX
Method
                   q3096949
NCBI GI
                   187
BLAST score
                   1.0e-23
E value
Match length
                   96
                   59
% identity
                   (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                    [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic
                   nucleotide-gated cation channel [Arabidopsis thaliana]
Seq. No.
                   299868
                   LIB3159-007-Q1-K1-G12
Seq. ID
Method
                   BLASTX
                   q3885344
NCBI GI
                   173
BLAST score
                    2.0e-12
E value
                    94
Match length
                    37
% identity
                    (AC005623) unknown protein [Arabidopsis thaliana]
NCBI Description
                    >gi_4557057_gb_AAD22497.1_AC007154_1 (AC007154) unknown
                   protein [Arabidopsis thaliana]
                    299869
Seq. No.
Seq. ID
                    LIB3159-007-Q1-K1-G9
                    BLASTX
Method
                    q118104
NCBI GI
BLAST score
                    187
                    1.0e-14
E value
                    45
Match length
% identity
                    PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                    (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                    >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
                    >gi_82914\overline{8}_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
                    299870
Seq. No.
                    LIB3159-007-Q1-K1-H2
Seq. ID
Method
                    BLASTX
                    g2511590
NCBI GI
BLAST score
                    174
```

1.0e-12

66

53

E value Match length

% identity



NCBI Description (Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] >gi_3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]

Seq. No. 299871

Seq. ID LIB3159-008-Q1-K1-A1

Method BLASTX
NCBI GI g3193303
BLAST score 168
E value 2.0e-12
Match length 64
% identity 55

NCBI Description (AF069298) similar to several proteins containing a tandem

repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis

thaliana]

Seq. No. 299872

Seq. ID LIB3159-008-Q1-K1-B2

Method BLASTX
NCBI GI g4206306
BLAST score 503
E value 3.0e-51
Match length 110
% identity 91

NCBI Description (AF049110) prpol [Zea mays]

Seq. No. 299873

Seq. ID LIB3159-008-Q1-K1-B4

Method BLASTX
NCBI GI g1129145
BLAST score 223
E value 4.0e-18
Match length 94

% identity 62

NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No. 299874

Seq. ID LIB3159-008-Q1-K1-C5

Method BLASTX
NCBI GI g3914006
BLAST score 186
E value 1.0e-19
Match length 64
% identity 84

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1816588

(U85495) LON2 [Zea mays]

Seq. No. 299875

Seq. ID LIB3159-008-Q1-K1-C6

Method BLASTX
NCBI GI g1498053
BLAST score 203
E value 3.0e-16
Match length 66
% identity 67

```
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
                    299876
Seq. No.
                    LIB3159-008-Q1-K1-D3
Seq. ID
                    BLASTX
Method
                    q3021270
NCBI GI
                    470
BLAST score
                    3.0e-47
E value
                    122
Match length
% identity
                    72
NCBI Description (AL022347) serine/threonine kinase -like protein
                    [Arabidopsis thaliana]
                    299877
Seq. No.
                    LIB3159-008-Q1-K1-E10
Seq. ID
                    BLASTX
Method
                    g115771
NCBI GI
                    364
BLAST score
                    4.0e-35
E value
                    67
Match length
% identity
                    99
                    CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                    (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll a/b-binding protein precursor - maize
                    >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]
                    299878
Seq. No.
                    LIB3159-008-Q1-K1-E7
Seq. ID
                    BLASTX
Method
                    g4104561
NCBI GI
                    165
BLAST score
                    1.0e-11
E value
                     65
Match length
                     49
% identity
                    (AF036960) subtilisin-like protease [Glycine max]
NCBI Description
                     299879
Seq. No.
                     LIB3159-008-Q1-K1-F1
 Seq. ID
                     BLASTX
Method
                     q2541876
NCBI GI
                     273
BLAST score
                     5.0e-24
E value
```

137 Match length 42 % identity

(D26015) CND41, chloroplast nucleoid DNA binding protein NCBI Description

[Nicotiana tabacum]

299880 Seq. No.

LIB3159-008-Q1-K1-G10 Seq. ID

Method BLASTX q100728 NCBI GI BLAST score 195 4.0e-15 E value 70 Match length 61 % identity

NCBI Description aspartate transaminase (EC 2.6.1.1) AAT3 precursor - proso



millet >gi_1084464_pir__S53304 aspartate aminotransferase -proso millet >gi_20601_emb_CAA45024_ (X63430) aspartate aminotransferase [Panicum miliaceum] >gi_435459_dbj_BAA04993_ (D25323) aspartate aminotransferase [Panicum miliaceum]

Seq. No. 299881

Seq. ID LIB3159-008-Q1-K1-G7

Method BLASTX
NCBI GI g2842480
BLAST score 189
E value 2.0e-16
Match length 86
% identity 57

NCBI Description (ALO21749) ADP, ATP carrier-like protein [Arabidopsis

thaliana]

Seq. No. 299882

Seq. ID LIB3159-009-Q1-K1-D7

Method BLASTX
NCBI GI g135060
BLAST score 245
E value 2.0e-26
Match length 101
% identity 68

NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)

(SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose

synthase [Zea mays] $\overline{>}$ gi_224 $\overline{8}$ 8_emb_CAA262 $\overline{2}$ 9_ (X02382)

sucrose synthase [Zea mays]

Seq. No. 299883

Seq. ID LIB3159-009-Q1-K1-E8

Method BLASTX
NCBI GI g3914899
BLAST score 272
E value 1.0e-31
Match length 88
% identity 83

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal

protein S4 type I [Zea mays]

Seq. No. 299884

Seq. ID LIB3159-009-Q1-K1-F6

Method BLASTX
NCBI GI g4160432
BLAST score 193
E value 9.0e-15
Match length 116
% identity 35

NCBI Description (AF071592) kinesin superfamily motor KIF4 [Homo sapiens]

Seq. No. 299885

Seq. ID LIB3159-009-Q1-K1-G3

Method BLASTX
NCBI GI g1514643
BLAST score 149

```
4.0e-11
E value
Match length
                  81
% identity
                  53
NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
                  299886
Seq. No.
Seq. ID
                  LIB3159-009-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  g4096756
BLAST score
                  151
                  5.0e-10
E value
                  79
Match length
                  42
% identity
                  (U39394) alpha-1,3/4-fucosidase precursor [Streptomyces
NCBI Description
                  sp.]
                  299887
Seq. No.
                  LIB3159-009-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  g4406764
NCBI GI
BLAST score
                  176
                  3.0e-13
E value
Match length
                  69 .
                  54 >
% identity
                  (AC006836) putative uridylyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                  299888
Seq. No.
                  LIB3159-010-Q1-K1-B5
Seq. ID
Method
                  BLASTX
                  g1084481
NCBI GI
BLAST score
                  332
                  3.0e-31
E value
Match length
                  103
% identity
                  71
NCBI Description heat shock protein 70 - Maize
                  299889
Seq. No.
                  LIB3159-010-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3850581
BLAST score
                  276
                  2.0e-24
E value
                  95
Match length
% identity
                  58
                  (AC005278) EST gb N96383 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  299890
Seq. ID
                  LIB3159-010-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q4309734
BLAST score
                  273
                  1.0e-25
E value
Match length
                  101
% identity
                   61
NCBI Description (AC006439) putative 26S proteosome regulatory subunit 8
```

Seq. ID

Method



[Arabidopsis thaliana]

```
299891
Seq. No.
                  LIB3159-011-Q1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22356
BLAST score
                  116
E value
                  1.0e-58
Match length
                  176
                  93
% identity
NCBI Description Maize mRNA for light-harvesting chlorophyll a/b binding
                  protein LHCP
Seq. No.
                  299892
                  LIB3159-011-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                  g3163946
NCBI GI
BLAST score
                  604
E value
                  7.0e-63
Match length
                  112
                  99
% identity
                  (AJ005599) alpha-tubulin 1 [Eleusine indica]
NCBI Description
Seq. No.
                  299893
Seq. ID
                  LIB3159-011-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2894568
BLAST score
                  333
E value
                  4.0e-31
Match length
                  85
                  69
% identity
NCBI Description
                  (AL021890) putative protein [Arabidopsis thaliana]
Seq. No.
                  299894
                  LIB3159-011-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4586027
BLAST score
                  190
E value
                  1.0e-14
Match length
                  93
% identity
                   44
                   (AC007109) putative ribosomal protein L14 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  299895
Seq. ID
                  LIB3159-011-Q1-K1-F4
Method
                  BLASTN
NCBI GI
                  q473602
BLAST score
                  53
E value
                  5.0e-21
Match length
                  197
                  82
% identity
NCBI Description Zea mays W-22 histone H2A mRNA, complete cds
Seq. No.
                  299896
```

42194

LIB3159-011-Q1-K1-F5

BLASTX



NCBI GI q544421 BLAST score 141 7.0e-09 E value Match length 41 % identity 73 NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 1 >gi_485420_pir__S12311 glycine-rich RNA-binding protein (clone S1) - sorghum $(fragment) > gi_21623_emb_CAA40863_ (X57663) \ glycine-rich$ RNA-binding protein [Sorghum bicolor] Seq. No. 299897 Seq. ID LIB3159-011-Q1-K1-H11 Method BLASTX NCBI GI q3914899

BLAST score 198 E value 2.0e-15 Match length 118 % identity 40

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 2331301 (AF013487) ribosomal

protein S4 type I [Zea mays]

299898 Seq. No.

Seq. ID LIB3159-011-Q1-K1-H9

Method BLASTX NCBI GI q115771 BLAST score 583 E value 2.0e-60 Match length 107 % identity 100

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 299899

Seq. ID LIB3159-012-Q1-K1-B3

Method BLASTN NCBI GI q22091 BLAST score 171 E value 2.0e-91 255 Match length % identity 92

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

299900 Seq. No.

Seq. ID LIB3159-012-Q1-K1-C12

Method BLASTX g2529677 NCBI GI 190 BLAST score E value 2.0e-14 Match length 91 % identity 45

NCBI Description (AC002535) kinesin-like protein, heavy chain [Arabidopsis

thaliana]

Seq. No. 299901



```
LIB3159-012-Q1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2160177
                  402
BLAST score
                  3.0e - 39
E value
                  120
Match length
                  62
% identity
                  (AC000132) EST gb_R64758 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  299902
Seq. No.
                  LIB3159-012-Q1-K1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3236242
BLAST score
                  221
                  6.0e-18
E value
                  86
Match length
                  57
% identity
                  (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                  thaliana]
                  299903
Seq. No.
                  LIB3159-012-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  g4454051
NCBI GI
BLAST score
                  171
                  3.0e-12
E value
Match length
                  45
                  71
% identity
                  (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                  299904
Seq. No.
                  LIB3159-012-Q1-K1-G12
Seq. ID
Method
                  BLASTN
                  g2589161
NCBI GI
BLAST score
                  127
E value
                  5.0e-65
Match length
                  181
% identity
                  92
NCBI Description Zea mays mRNA for aldehyde oxidase, complete cds
                  299905
Seq. No.
                  LIB3159-013-Q1-K1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1206013
BLAST score
                   337
                   1.0e-31
E value
Match length
                   64
                   97
% identity
NCBI Description (U44087) beta-D-glucosidase precursor [Zea mays]
                   299906
Seq. No.
                  LIB3159-013-Q1-K1-C4
Seq. ID
Method
                  BLASTX
```

42196

g4105269

153

NCBI GI BLAST score



E value 4.0e-10 Match length 102 % identity NCBI Description [Rattus norvegicus]

(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase

Seq. No. 299907

Seq. ID LIB3159-013-Q1-K1-F10

Method BLASTX q3252807 NCBI GI BLAST score 279 E value 8.0e-25 Match length 133 % identity 45

(AC004705) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 299908

Seq. ID LIB3159-013-Q1-K1-G1

Method BLASTX g1495804 NCBI GI BLAST score 390 E value 7.0e-38 Match length 125 % identity 59

NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]

299909 Seq. No.

Seq. ID LIB3159-013-Q1-K1-G11

Method BLASTX NCBI GI q730526 BLAST score 195 E value 5.0e-15 Match length 95 % identity 46

60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) NCBI Description

> >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein

[Arabidopsis thaliana]

299910 Seq. No.

Seq. ID LIB3159-013-Q1-K1-G3

Method BLASTX g4210330 NCBI GI BLAST score 284 1.0e-25 E value Match length 101 % identity 58

NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit

[Arabidopsis thaliana]

299911 Seq. No.

Seq. ID LIB3159-013-Q1-K1-H3

BLASTN Method NCBI GI g758352 BLAST score 92 2.0e-44 E value Match length 234



% identity 85
NCBI Description Z.mays mRNA for cysteine synthase
Seq. No. 299912

Seq. ID LIB3159-013-Q1-K1-H6
Method BLASTX
NCBI GI g2851508
BLAST score 410
E value 4.0e-40
Match length 81
% identity 86

NCBI Description 60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to

ribosomal protein L21 (gb L38826). ESTs

gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein

L21 [Arabidopsis thaliana]

Seq. No. 299913

Seq. ID LIB3159-015-Q1-K1-A2

Method BLASTN
NCBI GI g3789953
BLAST score 42
E value 1.0e-14
Match length 54
% identity 94

NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor

(Cab26) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 299914

Seq. ID LIB3159-015-Q1-K1-B1

Method BLASTX
NCBI GI g4105798
BLAST score 172
E value 2.0e-12
Match length 96
% identity 34

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 299915

Seq. ID LIB3159-015-Q1-K1-E3

Method BLASTX
NCBI GI g2129668
BLAST score 161
E value 1.0e-11
Match length 63
% identity 57

NCBI Description phosphoglycerate kinase - Arabidopsis thaliana (fragment)

>gi 1022803 (U37700) phosphoglycerate kinase [Arabidopsis

thaliana]

Seq. No. 299916

Seq. ID LIB3159-015-Q1-K1-E4

Method BLASTX
NCBI GI g2827663
BLAST score 180
E value 4.0e-13



```
Match length
                  12
% identity
                   (AL021637) membrane-associated salt-inducible-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  299917
Seq. ID
                  LIB3159-015-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q4651204
BLAST score
                  267
E value
                  1.0e-23
Match length
                  92
% identity
                   49
NCBI Description
                  (AB026262) ring finger protein [Cicer arietinum]
                  299918
Seq. No.
                  LIB3159-015-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3522956
                  141
BLAST score
E value
                  4.0e-09
                   67
Match length
% identity
                   48
NCBI Description
                   (AC004411) putative pectinacetylesterase precursor
                   [Arabidopsis thaliana]
                  299919
Seq. No.
Seq. ID
                  LIB3159-015-01-K1-H5
Method
                  BLASTX
NCBI GI
                  q1170937
BLAST score
                   511
E value
                   5.0e-52
Match length
                  103
% identity
                   95
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   299920
Seq. No.
Seq. ID
                  LIB3159-016-Q1-K1-C11
Method
                  BLASTX
                  g3775987
NCBI GI
BLAST score
                   351
E value
                   4.0e-33
Match length
                  128
% identity
                  58
NCBI Description
                  (AJ010457) RNA helicase [Arabidopsis thaliana]
                  299921
Seq. No.
```

Seq. ID LIB3159-016-Q1-K1-C12

Method BLASTX NCBI GI g729135 BLAST score 386 E value 2.0e-37 Match length 106 % identity 76



NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi 283034 pir S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi 168532 (M73235) O-methyltransferase [Zea mays] 299922 Seq. No. Seq. ID LIB3159-016-Q1-K1-E8 Method BLASTX NCBI GI g3294467 BLAST score 164 E value 6.0e-12 Match length 71 % identity 49 NCBI Description (U89341) phosphoglucomutase 1 [Zea mays] Seq. No. 299923 Seq. ID LIB3159-016-Q1-K1-F4 Method BLASTX NCBI GI g1661160 BLAST score 347 E value 6.0e-35 Match length 97 % identity 75 NCBI Description (U74295) chlorophyll a/b binding protein [Oryza sativa] Seq. No. 299924 Seq. ID LIB3159-016-Q1-K1-F8 Method BLASTN NCBI GI g2326946 BLAST score 54 E value 2.0e-21 Match length 118 % identity 86 NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29 Seq. No. 299925 Seq. ID LIB3159-016-Q1-K1-G11 Method BLASTX NCBI GI g120670 BLAST score 236 E value 1.0e-19 Match length 49 98 % identity NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 100879_pir S06879 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C - maize >gi_295853_emb_CAA33620 (X15596) GAPDH [Zea mays] Seq. No. 299926 Seq. ID LIB3159-016-Q1-K1-H8 Method BLASTX

NCBI GI g4505743 BLAST score 175 E value 1.0e-12 Match length 93 % identity 42



NCBI Description prefoldin 5 >gi_2498565_sp_Q99471_MM1_HUMAN C-MYC BINDING PROTEIN MM-1 >gi_1731809_dbj_BAA14006_ (D89667) c-myc

binding protein [Homo sapiens]

Seq. No. 299927

Seq. ID LIB3159-017-Q1-K1-C3

Method BLASTX
NCBI GI g2827621
BLAST score 165
E value 2.0e-11
Match length 83
% identity 51

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 299928

Seq. ID LIB3159-017-Q1-K1-C4

Method BLASTX
NCBI GI g3877997
BLAST score 164
E value 1.0e-11
Match length 83
% identity 35

NCBI Description (Z92970) predicted using Genefinder; Similarity to Bovine

protien disulphide isomerase ER-60 (SW:P38657); cDNA EST EMBL:D69661 comes from this gene; cDNA EST EMBL:T01819 comes from this gene; cDNA EST EMBL:T01942 comes from thi

Seq. No. 299929

Seq. ID LIB3159-017-Q1-K1-F5

Method BLASTX
NCBI GI g1658313
BLAST score 138
E value 3.0e-17
Match length 60
% identity 38

NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 299930

Seq. ID LIB3159-017-Q1-K1-G12

Method BLASTX
NCBI GI g226261
BLAST score 152
E value 2.0e-10
Match length 39
% identity 74

NCBI Description alphal tubulin [Arabidopsis thaliana]

Seq. No. 299931

Seq. ID LIB3159-017-Q1-K1-G8

Method BLASTX
NCBI GI g3393044
BLAST score 177
E value 2.0e-13
Match length 53
% identity 68

NCBI Description (AJ000153) sucrose synthase type 2 [Triticum aestivum]

```
Seq. No.
                   299932
                   LIB3159-018-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g115771
NCBI GI
                   264
BLAST score
                   3.0e-23
E value
                    69
Match length
                   78
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                    (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll a/b-binding protein precursor - maize
                   >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]
Seq. No.
                    299933
                    LIB3159-018-Q1-K1-C12
Seq. ID
                    BLASTX
Method
                    g729671
NCBI GI
                    173
BLAST score
                    1.0e-14
E value
Match length
                    69
                    70
% identity
NCBI Description HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]
                    299934
Seq. No.
                    LIB3159-018-Q1-K1-C3
Seq. ID
                    BLASTX
Method
                    g4587585
NCBI GI
                    240
BLAST score
                    3.0e-20
E value
                    105
Match length
% identity
                    51
                    (AC007232) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    299935
Seq. No.
                    LIB3159-018-Q1-K1-D3
Seq. ID
                    BLASTX
Method
                    g595768
NCBI GI
                    155
BLAST score
                     3.0e-10
E value
                     47
Match length
                     62
 % identity
NCBI Description (U13866) non-functional lacZ alpha peptide [Cloning vector]
                     299936
 Seq. No.
                     LIB3159-018-Q1-K1-F12
 Seq. ID
                     BLASTX
 Method
```

Method BLASTX
NCBI GI g4512649
BLAST score 173
E value 7.0e-15
Match length 85
% identity 58

NCBI Description (AC007048) hypothetical protein [Arabidopsis thaliana]

Seq. No. 299937

Seq. ID LIB3159-018-Q1-K1-F2

Method BLASTX



```
g2842648
NCBI GI
                  171
BLAST score
                  5.0e-21
E value
Match length
                  119
% identity
                  43
                  U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR 35 KD
NCBI Description
                  SUBUNIT RELATED-PROTEIN 2 >gi_2137782_pir__A57120 small
                  nuclear ribonucleoprotein auxiliary factor U2 - mouse
                  >gi 927659_dbj_BAA08143_ (D45205) U2af1-rs2 [Mus musculus]
                  299938
Seq. No.
                  LIB3159-019-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                   g3335359
NCBI GI
BLAST score
                   175
E value
                   1.0e-12
Match length
                   115
% identity
                   35
                  (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
                   299939
Seq. No.
                   LIB3159-019-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   q641905
NCBI GI
BLAST score
                   202
                   6.0e-16
E value
Match length
                   92
                   48
% identity
                   (U19267) cysteine proteinase [Zinnia elegans]
NCBI Description
                   299940
Seq. No.
                   LIB3159-019-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   g1519251
NCBI GI
                   248
BLAST score
                   2.0e-30
E value
                   109
Match length
                   70
 % identity
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                   299941
 Seq. No.
                   LIB3159-019-Q1-K1-C6
 Seq. ID
                   BLASTN
 Method
                   g551482
 NCBI GI
                   134
 BLAST score
                   3.0e-69
 E value
                   306
 Match length
                   90
 % identity
                   Zea mays ABA- and ripening-inducible-like protein mRNA,
 NCBI Description
                   complete cds
                    299942
 Seq. No.
                   LIB3159-019-Q1-K1-D11
```

Seq. ID

BLASTX Method g3386617 NCBI GI BLAST score 186 4.0e-14 E value



```
Match length
                  63
                  59
% identity
                  (AC004665) putative cell division protein (ftsY)
NCBI Description
                  [Arabidopsis thaliana]
                  299943
Seq. No.
                  LIB3159-019-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g2344894
NCBI GI
                  296
BLAST score
                  7.0e-27
E value
                  73
Match length
% identity
                  (AC002388) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  299944
Seq. No.
                  LIB3159-019-Q1-K1-E5
Seq. ID
                  BLASTX
Method
                   g116317
NCBI GI
                  149
BLAST score
                   1.0e-09
E value
                  55
Match length
                   55
% identity
                  BASIC ENDOCHITINASE 2 PRECURSOR >gi_100669_pir__S15997
NCBI Description
                   chitinase (EC 3.2.1.14) - rice >gi_227845_prf__1712313A
                   basic chitinase [Oryza sativa]
                   299945
Seq. No.
                   LIB3159-019-Q1-K1-F3
Seq. ID
                   BLASTN
Method
                   g294844
NCBI GI
                   68
BLAST score
                   5.0e-30
E value
                   156
Match length
% identity
                   Saccharum hybrid cultivar H65-7052 membrane protein mRNA,
NCBI Description
                   complete cds
                   299946
Seq. No.
                   LIB3159-019-Q1-K1-F4
Seq. ID
```

BLASTX

Method q2559012 NCBI GI 233 BLAST score 1.0e-19 E value 78 Match length 62 % identity

(AF026293) chaperonin containing t-complex polypeptide 1, NCBI Description

beta subunit; CCT-beta [Homo sapiens] >gi_4090929

(AF026166) chaperonin-containing TCP-1 beta subunit homolog

[Homo sapiens]

299947 Seq. No.

LIB3159-019-Q1-K1-G1 Seq. ID

BLASTX Method g1370603 NCBI GI BLAST score 439 1.0e-43 E value



93

87

Match length

% identity

```
Match length
                  80
% identity
NCBI Description (X98245) annexin p35 [Zea mays]
                  299948
Seq. No.
                  LIB3159-019-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                  g1877026
NCBI GI
                  177
BLAST score
                  7.0e-13
E value
                  50
Match length
                  74
% identity
NCBI Description (D78336) ribosomal protein S19 [Oryza sativa]
Seq. No.
                  299949
                  LIB3159-020-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                   g3059131
NCBI GI
                   162
BLAST score
                   3.0e-11
E value
Match length
                   105
                   39
% identity
                  (AJ000478) cytochrome P450 [Helianthus tuberosus]
NCBI Description
                   299950
Seq. No.
                   LIB3159-020-Q1-K1-A5
Seq. ID
                   BLASTN
Method
                   g22274
NCBI GI
                   90
BLAST score
                   2.0e-43
E value
                   97
Match length
                   99
% identity
                  Maize 26S - 17S rDNA spacer region from Black Mexican Sweet
NCBI Description
                   (BMS) suspension cells
                   299951
Seq. No.
                   LIB3159-020-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   g1169782
NCBI GI
                   202
BLAST score
                   4.0e-16
E value
                   73
Match length
                   53
 % identity
                   FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis
NCBI Description
                   thaliana]
                   299952
 Seq. No.
                   LIB3159-020-Q1-K1-D1
 Seq. ID
                   BLASTX
 Method
                   g115786
 NCBI GI
 BLAST score
                   416
                   5.0e-41
 E value
```

42205

(CAB) (LHCP) >gi 82680_pir__A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

NCBI Description



mays]

```
299953
Seq. No.
                  LIB3159-020-Q1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1370602
BLAST score
                  121
                  1.0e-61
E value
                  225
Match length
                  88
% identity
NCBI Description Z.mays mRNA for annexin p35
                  299954
Seq. No.
Seq. ID
                  LIB3159-021-Q1-K1-A11
Method
                  BLASTN
NCBI GI
                  q168704
BLAST score
                  60
E value
                  2.0e-25
Match length
                  92
                  91
% identity
NCBI Description Zea mays zein protein gene, complete cds
                  299955
Seq. No.
                  LIB3159-021-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q310587
BLAST score
                  266
                  1.0e-37
E value
Match length
                  126
                  66
% identity
NCBI Description
                  (L20864) ascorbate peroxidase [Spinacia oleracea]
                  >gi 1384110 dbj BAA12890 (D85864) cytosolic ascorbate
                  peroxidase [Spinacia oleracea]
                  299956
Seq. No.
Seq. ID
                  LIB3159-021-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g115764
BLAST score
                  248
E value
                  4.0e-28
Match length
                  96
                  71
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE I PRECURSOR
                   (CAB-6A) (LIGHT-HARVESTING COMPLEX I 26 KD PROTEIN)
                  >gi_170494 (J03558) chlorophyll a/b binding protein
                  precursor [Lycopersicon esculentum]
Seq. No.
                  299957
                  LIB3159-021-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024018
BLAST score
                  467
E value
                  7.0e-47
Match length
                  115
% identity
                  78
```

42206

>gi 1546919 emb CAA69225 (Y07920) translation initiation

INITIATION FACTOR 5A (EIF-5A) (EIF-4D)



factor 5A [Zea mays] >gi_2668738 (AF034943) translation
initiation factor 5A [Zea mays]

Seq. No. 299958 LIB3159-021-Q1-K1-E3 Seq. ID BLASTX Method q4006913 NCBI GI 235 BLAST score 8.0e-20 E value Match length 77 % identity (Z99708) hypothetical protein [Arabidopsis thaliana] NCBI Description 299959 Seq. No. LIB3159-021-Q1-K1-E6 Seq. ID Method BLASTX g1706082 NCBI GI BLAST score 215 1.0e-17 E value 85 Match length 52 % identity SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) NCBI Description >gi 629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3 [Hordeum vulgare] Seq. No. 299960 LIB3159-021-Q1-K1-F11 Seq. ID BLASTX Method q2190552 NCBI GI 389 BLAST score 1.0e-37 E value 114 Match length % identity 64 (AC001229) Similar to Holcus major pollen allergen NCBI Description (gb_Z27084). [Arabidopsis thaliana] 299961 Seq. No. LIB3159-021-Q1-K1-F5 Seq. ID BLASTX Method g3702338 NCBI GI 272 BLAST score 4.0e-24 E value 101 Match length 50 % identity (AC005397) unknown protein [Arabidopsis thaliana] NCBI Description 299962 Seq. No. LIB3159-021-Q1-K1-H3 Seq. ID BLASTX Method g118104 NCBI GI

42207

144

83

2.0e-10

BLAST score

Match length

E value



```
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi 68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi_168461 (M55021) cyclophilin [Zea mays]
                  >gi_82914\overline{8}_{emb}CAA48638_{(X68678)} cyclophilin [Zea mays]
                  299963
Seq. No.
                  LIB3179-001-P1-K2-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2687358
                  336
BLAST score
                  1.0e-35
E value
                  124
Match length
% identity
NCBI Description (AF033263) nonphototropic hypocotyl 1 [Zea mays]
                  299964
Seq. No.
                  LIB3179-001-P2-K1-A3
Seq. ID
                  BLASTX
Method
                  q1172861
NCBI GI
BLAST score
                  286
                   8.0e-26
E value
                   90
Match length
                   63
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR
NCBI Description
                   (RUBISCO LARGE SUBUNIT) >gi_1363613_pir__S58560
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain
                   - maize chloroplast >gi_18036_emb_CAA78027_ (Z11973)
                   Ribulose bisphosphate carboxylase [Zea mays]
                   >gi 902230 emb CAA60294 (X86563) rubisco large subunit
                   [Zea mays]
                   299965
Seq. No.
                   LIB3179-001-P2-K1-C10
Seq. ID
                   BLASTX
Method
                   q4539677
NCBI GI
BLAST score
                   147
                   1.0e-09
E value
                   88
Match length
                   43
% identity
NCBI Description (AF061282) patatin-like protein [Sorghum bicolor]
                   299966
Seq. No.
                   LIB3179-001-P2-K1-D12
Seq. ID
                   BLASTX
Method
                   g2944088
NCBI GI
BLAST score
                   179
                   3.0e-13
E value
                   68
Match length
                   53
 % identity
 NCBI Description (AF050102) glutathione s-transferase [Oryza sativa]
```

Seq. No. 299967

Seq. ID LIB3179-001-P2-K1-D4

Method BLASTX NCBI GI g131225



```
BLAST score
E value
                  4.0e-35
Match length
                  130
                  57
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  299968
Seq. No.
Seq. ID
                  LIB3179-001-P2-K1-D6
Method
                  BLASTX
NCBI GI
                  q2879811
                  238
BLAST score
E value
                  4.0e-20
                  89
Match length
% identity
                  (AJ223316) ribosomal protein L30 [Lupinus luteus]
NCBI Description
                  299969
Seq. No.
                  LIB3179-001-P2-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g531829
BLAST score
                  189
E value
                  2.0e-14
Match length
                   78
                   53
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                   299970
Seq. No.
                  LIB3179-001-P2-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q531829
BLAST score
                   138
E value
                   1.0e-08
Match length
                   75
                   49
% identity
NCBI Description
                  (U12390) beta-galactosidase alpha peptide [cloning vector
                   pSport1]
                   299971
Seq. No.
                   LIB3179-001-P2-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2687358
                   220
BLAST score
E value
                   5.0e-18
Match length
                   109
% identity
                   50
                  (AF033263) nonphototropic hypocotyl 1 [Zea mays]
NCBI Description
                   299972
Seq. No.
```

Seq. ID LIB3179-001-P2-K1-F9

Method BLASTX
NCBI GI g3599491
BLAST score 285
E value 1.0e-25



```
Match length 118 % identity 48
```

NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.

299973

Seq. ID

LIB3179-001-P2-K1-G1

Method NCBI GI BLASTX g1362086

BLAST score E value 388 1.0e-37

Match length % identity

99 76

NCBI Description

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi 2129919_pir _S65957

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >qi 886471 emb CAA58474 (X83499) methionine synthase

[Catharanthus roseus]

Seq. No.

299974

Seq. ID

LIB3179-001-P2-K1-G11

Method BLASTX
NCBI GI g445612
BLAST score 171
E value 3.0e-12
Match length 52

Match length 52 % identity 65

NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No.

299975

Seq. ID

LIB3179-001-P2-K1-H12

Method BLASTN
NCBI GI g475252
BLAST score 44
E value 9.0e-16
Match length 131
% identity 85

NCBI Description Z.mays MPI gene

Seq. No.

299976

Seq. ID

LIB3179-001-P2-K1-H4

Method BLASTX
NCBI GI g2494261
BLAST score 222
E value 7.0e-32
Match length 116
% identity 61

NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)

>gi_99903_pir__S21567 translation elongation factor Tu
precursor - soybean chloroplast >gi_18776_emb_CAA46864_
(X66062) EF-Tu [Glycine max] >gi_448921_prf__1918220A

elongation factor Tu [Glycine max]

Seq. No.

299977

Seq. ID

LIB3179-001-P2-K1-H7

Method

BLASTX



q2501189 NCBI GI BLAST score 227 8.0e-19 E value 114 Match length % identity THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR NCBI Description >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi 596078 (U17350) thiamine biosynthetic enzyme [Zea mays] 299978 Seq. No. LIB3179-002-P1-K1-C1 Seq. ID BLASTX Method NCBI GI g461550 BLAST score 241 2.0e-20 E value 59 Match length 80 % identity ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR NCBI Description >gi 81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast -Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana] Seq. No. 299979 LIB3179-002-P1-K1-D4 Seq. ID Method BLASTN g559535 NCBI GI BLAST score 64 E value 1.0e-27 136 Match length 87 % identity NCBI Description Z.mays mRNA for metallothionein 299980 Seq. No. LIB3179-002-P1-K1-D7 Seq. ID Method BLASTX NCBI GI q994736 147 BLAST score 9.0e-10 E value Match length 46 65 % identity (M18327) LacOPZ-alpha peptide from pUC9; putative [cloning NCBI Description vectors] >gi_994738 (M18328) LacOPZ-alpha peptide from pUC9; putative [cloning vectors] >gi_994740 (M18329) LacOPZ-alpha peptide from pUC9; putative [cloning vectors]

Sea. No. 299981

Seq. No. 299981 Seq. ID LIB3179-002-P1-K1-G4

Method BLASTN
NCBI GI g342630
BLAST score 39
E value 9.0e-13
Match length 148
% identity 82

NCBI Description Maize chloroplast His-tRNA gene on Ecol fragment



```
Seq. No.
Seq. ID
                  LIB3179-002-P1-K2-F4
Method
                  BLASTN
NCBI GI
                  g405634
BLAST score
                  294
E value
                  1.0e-164
Match length
                  334
                  97
% identity
NCBI Description Z.mays zmcpt mRNA triose phosphate/phosphate translocator
Seq. No.
                  299983
Seq. ID
                  LIB3179-002-P2-K1-A3
Method
                  BLASTX
NCBI GI
                  g1174613
BLAST score
                  423
E value
                  1.0e-41
Match length
                  144
% identity
                  63
                 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 1) (TBP-1) >qi 556560 dbj BAA04614
                  (D17788) rice homologue of Tat binding protein [Oryza
                  sativa]
Seq. No.
                  299984
Seq. ID
                  LIB3179-002-P2-K1-A5
Method
                  BLASTX
NCBI GI
                  q567893
BLAST score
                  223
E value
                  4.0e-18
Match length
                  95
                  45
% identity
NCBI Description
                  (L37382) beta-galactosidase-complementation protein
                  [Cloning vector]
Seq. No.
                  299985
Seq. ID
                  LIB3179-002-P2-K1-B10
                  BLASTN
Method
NCBI GI
                  g475252
BLAST score
                  37
                  3.0e-11
E value
Match length
                  296
% identity
                  78
NCBI Description Z.mays MPI gene
                  299986
Seq. No.
Seq. ID
                  LIB3179-002-P2-K1-C1
Method
                  BLASTX
NCBI GI
                  g461550
BLAST score
                  180
                  3.0e-13
E value
Match length
                  65
% identity
                  63
```

% identity 63
NCBI Description ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR
>gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast Arabidopsis thaliana >gi 166632 (M61741) ATP synthase

gamma-subunit [Arabidopsis thaliana]

Seq. ID Method



```
Seq. No.
                  299987
Seq. ID
                  LIB3179-002-P2-K1-C10
Method
                  BLASTX
                  q1853970
NCBI GI
                  262
BLAST score
E value
                   9.0e-23
                  136
Match length
% identity
NCBI Description
                  (D88122) CPRD46 protein [Vigna unguiculata]
Seq. No.
                  299988
Seq. ID
                  LIB3179-002-P2-K1-D1
Method
                  BLASTN
                   q3264597
NCBI GI
BLAST score
                   75
                   5.0e-34
E value
Match length
                   242
% identity
                   84
NCBI Description Zea mays trypsin inhibitor mRNA, complete cds
                   299989
Seq. No.
Seq. ID
                  LIB3179-002-P2-K1-D10
Method
                  BLASTX
                   q2501578
NCBI GI
                   400
BLAST score
                   5.0e+39
E value
Match length
                   124
% identity
                   59
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047
NCBI Description
                   ethylene-responsive protein 1 - Para rubber tree
                   >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                   brasiliensis]
Seq. No.
                   299990
Seq. ID
                   LIB3179-002-P2-K1-D3
Method
                   BLASTX
NCBI GI
                   q3287494
BLAST score
                   289
                   7.0e-26
E value
Match length
                   129
% identity
                   53
NCBI Description (D78504) similar to yeast SRP1 [Oryza sativa]
                   299991
Seq. No.
                   LIB3179-002-P2-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3287494
BLAST score
                   236
                   8.0e-20
E value
                   100
Match length
                   57
% identity
NCBI Description (D78504) similar to yeast SRP1 [Oryza sativa]
                   299992
Seq. No.
```

42213

LIB3179-002-P2-K1-D6

BLASTX



```
g4544419
NCBI GI
                   149
BLAST score
                   2.0e-09
E value
Match length
                   79
% identity
                   48
                   (AC006955) unknown protein [Arabidopsis thaliana]
NCBI Description
                   299993
Seq. No.
                   LIB3179-002-P2-K1-E2
Seq. ID
                   BLASTX
Method
                   g131134
NCBI GI
                   384
BLAST score
                   4.0e-37
E value
                   117
Match length
% identity
                    64
                   PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1
NCBI Description
                   >gi_1363576_pir__S58552 photosystem I protein A1 - maize
chloroplast >gi_342595 (M11203) P700 chlorophyll a-protein
                    PSI-A1 [Zea mays] >gi_902222_emb_CAA60286_ (X86563) PSI
                    P700 apoprotein Al [Zea mays]
                    299994
Seq. No.
                    LIB3179-002-P2-K1-F1
Seq. ID
                    BLASTX
Method
                    q1657851
NCBI GI
BLAST score
                    172
                    2.0e-12
E value
Match length
                    51
                    35
% identity
                    (U73214) cold acclimation protein WCOR518 [Triticum
NCBI Description
                    aestivum]
                    299995
Seq. No.
                    LIB3179-002-P2-K1-F10
Seq. ID
                    BLASTX
Method
                    g1698670
NCBI GI
                    383
BLAST score
                    5.0e-37
E value
                    128
Match length
                    58
 % identity
                   (U66241) S-like RNase [Zea mays]
NCBI Description
                    299996
 Seq. No.
                    LIB3179-002-P2-K1-G3
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q133852
                    221
 BLAST score
                    6.0e-18
 E value
                    74
 Match length
                    64
 % identity
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S19 >gi 71030 pir R3ZM19
 NCBI Description
                    ribosomal protein S19 - maize chloroplast
                    >gi_1208517_emb_CAA60374_ (X86563) ribosomal protein S19
                     [Zea mays] >gi_2654314_emb_CAA60326_ (X86563) ribosomal
```

Seq. No. 299997

protein S19 [Zea mays]



```
LIB3179-002-P2-K1-G7
Seq. ID
Method
                   BLASTX
                   g1550814
NCBI GI
BLAST score
                   281
                   6.0e-25
E value
                   119
Match length
                   52
% identity
                   (Y07959) 60S acidic ribosomal protein PO [Zea mays]
NCBI Description
                   299998
Seq. No.
                   LIB3179-002-P2-K1-H1
Seq. ID
                   BLASTX
Method
                   g135535
NCBI GI
                   297
BLAST score
                   5.0e-27
E value
                   95
Match length
                   67
% identity
                   T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
NCBI Description
                   (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide
                   Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_
(D11351) t-complex polypeptide 1 homologue [Arabidopsis
                   thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT
                   alpha/TCP-1 [Arabidopsis thaliana]
                   299999
Seq. No.
                   LIB3179-002-P2-K1-H3
Seq. ID
                   BLASTN
Method
                   g1698669
NCBI GI
                   121
BLAST score
                   2.0e-61
E value
Match length
                   385
                   83
% identity
NCBI Description Zea mays S-like RNase (kin1) mRNA, complete cds
                   300000
Seq. No.
                   LIB3179-002-P2-K1-H5
Seq. ID
                   BLASTX
Method
                   g1351271
NCBI GI
BLAST score
                   192
                   1.0e-14
E value
Match length
                    55
                    67
% identity
                   TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                    >gi_1084309_pir__S52032 triose-phosphate isomerase (EC
                    5.3.1.1) precursor, chloroplast - spinach >gi_806312
                    (L36387) triosephosphate isomerase, chloroplast isozyme
                    [Spinacia oleracea]
                    300001
Seq. No.
                    LIB3179-019-P1-K1-D11
Seq. ID
Method
                    BLASTX
                    q1778147
NCBI GI
BLAST score
                    270
                    1.0e-23
E value
                    58
Match length
% identity
                    95
NCBI Description (U66403) phosphate/phosphoenolpyruvate translocator
```

BLAST score

Match length

% identity

E value

221

67

58

6.0e-18



precursor [Zea mays]

```
Seq. No.
                  300002
Seq. ID
                  LIB3179-019-P1-K1-E8
Method
                  BLASTN
NCBI GI
                  g474945
BLAST score
                  118
E value
                  1.0e-59
                  258
Match length
% identity
                  86
NCBI Description Z.mays mRNA for subtilisin-chymotrypsin inhibitor
Seq. No.
                  300003
                  LIB3179-020-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266578
BLAST score
                  205
                  3.0e-16
E value
Match length
                  56
% identity
                  68
                  METALLOTHIONEIN-LIKE PROTEIN 1 >gi 100898 pir S17560
NCBI Description
                  metallothionein-like protein - maize >gi_236730 bbs_57629
                  (S57628) metallothionein homologue [Zea mays, Peptide, 76
                  aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186)
                  metallothionein- like protein [Zea mays]
                  >gi 228095 prf 1717215A metallothionein-like protein [Zea
                  mays]
Seq. No.
                  300004
Seq. ID
                  LIB3179-020-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  g559535
BLAST score
                  71
E value
                  7.0e-32
Match length
                  107
                  92
% identity
NCBI Description Z.mays mRNA for metallothionein
                  300005
Seq. No.
Seq. ID
                  LIB3179-020-P1-K1-C2
Method
                  BLASTN
NCBI GI
                  g596079
BLAST score
                  108
                  8.0e-54
E value
Match length
                  287
% identity
                  85
NCBI Description Zea mays thiamine biosynthetic enzyme (thi1-2) mRNA,
                  complete cds
Seq. No.
                  300006
                  LIB3179-020-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980793
```

Match length

% identity

83



NCBI Description

```
300007
Seq. No.
                  LIB3179-020-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115770
BLAST score
                  226
                  1.0e-18
E value
                  48
Match length
                  85
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB) (LHCP) >gi_100533_pir__S07448 chlorophyll a/b-binding
                  protein - swollen duckweed >gi 168290 (M12152) chlorophyll
                  a/b apoprotein [Lemna gibba]
                  300008
Seq. No.
                  LIB3179-020-P1-K1-G2
Seq. ID
Method
                  BLASTX
                  q3522946
NCBI GI
BLAST score
                  267
                  1.0e-23
E value
                  93
Match length
                  52
% identity
                  (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  300009
Seq. No.
                  LIB3179-021-P1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q114599
                   347
BLAST score
                   9.0e-33
E value
                   99
Match length
                   71
% identity
                  ATP SYNTHASE EPSILON CHAIN >gi 67867 pir PWZME
NCBI Description
                   H+-transporting ATP synthase (EC 3.6.1.34) epsilon chain -
                  maize chloroplast >gi_342578 (J01421) coupling factor
                   epsilon subunit [Zea mays] >gi_902228_emb_CAA60292
                   (X86563) ATPase epsilon subunit [Zea mays]
Seq. No.
                   300010
                   LIB3179-021-P1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4581163
BLAST score
                   335
                   3.0e-31
E value
Match length
                   104
% identity
                   66
                   (AC006220) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   300011
                   LIB3179-022-P1-K1-F1
Seq. ID
                   BLASTN
Method
                   g12455
NCBI GI
BLAST score
                   90
                   6.0e-43
E value
                   302
```

(AL022197) putative protein [Arabidopsis thaliana]

```
NCBI Description Maize chloroplast rpl16 gene for ribosomal protein L16 exon
                   300012
Seq. No.
                   LIB3179-023-P1-K1-C3
Seq. ID
                   BLASTX
Method
                   q2118425
NCBI GI
                   221
BLAST score
                   5.0e-18
E value
                   63
Match length
                   71
% identity
                   subtilisin/chymotrypsin inhibitor - maize
NCBI Description
                   >gi 475253 emb_CAA55588_ (X78988) proteinase inhibitor [Zea
                   mays] >gi_\overline{4}759\overline{2}2_emb_CA\overline{A}49593_ (X69972) proteinase
                   inhibitor [Zea mays] > gi_559538_emb_CAA57677_ (X82187)
                   substilin /chymotrypsin-like inhibitor [Zea mays]
Seq. No.
                   300013
                   LIB3179-023-P1-K1-E1
Seq. ID
Method
                   BLASTX
                    q132147
NCBI GI
BLAST score
                    296
                    5.0e-27
E value
                    99
Match length
```

63 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi_68089_pir_

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - maize >gi_22474_emb_CAA29784 (X06535)

ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi 217964_dbj_BAA00120_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi_359512_prf__1312317A ribulosebisphosphate carboxylase

[Zea mays]

300014 Seq. No.

LIB3179-023-P1-K1-H1 Seq. ID

BLASTX Method g115789 NCBI GI BLAST score 245 4.0e-21 E value 60 Match length 78 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-22L) (LHCP) >gi_20475_emb_CAA26212_ (X02359) cab 22L

precursor polypeptide (aa -34 to 233) [Petunia sp.]

300015 Seq. No.

LIB3180-001-P1-M1-B6 Seq. ID

BLASTX Method g553073 NCBI GI BLAST score 197 1.0e-21 E value 128 Match length 52 % identity

(M94481) reverse transcriptase [Zea mays] NCBI Description

300016 Seq. No.



```
LIB3180-001-P1-M1-D8
Seq. ID
Method
                  BLASTX
                  g3337356
NCBI GI
                  248
BLAST score
                  2.0e-21
E value
Match length
                  54
                  89
% identity
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
                  300017
Seq. No.
                  LIB3180-001-P1-M1-G11
Seq. ID
Method
                  BLASTX
                  g3176712
NCBI GI
BLAST score
                  180
                  3.0e-13
E value
                  91
Match length
                   37
% identity
                  (AC002392) putative zinc-finger protein [Arabidopsis
NCBI Description
                  thaliana]
                   300018
Seq. No.
                  LIB3180-002-P1-M1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4165327
BLAST score
                   42
                  1.0e-14
E value
Match length
                   54
                   96
% identity
                  Oryza sativa 3-hydroxy-3-methylglutaryl-CoA reductase gene,
NCBI Description
                   promoter region and complete cds
                   300019
Seq. No.
Seq. ID
                   LIB3180-002-P1-M1-E11
Method
                   BLASTX
NCBI GI
                   q3021513
BLAST score
                   232
                   2.0e-19
E value
                   65
Match length
% identity
                   69
                   (X96728) isocitrate dehydrogenase (NADP+) [Nicotiana
NCBI Description
                   tabacum]
                   300020
Seq. No.
Seq. ID
                   LIB3180-002-P1-M1-G10
                   BLASTX
Method
                   q133961
NCBI GI
BLAST score
                   199
E value
                   2.0e-15
Match length
                   63
% identity
                   67
                   40S RIBOSOMAL PROTEIN S4 (OMNIPOTENT SUPRESSOR PROTEIN
NCBI Description
                   SUP44) (RP12) (S2E) >gi 70888 pir R3BYS2 ribosomal protein
                   S2.e - yeast (Saccharomyces cerevisiae) >gi_172793 (M59375)
                   ribosomal protein S4 [Saccharomyces cerevisiae]
                   >gi 1322683 emb CAA96831_ (Z72645) ORF YGL123w
```

[Saccharomyces cerevisiae] >gi_1628451_emb_CAA63835_

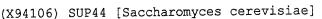


79

70

Match length

% identity



300021 Seq. No. LIB3180-003-P2-M1-C1 Seq. ID BLASTX Method g1184774 NCBI GI 152 BLAST score 2.0e-10 E value 48 Match length % identity 67 (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase NCBI Description GAPC3 [Zea mays] 300022 Seq. No. LIB3180-003-P2-M1-C9 Seq. ID Method BLASTX g3193284 NCBI GI BLAST score 379 1.0e-36 E value 102 Match length % identity 69 (AF069298) No definition line found [Arabidopsis thaliana] NCBI Description 300023 Seq. No. LIB3180-003-P2-M1-D12 Seq. ID Method BLASTX g3834321 NCBI GI BLAST score 412 2.0e-40 E value 127 Match length 65 % identity (AC005679) Strong similarity to F13P17.9 gi_3337356 NCBI Description transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana] 300024 Seq. No. LIB3180-003-P2-M1-F3 Seq. ID BLASTX Method g3122071 NCBI GI 499 BLAST score 8.0e-51 E value 104 Match length 93 % identity ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) NCBI Description >gi_2130148_pir__S66339 translation elongation factor eEF-1 alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408) alpha subunit of tlanslation elongation factor 1 [Zea mays] 300025 Seq. No. LIB3180-003-P2-M1-F9 Seq. ID BLASTX Method g553125 NCBI GI BLAST score 268 6.0e-24E value



NCBI Description (L13975) dihydroxyacid dehydratase [Saccharomyces cerevisiae]

Seq. No. 300026

Seq. ID LIB3180-003-P2-M1-G12

Method BLASTX
NCBI GI g121631
BLAST score 263
E value 5.0e-23
Match length 76
% identity 68

NCBI Description GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR

>gi_72323_pir__KNNT2S glycine-rich protein 2 - wood tobacco

>gi 19743 emb CAA42622 (X60007) nsGRP-2 [Nicotiana

sylvestris]

Seq. No. 300027

Seq. ID LIB3180-003-P2-M1-G9

Method BLASTX
NCBI GI g168691
BLAST score 311
E value 1.0e-28
Match length 95
% identity 69

NCBI Description (M29628) zein [Zea mays]

Seq. No. 300028

Seq. ID LIB3180-004-P2-M1-A11

Method BLASTN
NCBI GI g22292
BLAST score 36
E value 3.0e-11
Match length 80
% identity 86

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 300029

Seq. ID LIB3180-004-P2-M1-B6

Method BLASTN
NCBI GI g22516
BLAST score 115
E value 6.0e-58
Match length 323
% identity 84

NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 300030

Seq. ID LIB3180-004-P2-M1-B8

Method BLASTN
NCBI GI g168665
BLAST score 124
E value 2.0e-63
Match length 192
% identity 91

NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 300031



```
LIB3180-004-P2-M1-C6
Seq. ID
                  BLASTX
Method
                  g113217
NCBI GI
                  166
BLAST score
                  8.0e-12
E value
                  31
Match length
                  100
% identity
NCBI Description ACTIN 1 >gi_100149_pir__S07002 actin 1 - carrot
                  300032
Seq. No.
                  LIB3180-004-P2-M1-E4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3551838
BLAST score
                  164
                  2.0e-11
E value
                  59
Match length
                  54
% identity
NCBI Description (AF070967) SKP1-like protein [Nicotiana clevelandii]
                  300033
Seq. No.
                  LIB3180-004-P2-M1-F5
Seq. ID
                  BLASTN
Method
                  g928931
NCBI GI
                  43
BLAST score
                  5.0e-15
E value
                  79
Match length
                  89
% identity
NCBI Description A.thaliana mRNA for putative dTDP-glucose 4-6-dehydratases
Seq. No.
                  300034
                  LIB3180-004-P2-M1-G1
Seq. ID
                  BLASTX
Method
                  q1184774
NCBI GI
                  215
BLAST score
                  1.0e-17
E value
                   68
Match length
                   65
% identity
                  (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC3 [Zea mays]
                   300035
Seq. No.
                   LIB3180-005-P2-M1-A1
Seq. ID
                   BLASTX
Method
                   q141608
NCBI GI
BLAST score
                   250
E value
                   2.0e-21
                   106
Match length
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
NCBI Description
                   zein, 19K - maize >gi_22446 emb_CAA37651_ (X53582) 19 kDa
                   zein [Zea mays]
                   300036
 Seq. No.
                   LIB3180-005-P2-M1-A10
 Seq. ID
 Method
                   BLASTN
```

42222

q168696

40

NCBI GI

BLAST score

E value 3.0e-13 Match length 72 89 % identity Z.mays zein mRNA, 3' end NCBI Description 300037 Seq. No. Seq. ID LIB3180-005-P2-M1-A2 Method BLASTX q135060 NCBI GI 221 BLAST score E value 4.0e-18 Match length 94 % identity SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1) NCBI Description (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382) sucrose synthase [Zea mays] 300038 Seq. No. LIB3180-005-P2-M1-A3 Seq. ID Method BLASTX NCBI GI q3142302 BLAST score 299 3.0e-27 E value 98 Match length 63 % identity (AC002411) Strong similarity to myosin heavy chain NCBI Description gb_Z34293 from A. thaliana. [Arabidopsis thaliana] 300039 Seq. No. LIB3180-005-P2-M1-A7 Seq. ID BLASTX Method NCBI GI q16073 BLAST score 180 E value 2.0e-15

Match length 55 87 % identity

(X59526) zein protein [Acetabularia mediterranea] NCBI Description

300040 Seq. No.

LIB3180-005-P2-M1-B9 Seq. ID

Method BLASTX NCBI GI g141603 BLAST score 220 3.0e-18 E value Match length 69 % identity 71

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) NCBI Description

>qi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize

>gi 22529 emb CAA24723 (V01476) zein [Zea mays]

300041 Seq. No.

LIB3180-005-P2-M1-C12 Seq. ID

Method BLASTX g2668742 NCBI GI BLAST score 256



E value 3.0e-22 Match length 73 % identity 68 NCBI Description (AF0349

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 300042

Seq. ID LIB3180-005-P2-M1-C3

Method BLASTN
NCBI GI g168652
BLAST score 97
E value 3.0e-47
Match length 153
% identity 91

NCBI Description Maize amyloplast-specific transit protein (waxy; wx+

locus), complete cds

Seq. No. 300043

Seq. ID LIB3180-005-P2-M1-C6

Method BLASTX
NCBI GI g1076678
BLAST score 388
E value 1.0e-37
Match length 78
% identity 100

NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No. 300044

Seq. ID LIB3180-005-P2-M1-C8

Method BLASTN
NCBI GI g22509
BLAST score 179
E value 4.0e-96
Match length 283
% identity 91

NCBI Description Zea mays waxy (wx+) locus for UDP-glucose starch glycosyl

transferase

Seq. No. 300045

Seg. ID LIB3180-005-P2-M1-D8

Method BLASTX
NCBI GI g2109293
BLAST score 216
E value 2.0e-17
Match length 121
% identity 40

NCBI Description (U97568) serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 300046

Seq. ID LIB3180-005-P2-M1-F6

Method BLASTX
NCBI GI g1172833
BLAST score 331
E value 3.0e-31
Match length 68
% identity 91

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-1 >gi_495729 (L16789) small



ras-related protein [Arabidopsis thaliana] >gi_2058278_emb_CAA66047_ (X97379) atran1 [Arabidopsis thaliana]

Seq. No. 300047

Seq. ID LIB3180-005-P2-M1-G2

Method BLASTX
NCBI GI g2511531
BLAST score 330
E value 5.0e-31
Match length 66
% identity 94

NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]

>gi 3163944 emb CAA06618 (AJ005598) alpha-tubulin 1

[Eleusine indica]

Seq. No. 300048

Seq. ID LIB3180-005-P2-M1-H4

Method BLASTX
NCBI GI g141599
BLAST score 184
E value 5.0e-14
Match length 55
% identity 69

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)

>gi_72316_pir__ZIZMA2 19K zein precursor (clone cZ19A2) maize (fragment) >gi 168670 (M12142) 19 kDa zein protein

[Zea mays]

Seq. No. 300049

Seq. ID LIB3180-007-P2-M1-A12

Method BLASTX
NCBI GI g1169528
BLAST score 206
E value 7.0e-17
Match length 53
% identity 81

NCBI Description ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973)

enolase [Zea mays]

Seq. No. 300050

Seq. ID LIB3180-007-P2-M1-B10

Method BLASTN
NCBI GI g22549
BLAST score 51
E value 5.0e-20
Match length 67
% identity 94

NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 300051

Seq. ID LIB3180-007-P2-M1-B3

Method BLASTX
NCBI GI g113220
BLAST score 253
E value 7.0e-22

Seq. No.

Seq. ID



```
Match length
% identity
                   78
                  ACTIN 1 >gi_71640_pir__ATZM1 actin - maize
NCBI Description
Seq. No.
                  300052
                  LIB3180-007-P2-M1-B6
Seq. ID
Method
                  BLASTN
                  q786131
NCBI GI
                   34
BLAST score
                  2.0e-09
E value
Match length
                  70
% identity
                   87
NCBI Description Oryza sativa root-specific RCc3 mRNA, complete cds
                   300053
Seq. No.
                  LIB3180-007-P2-M1-C10
Seq. ID
Method
                  BLASTX
                   g4510348
NCBI GI
                   194
BLAST score
E value
                   2.0e-15
                   60
Match length
                   55
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   300054
                   LIB3180-007-P2-M1-C3
Seq. ID
Method
                   BLASTX
                   g2369714
NCBI GI
BLAST score
                   218
                   1.0e-17
E value
                   122
Match length
                   49
% identity
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   300055
Seq. No.
Seq. ID
                   LIB3180-007-P2-M1-D1
Method
                   BLASTN
NCBI GI
                   q22272
BLAST score
                   95
                   3.0e-46
E value
Match length
                   159
                   90
% identity
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
                   300056
Seq. No.
                   LIB3180-007-P2-M1-D11
Seq. ID
Method
                   BLASTX
                   g4519539
NCBI GI
BLAST score
                   158
E value
                   1.0e-10
                   67
Match length
                   48
% identity
                   (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
NCBI Description
                   domestica]
                   300057
```

42226

LIB3180-007-P2-M1-E10



```
BLASTX
Method
NCBI GI
                  a168691
                   360
BLAST score
                  2.0e-34
E value
Match length
                  104
                  73
% identity
NCBI Description
                  (M29628) zein [Zea mays]
                   300058
Seq. No.
                  LIB3180-007-P2-M1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q419803
BLAST score
                   290
                   2.0e-26
E value
                   79
Match length
                   73
% identity
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
                   300059
Seq. No.
                   LIB3180-007-P2-M1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4165488
BLAST score
                   408
                   4.0e-40
E value
Match length
                   101
                   77
% identity
                  (AJ132399) alpha-tubulin 3 [Hordeum vulgare]
NCBI Description
                   300060
Seq. No.
Seq. ID
                   LIB3180-007-P2-M1-F4
Method
                   BLASTX
                   q224509
NCBI GI
BLAST score
                   303
                   1.0e-27
E value
Match length
                   114
% identity
                   61
NCBI Description zein E19 [Zea mays]
                   300061
Seq. No.
                   LIB3180-007-P2-M1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141597
BLAST score
                   223
E value
                   3.0e-18
Match length
                   114
                   52
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
```

>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]

[Zea mays]

Seq. No. 300062

Seq. ID LIB3180-007-P2-M1-G5

Method BLASTX
NCBI GI g2316016
BLAST score 361



```
2.0e-34
E value
                  138
Match length
                  53
% identity
                  (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
NCBI Description
                  300063
Seq. No.
                  LIB3180-007-P2-M1-H1
Seq. ID
                  BLASTN
Method
                  g1519252
NCBI GI
                  38
BLAST score
                  3.0e-12
E value
                  78
Match length
                  87
% identity
NCBI Description Oryza sativa GF14-d protein mRNA, complete cds
                  300064
Seq. No.
                  LIB3180-007-P2-M1-H11
Seq. ID
                  BLASTX
Method
                  g136757
NCBI GI
                   374
BLAST score
                   4.0e-36
E value
                   103
Match length
                   71
% identity
                  GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
NCBI Description
                   >gi_100881_pir__S07314 UDPglucose--starch
                   glucosyltransferase (EC 2.4.1.11) precursor - maize
                   >gi 168653 (M24258) amyloplast-specific transit protein
                   [Zea mays] >gi_1644339_emb_CAA27574_ (X03935) glucosyl
                   transferase [Zea mays]
                   300065
Seq. No.
                   LIB3180-007-P2-M1-H5
Seq. ID
                   BLASTX
Method
                   q136063
NCBI GI
BLAST score
                   258
                   1.0e-22
E value
                   75
Match length
                   71
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi_68426_pir__ISZMT triose-phosphate isomerase (EC
                   5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
                   isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)
                   triosephosphate isomerase [Zea mays]
                   300066
Seq. No.
                   LIB3180-007-P2-M1-H6
 Seq. ID
                   BLASTX
Method
                   q551288
NCBI GI
 BLAST score
                   396
 E value
                   1.0e-38
Match length
                   95
                   80
 % identity
 NCBI Description (Z33611) phosphoglycerate mutase [Zea mays]
```

Seq. No.

300067

Seq. ID LIB3180-008-P2-M1-A2

Method BLASTN



```
q3342032
NCBI GI
BLAST score
                  141
                  2.0e-73
E value
Match length
                  141
                  100
% identity
                  Elegia sp. Hahn 6994 18S small subunit ribosomal RNA gene,
NCBI Description
                  complete sequence
                  300068
Seq. No.
                  LIB3180-008-P2-M1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168661
BLAST score
                  52
                  2.0e-20
E value
                  68
Match length
                  94
% identity
NCBI Description Maize 15 kDa zein mRNA, clone cZ15A3, complete cds
                   300069
Seq. No.
                  LIB3180-008-P2-M1-C9
Seq. ID
Method
                  BLASTX
                   g4210330
NCBI GI
BLAST score
                   220
E value
                   2.0e-18
                   78
Match length
                   56
% identity
                   (AJ223802) 2-oxoglutarate dehydrogenase, El subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   300070
                   LIB3180-008-P2-M1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g72307
BLAST score
                   326
E value
                   3.0e-30
Match length
                   110
% identity
                   65
                   22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   300071
Seq. No.
                   LIB3180-008-P2-M1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q419803
BLAST score
                   376
                   3.0e-36
E value
Match length
                   124
% identity
                   60
                   zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                   mays]
                   300072
Seq. No.
Seq. ID
                   LIB3180-008-P2-M1-E9
                   BLASTX
Method
```

BLAST score 141

NCBI GI

g4325342

E value 4.0e-09

Seq. ID



```
Match length
                   71
% identity
                   (AF128393) No definition line found [Arabidopsis thaliana]
NCBI Description
                   300073
Seq. No.
                  LIB3180-008-P2-M1-F3
Seq. ID
Method
                  BLASTX
                   g22216
NCBI GI
                   251
BLAST score
                   1.0e-21
E value
Match length
                   103
% identity
                   58
NCBI Description (X55722) 22kD zein [Zea mays]
                   300074
Seq. No.
                   LIB3180-008-P2-M1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4586246
                   176
BLAST score
                   7.0e-13
E value
                   83
Match length
                   46
% identity
NCBI Description (AL049640) putative protein [Arabidopsis thaliana]
                   300075
Seq. No.
                   LIB3180-008-P2-M1-G11
Seq. ID
                   BLASTN
Method
                   q22272
NCBI GI
BLAST score
                   36
                   5.0e-11
E value
                   108
Match length
                   83
% identity
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
                   300076
Seq. No.
                   LIB3180-008-P2-M1-G2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4416300
BLAST score
                   90
                   5.0e-43
E value
Match length
                   222
                   43
% identity
                   Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
                   300077
Seq. No.
                   LIB3180-009-P2-M1-A1
Seq. ID
Method
                   BLASTX
                   g2911052
NCBI GI
BLAST score
                   165
                   9.0e-12
E value
                   34
Match length
% identity
                   (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   300078
Seq. No.
```

42230

LIB3180-009-P2-M1-A2

Method

NCBI GI

BLASTX

g118390



```
Method
                  BLASTX
                  q3023816
NCBI GI
                  187
BLAST score
                  2.0e-14
E value
                  39
Match length
% identity
                  97
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                  300079
Seq. No.
                  LIB3180-009-P2-M1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3511235
BLAST score
                  46
                  9.0e-17
E value
Match length
                  90
% identity
                   88
                  Zea mays starch branching enzyme IIb (ae) gene, complete
NCBI Description
Seq. No.
                   300080
Seq. ID
                  LIB3180-009-P2-M1-B6
Method
                  BLASTN
                  q22237
NCBI GI
                   61
BLAST score
                   5.0e-26
E value
                   109
Match length
% identity
                  Maize mRNA for cytosolic GAPDH (GapC)
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase
Seq. No.
                   300081
                   LIB3180-009-P2-M1-B7
Seq. ID
Method
                   BLASTN
                   g22312
NCBI GI
BLAST score
                   72
                   9.0e-33
E value
Match length
                   112
% identity
                   91
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
Seq. No.
                   300082
                   LIB3180-009-P2-M1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2199566
                   293
BLAST score
                   7.0e-27
E value
                   76
Match length
                   75
% identity
                   (AF004210) cytochrome P-450 [Zea mays]
NCBI Description
                   300083
Seq. No.
Seq. ID
                   LIB3180-009-P2-M1-D8
```



```
BLAST score
                  3.0e-14
E value
Match length
                  45
% identity
                  84
                  PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
NCBI Description
                  >gi_2144526_pir__DCZMP pyruvate decarboxylase (EC 4.1.1.1)
                  - maize >gi 22395 emb CAA42120 (X59546) pyruvate
                  decarboxylase [Zea mays]
Seq. No.
                  300084
Seq. ID
                  LIB3180-009-P2-M1-E4
Method
                  BLASTX
NCBI GI
                  q3355311
BLAST score
                  158
                  6.0e-11
E value
Match length
                  33
                  88
% identity
                  (AJ009737) eukaryotic translation initiation factor 6 [Beta
NCBI Description
                  vulgaris]
                  300085
Seq. No.
                  LIB3180-009-P2-M1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q461498
BLAST score
                  224
                  1.0e-18
E value
                   63
Match length
                   73
% identity
                  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
NCBI Description
                   TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                   (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC
                   2.6.1.2) - proso millet >gi 296204 emb CAA49199 (X69421)
                   alanine aminotransferase [Panicum miliaceum]
Seq. No.
                   300086
                   LIB3180-009-P2-M1-F11
Seq. ID
Method
                   BLASTX
                   g3043612
NCBI GI
BLAST score
                   178
                   4.0e-13
E value
Match length
                   74
% identity
                   46
                  (AB011116) KIAA0544 protein [Homo sapiens]
NCBI Description
                   300087
Seq. No.
Seq. ID
                   LIB3180-009-P2-M1-H11
Method
                   BLASTX
NCBI GI
                   g3176714
BLAST score
                   164
                   1.0e-11
E value
```

Match length 77 40 % identity

(AC002392) putative tRNA-splicing endonuclease positive NCBI Description

effector [Arabidopsis thaliana]

300088 Seq. No.

Seq. ID LIB3180-009-P2-M1-H4



Method NCBI GI q1169228 BLAST score 179 2.0e-13 E value 55 Match length 58 % identity RNA HELICASE-LIKE PROTEIN DB10 >gi 1084413 pir__S42639 NCBI Description helicase-like protein - Wood tobacco >gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein DB10 [Nicotiana sylvestris] 300089 Seq. No. Seq. ID LIB3180-009-P2-M1-H8 Method BLASTX q1706958 NCBI GI 195 BLAST score E value 5.0e-15 Match length 91 % identity 49 NCBI Description (U58284) cellulose synthase [Gossypium hirsutum] 300090 Seq. No. LIB3180-010-P2-M1-A10 Seq. ID Method BLASTX NCBI GI q1495251 198 BLAST score 2.0e-15 E value 76 Match length % identity 55 NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana] 300091 Seq. No. LIB3180-010-P2-M1-B5 Seq. ID Method BLASTN NCBI GI q22516 BLAST score 102 E value 4.0e-50 Match length 178 % identity 89 NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2) 300092 Seq. No. LIB3180-010-P2-M1-D12 Seq. ID Method BLASTX g419803 NCBI GI 294 BLAST score 9.0e-27 E value Match length 82

74 % identity

zein protein - maize >gi 168705 (M72708) zein protein [Zea NCBI Description

mays]

300093 Seq. No.

Seq. ID LIB3180-010-P2-M1-D4

Method BLASTN g168484 NCBI GI BLAST score 203



```
E value
                  1.0e-110
Match length
                  382
% identity
                  Maize endosperm glutelin-2 gene, complete cds
NCBI Description
                  300094
Seq. No.
                  LIB3180-010-P2-M1-E5
Seq. ID
                  BLASTX
Method
                  q4539292
NCBI GI
                  249
BLAST score
E value
                  3.0e-21
Match length
                  114
% identity
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                  thaliana]
                  300095
Seq. No.
                  LIB3180-010-P2-M1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q119152
BLAST score
                  153
                   2.0e-17
E value
                  109
Match length
                   50
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi_345384_pir__A45618 translation elongation factor eEF-1
                   alpha chain - nematode (Onchocerca volvulus) >gi_159885
                   (M64333) elongation factor [Onchocerca volvulus]
                   300096
Seq. No.
                   LIB3180-010-P2-M1-F2
Seq. ID
Method
                   BLASTX
                   q3176662
NCBI GI
BLAST score
                   232
                   2.0e-19
E value
Match length
                   104
% identity
                   (AC004393) Similar to mannosyl-oligosaccharide glucosidase
NCBI Description
                   gb X87237 from Homo sapiens. [Arabidopsis thaliana]
                   300097
Seq. No.
                   LIB3180-010-P2-M1-F6
Seq. ID
Method
                   BLASTX
                   g548770
NCBI GI
                   233
BLAST score
                   9.0e-20
E value
Match length
                   75
% identity
                   61
                   60S RIBOSOMAL PROTEIN L3 >gi_481228 pir _S38359 ribosomal
NCBI Description
                   protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                   ribosomal protein L3 [Oryza sativa]
```

Seq. No.

300098

Seq. ID LIB3180-010-P2-M1-F9

Method BLASTX
NCBI GI g3269288
BLAST score 139



E value 5.0e-09
Match length 44
% identity 61

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 300099

Seq. ID LIB3180-011-P2-M1-A6

Method BLASTX
NCBI GI g3786011
BLAST score 406
E value 6.0e-40
Match length 101
% identity 72

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

Seq. No. 300100

Seq. ID LIB3180-011-P2-M1-B11

Method BLASTX
NCBI GI g113621
BLAST score 288
E value 5.0e-50
Match length 110
% identity 96

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 300101

Seq. ID LIB3180-011-P2-M1-B3

Method BLASTX
NCBI GI g3138799
BLAST score 267
E value 1.0e-23
Match length 60
% identity 85

NCBI Description (AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]

Seq. No. 300102

Seq. ID LIB3180-011-P2-M1-C3

Method BLASTN
NCBI GI g602252
BLAST score 179
E value 4.0e-96
Match length 187
% identity 99

NCBI Description Zea mays enolase (eno2) mRNA, complete cds

Seq. No. 300103

Seq. ID LIB3180-011-P2-M1-F4

Method BLASTX
NCBI GI g129881
BLAST score 316
E value 3.0e-29



```
Match length
                  63
% identity
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                  (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                  (PPI-PFK) >gi_482294_pir__A36094
                  pyrophosphate--fructose-6-phosphate 1-phosphotransferase
                  (EC 2.7.1.90) alpha chain - potato (cv. Kennebec)
                  >gi 169538 (M55190) pyrophosphate-fructose 6-phosphate
                  1-phosphotransferase alpha-subunit [Solanum tuberosum]
                  300104
Seq. No.
                  LIB3180-011-P2-M1-H7
Seq. ID
Method
                  BLASTX
                  g4415916
NCBI GI
                  146
BLAST score
                  2.0e-09
E value
                  52
Match length
                  56
% identity
                  (AC006282) putative pectin methylesterase [Arabidopsis
NCBI Description
                  thaliana]
                  300105
Seq. No.
                  LIB3180-012-P2-M1-A8
Seq. ID
Method
                  BLASTN
                  g22172
NCBI GI
BLAST score
                   61
                  7.0e-26
E value
Match length
                  101
                   91
% identity
NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit
                   300106
Seq. No.
                   LIB3180-012-P2-M1-B4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q22542
BLAST score
                   54
                   1.0e-21
E value
Match length
                   66
% identity
                   95
NCBI Description Maize gene for Mr 19000 alpha zein and 5'-flanking region
                   300107
Seq. No.
                   LIB3180-012-P2-M1-C12
Seq. ID
Method
                   BLASTN
                   g1519248
NCBI GI
                   39
BLAST score
                   9.0e-13
E value
Match length
                   67
                   90
% identity
NCBI Description Oryza sativa GF14-b protein mRNA, complete cds
```

300108 Seq. No.

LIB3180-012-P2-M1-C4 Seq. ID

Method BLASTN g22272 NCBI GI BLAST score 94



E value 1.0e-45
Match length 138
% identity 93

NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 300109

Seq. ID LIB3180-012-P2-M1-D2

Method BLASTN
NCBI GI g2264311
BLAST score 37
E value 3.0e-11
Match length 65
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MLN1, complete sequence [Arabidopsis thaliana]

Seq. No. 300110

Seq. ID LIB3180-012-P2-M1-E3

Method BLASTN
NCBI GI g416150
BLAST score 64
E value 9.0e-28
Match length 116
% identity 89

NCBI Description Zea mays beta-8 tubulin (tub8) mRNA, complete cds

Seq. No. 300111

Seq. ID LIB3180-012-P2-M1-E5

Method BLASTN
NCBI GI g168704
BLAST score 127
E value 2.0e-65
Match length 175
% identity 93

NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 300112

Seq. ID LIB3180-012-P2-M1-G6

Method BLASTN
NCBI GI g22549
BLAST score 151
E value 1.0e-79
Match length 231
% identity 91

NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 300113

Seq. ID LIB3180-013-P2-M1-A4

Method BLASTX
NCBI GI g2789660
BLAST score 156
E value 2.0e-10
Match length 51
% identity 63

NCBI Description (AF040102) p105 [Arabidopsis thaliana]

Seq. No. 300114

```
LIB3180-013-P2-M1-B1
Seq. ID
                   BLASTX
Method
                   g82718
NCBI GI
                   291
BLAST score
                   2.0e-26
E value
Match length
                   68
% identity
                   pyruvate, orthophosphate dikinase (EC 2.7.9.1) 2, cytosolic
NCBI Description
                   - maize (fragment) >gi 257810_bbs_117087 (S46967)
                   orthophosphate dikinase, PPDK {N-terminal} [maize, Peptide
                   Partial, 90 aa] [Zea mays]
                   300115
Seq. No.
                   LIB3180-013-P2-M1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q548770
BLAST score
                   346
                   8.0e-46
E value
Match length
                   133
                   75
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                   protein L3 - rice >gi 303853 dbj BAA02155 (D12630)
                   ribosomal protein L3 [Oryza sativa]
Seq. No.
                   300116
                   LIB3180-013-P2-M1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g121631
BLAST score
                   200
                   1.0e-15
E value
Match length
                   83
% identity
                   54
                   GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR
NCBI Description
                   >gi_72323_pir__KNNT2S glycine-rich protein 2 - wood tobacco
>gi_19743_emb_CAA42622_ (X60007) nsGRP-2 [Nicotiana
                   sylvestris]
                    300117
Seq. No.
                   LIB3180-013-P2-M1-D3
Seq. ID
```

BLASTX Method g3914557 NCBI GI BLAST score 442 4.0e-46 E value 111 Match length 92 % identity

RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED NCBI Description

PROTEIN) >gi 1155265 (U40219) possible apospory-associated

protein [Pennisetum ciliare]

300118 Seq. No.

Seq. ID LIB3180-013-P2-M1-F2

BLASTN Method NCBI GI g342659 BLAST score 319 1.0e-179 E value Match length 327 % identity 100



NCBI Description Maize (Black Mexican Sweet) mitochondrial 1.9 kb plasmid, complete

Seq. No. 300119

Seq. ID LIB3180-013-P2-M1-H5

Method BLASTN
NCBI GI g22524
BLAST score 50
E value 3.0e-19
Match length 81
% identity 93

NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 300120

Seq. ID LIB3180-014-P2-M1-A5

Method BLASTX
NCBI GI g4033330
BLAST score 215
E value 2.0e-17
Match length 119
% identity 39

NCBI Description (Y18523) dTDP-glucose 4,6-dehydratase [Actinoplanes sp.]

Seq. No. 300121

Seq. ID LIB3180-014-P2-M1-C2

Method BLASTX
NCBI GI g3599491
BLAST score 302
E value 1.0e-27
Match length 119
% identity 51

NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]

Seq. No. 300122

Seq. ID LIB3180-014-P2-M1-D8

Method BLASTX
NCBI GI g168699
BLAST score 365
E value 7.0e-35
Match length 118
% identity 71

NCBI Description (M60836) zein [Zea mays]

Seq. No. 300123

Seq. ID LIB3180-014-P2-M1-E1

Method BLASTX
NCBI GI g114420
BLAST score 142
E value 7.0e-09
Match length 57
% identity 53

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

>gi 100882 pir S11491 H+-transporting ATP synthase (EC

3.6.1.34) beta chain, mitochondrial - maize

>gi_22173_emb_CAA38140_ (X54233) ATPase F1 subunit protein
[Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea

mays]



```
300124
Seq. No.
                  LIB3180-014-P2-M1-E3
Seq. ID
Method
                  BLASTN
                  g2687433
NCBI GI
                  43
BLAST score
                  7.0e-15
E value
Match length
                  95
                  86
% identity
                  Tragopogon dubius large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
                  300125
Seq. No.
                  LIB3180-014-P2-M1-F3
Seq. ID
                  BLASTX
Method
                  g114420
NCBI GI
                  498
BLAST score
                  2.0e-50
E value
                  110
Match length
% identity
                  91
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_100882_pir__S11491 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - maize
                  >gi_22173_emb_CAA38140_ (X54233) ATPase F1 subunit protein
                   [Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea
                  mays]
                  300126
Seq. No.
                  LIB3180-014-P2-M1-H10
Seq. ID
Method
                  BLASTN
                  g22549
NCBI GI
                  42
BLAST score
                  8.0e-15
E value
Match length
                  70
% identity
                   90
NCBI Description Maize gene for a 27kDa storage protein, zein
                   300127
Seq. No.
                  LIB3180-015-P2-M1-D1
Seq. ID
Method
                  BLASTX
                   g3402679
NCBI GI
                   161
BLAST score
                   4.0e-11
E value
                   68
Match length
% identity
                   59
                  (AC004697) unknown protein [Arabidopsis thaliana]
NCBI Description
                   300128
Seq. No.
                   LIB3180-015-P2-M1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512685
BLAST score
                   148
                   2.0e-09
E value
Match length
                   38
% identity
                   66
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

>gi 4559325_gb_AAD22987.1_AC007087_6 (AC007087)

Seq. ID

Method





hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
                  LIB3180-015-P2-M1-G3
Seq. ID
                  BLASTX
Method
                  g3360293
NCBI GI
BLAST score
                  263
                  7.0e-28
E value
                  99
Match length
% identity
                  70
                  (AF023166) leucine-rich repeat transmembrane protein kinase
NCBI Description
                  3 [Zea mays]
                  300130
Seq. No.
                  LIB3180-015-P2-M1-G4
Seq. ID
Method
                  BLASTX
                  q2760345
NCBI GI
BLAST score
                  441
                  7.0e-44
E value
Match length
                  90
                  26
% identity
NCBI Description (U84967) ubiquitin [Arabidopsis thaliana]
Seq. No.
                  300131
                  LIB3180-015-P2-M1-H5
Seq. ID
                  BLASTX
Method
                  g872116
NCBI GI
                  242
BLAST score
E value
                  2.0e-20
                  125
Match length
                  22
% identity
NCBI Description (X79770) sti (stress inducible protein) [Glycine max]
Seq. No.
                   300132
Seq. ID
                   LIB3180-015-P2-M1-H7
Method
                  BLASTX
NCBI GI
                   g2688619
BLAST score
                   398
E value
                   9.0e-39
Match length
                   135
% identity
                  (AE001169) conserved hypothetical protein [Borrelia
NCBI Description
                   burgdorferi]
                   300133
Seq. No.
                   LIB3180-016-P2-M1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3915826
BLAST score
                   302
                   8.0e-28
E value
                   71
Match length
                   80
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
                   300134
Seq. No.
```

42241

LIB3180-016-P2-M1-B3

BLASTX



```
NCBI GI
                  q1709619
BLAST score
                  274
                  3.0e-24
E value
                  80
Match length
                  68
% identity
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
NCBI Description
                  DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
                  (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
                  >gi_2146814_pir__S69181 protein disulfide isomerase (EC
                  5.3.4.1) precursor - maize >gi_625148 (L39014) protein
                  disulfide isomerase [Zea mays]
Seq. No.
                  300135
                  LIB3180-016-P2-M1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168425
BLAST score
                  61
E value
                  3.0e-26
Match length
                  61
                  100
% identity
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds
                  300136
Seq. No.
Seq. ID
                  LIB3180-016-P2-M1-F12
Method
                  BLASTN
                  g413792
NCBI GI
BLAST score
                  35
E value
                  3.0e-10
Match length
                  139
% identity
                  81
NCBI Description Cloning vector lambda EMBL3 SP6/T7, left arm
Seq. No.
                  300137
Seq. ID
                  LIB3180-016-P2-M1-G6
Method
                  BLASTX
NCBI GI
                  q4210330
BLAST score
                  209
E value
                  3.0e-17
Match length
                  49
% identity
                  80
                   (AJ223802) 2-oxoglutarate dehydrogenase, El subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  300138
Seq. ID
                  LIB3180-016-P2-M1-G9
Method
                  BLASTX
NCBI GI
                  g4322327
BLAST score
                  234
```

6.0e-20 E value Match length 71 % identity 61

(AF080545) peptide transporter [Nepenthes alata] NCBI Description

Seq. No. 300139

LIB3180-017-P2-M1-A12 Seq. ID

BLASTX Method NCBI GI g4432841



```
BLAST score
                   7.0e-18
E value
Match length
                  82
                   54
% identity
                  (AC006283) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                   LIB3180-017-P2-M1-B12
Method
                   BLASTX
NCBI GI
                   q168691
BLAST score
                   246
E value
                   6.0e-21
Match length
                   121
                   49
% identity
                  (M29628) zein [Zea mays]
NCBI Description
                   300141
Seq. No.
Seq. ID
                   LIB3180-017-P2-M1-B5
                   BLASTN
Method
                   q984755
NCBI GI
                   43
BLAST score
                   6.0e-15
E value
Match length
                   111
% identity
                   85
NCBI Description O.sativa mRNA for chilling-inducible protein
Seq. No.
                   300142
                   LIB3180-017-P2-M1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1658313
BLAST score
                   276
E value
                   2.0e-29
Match length
                   93
% identity
                   39
NCBI Description
                  (Y08987) osr40g2 [Oryza sativa]
Seq. No.
                   300143
                   LIB3180-017-P2-M1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832247
BLAST score
                   210
                   5.0e-17
E value
                   82
Match length
% identity
                   56
                   (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
Seq. No.
                   300144
                   LIB3180-017-P2-M1-D2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3914424
                   258
BLAST score
                   2.0e-22
E value
                   70
Match length
                   74
% identity
                  PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)
NCBI Description
```

42243

(MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi 2511592 emb CAA74027.1 (Y13693) multicatalytic

NCBI Description

maize



endopeptidase complex, proteasome component; alpha subunit
[Arabidopsis thaliana]

Seq. No. 300145 LIB3180-017-P2-M1-D7 Seq. ID Method BLASTN NCBI GI g3747049 BLAST score 79 2.0e-36 E value 111 Match length % identity NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds 300146 Seq. No. LIB3180-017-P2-M1-E1 Seq. ID Method BLASTX g2506139 NCBI GI BLAST score 295 1.0e-26 E value 76 Match length % identity 84 COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) NCBI Description (ARCHAIN) >gi 1314049 emb CAA91901 (Z67962) archain/delta-COP [Oryza sativa] 300147 Seq. No. LIB3180-017-P2-M1-E9 Seq. ID Method BLASTX NCBI GI q3372518 BLAST score 205 E value 3.0e-16 Match length 76 55 % identity NCBI Description (AF050631) invertase [Zea mays] Seq. No. 300148 LIB3180-017-P2-M1-F3 Seq. ID Method BLASTX NCBI GI g1345587 175 BLAST score 5.0e-13 E value Match length 64 % identity 62 14-3-3-LIKE PROTEIN GF14-6 >gi 998430 bbs 164522 (S77133) NCBI Description GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261 aa] [Zea mays] 300149 Seq. No. Seq. ID LIB3180-017-P2-M1-F4 Method BLASTX NCBI GI q67155 BLAST score 228 4.0e-19 E value Match length 91 53 % identity

pyruvate, orthophosphate dikinase (EC 2.7.9.1) precursor -

E value

Match length

% identity

270

92



```
300150
Seq. No.
                  LIB3180-017-P2-M1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168514
BLAST score
                  140
                  8.0e-73
E value
Match length
                  304
                  87
% identity
NCBI Description Z.mays cl locus myb homologue cDNA, exons 1-3
                  300151
Seq. No.
                  LIB3180-017-P2-M1-G5
Seq. ID
Method
                  BLASTX
                  g119150
NCBI GI
                  160
BLAST score
                  2.0e-11
E value
                  49
Match length
                  69
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_82081_pir__S10507 translation elongation factor eEF-1
                  alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF
                   1-alpha (AA 1-448) [Lycopersicon esculentum]
                   >gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha
                   [Lycopersicon esculentum]
                   300152
Seq. No.
                  LIB3180-017-P2-M1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2921209
                   268
BLAST score
E value
                   2.0e-23
                   72
Match length
                   78
% identity
                   (AF026148) beta-ketoacyl-ACP synthase I [Perilla
NCBI Description
                   frutescens]
                   300153
Seq. No.
                   LIB3180-018-P2-M1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3236238
BLAST score
                   172
                   2.0e-12
E value
Match length
                   59
% identity
                   59
                   (AC004684) putative ARF1 GTPase activating protein
NCBI Description
                   [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_
                   (AB017876) Aspl [Arabidopsis thaliana]
Seq. No.
                   300154
                   LIB3180-018-P2-M1-E1
Seq. ID
                   BLASTN
Method
                   g22549
NCBI GI
BLAST score
                   178
                   2.0e-95
```



NCBI Description Maize gene for a 27kDa storage protein, zein Seq. No. 300155

LIB3180-018-P2-M1-E5

Method BLASTX
NCBI GI g3334474
BLAST score 190
E value 1.0e-14
Match length 71
% identity 59

Seq. ID

NCBI Description OLEOSIN ZM-I (OLEOSIN 16 KD) (LIPID BODY-ASSOCIATED MAJOR

PROTEIN) (LIPID BODY-ASSOCIATED PROTEIN L3)

>gi_1076817_pir__S52029 oleosin 16 - maize >gi_687245

 $(U1\overline{3}701)$ 16 kDa oleosin [Zea mays]

Seq. No. 300156

Seq. ID LIB3180-018-P2-M1-E8

Method BLASTX
NCBI GI g578545
BLAST score 179
E value 3.0e-13
Match length 112
% identity 10

NCBI Description (Z35759) ubiquitin [Tetrahymena pyriformis]

Seq. No. 300157

Seq. ID LIB3180-018-P2-M1-G10

Method BLASTX
NCBI GI g2369714
BLAST score 177
E value 3.0e-13
Match length 76
% identity 51

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 300158

Seq. ID LIB3180-018-P2-M1-G9

Method BLASTN
NCBI GI g556672
BLAST score 46
E value 5.0e-17
Match length 66
% identity 92

NCBI Description S.cereale (Halo) chloroplast mRNA for heat-shock protein

Seq. No. 300159

Seq. ID LIB3180-018-P2-M1-H3

Method BLASTX
NCBI GI g548770
BLAST score 440
E value 1.0e-43
Match length 101
% identity 83

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal

protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. ID

Method NCBI GI



```
Seq. No.
                  300160
                  LIB3180-019-P2-M1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2117937
BLAST score
                  240
E value
                  2.0e-20
Match length
                  65
                  75
% identity
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                  barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
Seq. No.
                  300161
Seq. ID
                  LIB3180-019-P2-M1-A2
Method
                  BLASTX
NCBI GI
                  q1181673
BLAST score
                  234
E value
                   1.0e-19
                  73
Match length
                   66
% identity
                  (U41652) heat shock protein cognate 70 [Sorghum bicolor]
NCBI Description
Seq. No.
                   300162
Seq. ID
                  LIB3180-019-P2-M1-D11
Method
                   BLASTX
NCBI GI
                   q4510423
BLAST score
                   163
E value
                   1.0e-11
Match length
                   52
                   65
% identity
                   (AC006929) unknown protein [Arabidopsis thaliana]
NCBI Description
                   300163
Seq. No.
                   LIB3180-019-P2-M1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22524
BLAST score
                   121
                   7.0e-62
E value
Match length
                   125
% identity
                   99
                  Zea mays mRNA encoding a zein (clone ZG31A)
NCBI Description
                   300164
Seq. No.
                   LIB3180-019-P2-M1-G6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1762945
BLAST score
                   158
                   1.0e-10
E value
Match length
                   50
% identity
                   60
                   (U66269) ORF; able to induce HR-like lesions [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   300165
```

42247

LIB3180-019-P2-M1-H6

BLASTX

g3599491



```
BLAST score 250
E value 1.0e-21
Match length 76
% identity 62
NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]
```

Seq. No. 300166 Seq. ID LIB3180-020-P2-M1-B7

Method BLASTN
NCBI GI g1532072
BLAST score 85
Figure 3.0e-40

E value 3.0e-40
Match length 137
% identity 91

NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 300167

Seq. ID LIB3180-020-P2-M1-C1

Method BLASTX
NCBI GI g1076809
BLAST score 156
E value 7.0e-11
Match length 71
% identity 51

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize

>gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase

[Zea mays]

Seq. No. 300168

Seq. ID LIB3180-020-P2-M1-D3

Method BLASTX
NCBI GI g2959732
BLAST score 256
E value 2.0e-22
Match length 52
% identity 83

NCBI Description (Y13649) homologous to GATA-binding transcription factors

[Arabidopsis thaliana]

Seq. No. 300169

Seq. ID LIB3180-020-P2-M1-H4

Method BLASTX
NCBI GI g3152587
BLAST score 258
E value 2.0e-22
Match length 87
% identity 68

NCBI Description (AC002986) Similar to CREB-binding protein homolog

gb_U88570 from D. melanogaster and contains similarity to callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb_W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No. 300170

Seq. ID LIB3180-021-P2-M1-A12

Method BLASTX NCBI GI g3608171 BLAST score 398



E value 6.0e-39 Match length 103 % identity 80 (D86306) proton-translocating inorganic pyrophosphatase NCBI Description [Cucurbita moschata] Seq. No. 300171 LIB3180-021-P2-M1-A6 Seq. ID Method BLASTX NCBI GI g141597 BLAST score 363 E value 1.0e-34 Match length 130 64 % identity ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) NCBI Description >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2] [Zea mays] 300172 Seq. No. LIB3180-021-P2-M1-B11 Seq. ID Method BLASTN NCBI GI q22549 BLAST score 106 7.0e-53 E value 158 Match length % identity NCBI Description Maize gene for a 27kDa storage protein, zein 300173 Seq. No. LIB3180-021-P2-M1-C8 Seq. ID Method BLASTN NCBI GI g2668743 BLAST score 64 E value 2.0e-27 Match length 80 % identity 95 Zea mays ubiquitin conjugating enzyme (UBC) mRNA, complete NCBI Description cds 300174 Seq. No. Seq. ID LIB3180-021-P2-M1-D1 BLASTN Method NCBI GI g22516 BLAST score 123 8.0e-63 E value Match length 213 % identity 89 NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

300175 Seq. No.

Seq. ID LIB3180-021-P2-M1-E9

BLASTN Method NCBI GI g311238 BLAST score 84 7.0e-40 E value Match length 136

% identity NCBI Description Z.mays cat1 gene for catalase 300176 Seq. No. LIB3180-021-P2-M1-F5 Seq. ID Method BLASTN NCBI GI q1184771 95 BLAST score 3.0e-46E value 185 Match length % identity 89 Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC2 NCBI Description (gpc2) mRNA, complete cds 300177 Seq. No. LIB3180-021-P2-M1-G4 Seq. ID BLASTN Method NCBI GI q168425 165 BLAST score 7.0e-88 E value 205 Match length

% identity 95
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 300178

Seq. ID LIB3180-022-P2-M1-C11

Method BLASTX
NCBI GI g119355
BLAST score 216
E value 2.0e-17
Match length 55
% identity 82

NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)

>gi 100869 pir S16257 phosphopyruvate hydratase (EC

4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase

[Zea mays]

Seq. No. 300179

Seq. ID LIB3180-022-P2-M1-C4

Method BLASTX
NCBI GI g113621
BLAST score 211
E value 2.0e-17
Match length 44
% identity 95

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 300180

Seq. ID LIB3180-022-P2-M1-C7

Method BLASTN NCBI GI g260041



```
BLAST score
E value
                  3.0e-12
Match length
                  66
                  89
% identity
                  Sh2=shrunken-2 locus [maize, mRNA Partial, 1867 nt]
NCBI Description
                  300181
Seq. No.
                  LIB3180-022-P2-M1-E6
Seq. ID
Method
                  BLASTX
                  g232172
NCBI GI
BLAST score
                  239
                  1.0e-20
E value
Match length
                  77
% identity
                  66
                  GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT
NCBI Description
                  PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
                  PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE
                  ADENYL TRANSFERASE) >gi_481816_pir__S39504
                  glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
                  wheat >gi 21687_emb_CAA46879_ (X66080) ADP-glucose
                  pyrophosphorylase [Triticum aestivum]
                  300182
Seq. No.
Seq. ID
                  LIB3180-022-P2-M1-E7
Method
                  BLASTX
NCBI GI
                  q421929
BLAST score
                   215
                  2.0e-17
E value
                   60
Match length
% identity
                  11
                  ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156)
NCBI Description
                  ubiquitin [Lycopersicon esculentum]
Seq. No.
                   300183
                   LIB3180-022-P2-M1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3641839
BLAST score
                   197
E value
                   3.0e-15
Match length
                   52
                   67
% identity
                   (AL023094) isoflavone reductase - like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   300184
                   LIB3180-023-P2-M1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g168586
```

428 BLAST score 2.0e-46 E value 112 Match length % identity 91

(M58656) pyruvate, orthophosphate dikinase [Zea mays] NCBI Description

300185 Seq. No.

LIB3180-023-P2-M1-D6 Seq. ID

BLASTX Method

```
NCBI GI ~
                  q3121867
BLAST score
                  186
                  2.0e-14
E value
Match length
                  71
                  54
% identity
                  COP1 REGULATORY PROTEIN >gi 1694900 emb CAA70768_ (Y09579)
NCBI Description
                  Cop1 protein [Pisum sativum]
                  300186
Seq. No.
                  LIB3180-023-P2-M1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4105719
BLAST score
                  286
                  3.0e-26
E value
Match length
                  54
% identity
                  93
                   (AF050128) cell wall invertase Incw2; beta-fructosidase
NCBI Description
                   [Zea mays]
                  300187
Seq. No.
                  LIB3180-023-P2-M1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2507281
BLAST score
                  238
                   3.0e-20
E value
                   50
Match length
                  92
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi 1668706 emb CAA66048_
NCBI Description
                   (X97380) atran2 [Arabidopsis thaliana]
                   300188
Seq. No.
                   LIB3180-024-P2-M1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3135543
BLAST score
                   182
                   5.0e-14
E value
Match length
                   52
                   67
% identity
NCBI Description
                  (AF062393) aquaporin [Oryza sativa]
                   300189
Seq. No.
                   LIB3180-024-P2-M1-A8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g602252
BLAST score
                   36
```

6.0e-11 E value Match length 40 % identity 97

NCBI Description Zea mays enolase (eno2) mRNA, complete cds

300190 Seq. No.

Seq. ID LIB3180-024-P2-M1-B3

Method BLASTX g3212871 NCBI GI 195 BLAST score 2.0e-15 E value 76 Match length

% identity (AC004005) putative translation initiation factor NCBI Description [Arabidopsis thaliana] Seq. No. 300191 Seq. ID LIB3180-024-P2-M1-B9 Method BLASTX NCBI GI q2655291 BLAST score 144 E value 1.0e-09 Match length 43 % identity 67 NCBI Description (AF032974) germin-like protein 4 [Oryza sativa] 300192 Seq. No. Seq. ID LIB3180-024-P2-M1-C1 Method BLASTX NCBI GI g22216 BLAST score 296 E value 8.0e-27 94 Match length % identity 66 NCBI Description (X55722) 22kD zein [Zea mays] 300193 Seq. No. Seq. ID LIB3180-024-P2-M1-C2 Method BLASTN NCBI GI q602252 BLAST score 60 E value 2.0e-25 Match length 128 87 % identity NCBI Description Zea mays enolase (eno2) mRNA, complete cds

Seq. No. 300194

Seq. ID LIB3180-024-P2-M1-D12

Method BLASTN
NCBI GI g168654
BLAST score 107
E value 4.0e-53
Match length 162
% identity 92

NCBI Description Zea mays ADP glucose pyrophosphorylase (shrunken-2) gene,

complete cds

Seq. No. 300195

Seq. ID LIB3180-024-P2-M1-D8

Method BLASTX
NCBI GI g141605
BLAST score 455
E value 2.0e-45
Match length 124
% identity 73

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)

>gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

BLAST score

E value

387

7.0e-38



```
Seq. No.
                   300196
Seq. ID
                  LIB3180-024-P2-M1-E8
Method
                   BLASTX
NCBI GI
                   g4115371
BLAST score
                   265
E value
                   3.0e-23
Match length
                   113
% identity
                   52
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                   300197
Seq. ID
                  LIB3180-024-P2-M1-F2
Method
                   BLASTX
NCBI GI
                   q4104056
BLAST score
                   245
                   3.0e-21
E value
Match length
                   54
% identity
                   83
NCBI Description
                  (AF031194) S276 [Triticum aestivum]
Seq. No.
                   300198
Seq. ID
                   LIB3180-024-P2-M1-H3
Method
                   BLASTX
NCBI GI
                   q3043415
BLAST score
                   331
E value
                   4.0e-31
Match length
                   70
% identity
                   91
NCBI Description
                  (Y17053) At-hsc70-3 [Arabidopsis thaliana]
Seq. No.
                   300199
                   LIB3180-024-P2-M1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3319882
BLAST score
                   152
                   4.0e-10
E value
Match length
                   86
                   45
% identity
                   (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                   arietinum]
Seq. No.
                   300200
Seq. ID
                   LIB3180-024-P2-M1-H7
Method
                   BLASTX
NCBI GI
                   g2275211
BLAST score
                   165
                   2.0e-11
E value
Match length
                   87
                   68
% identity
                   (AC002337) RNA helicase isolog [Arabidopsis thaliana]
NCBI Description
                   300201
Seq. No.
Seq. ID
                   LIB3180-027-P2-M2-B8
Method
                   BLASTX
NCBI GI
                   g119150
```



Match length % identity 86

ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) NCBI Description

>gi_82081_pir__S10507 translation elongation factor eEF-1 alpha chain - tomato >gi 19273 emb_CAA32618_ (X14449) EF

1-alpha (AA 1-448) [Lycopersicon esculentum]

>gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha

[Lycopersicon esculentum]

300202 Seq. No.

Seq. ID LIB3180-027-P2-M2-F11

Method BLASTX g2498329 NCBI GI BLAST score 172 E value 8.0e-13 Match length 53 60 % identity

PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__S65571 NCBI Description

pattern-formation protein GNOM - Arabidopsis thaliana >gi 1209633 (U36433) GNOM gene product [Arabidopsis

thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession

Number J03918 [Arabidopsis thaliana]

Seq. No. 300203

LIB3180-028-P2-M2-A6 Seq. ID

Method BLASTN g1491773 NCBI GI BLAST score 53 E value 3.0e-21 Match length 105

88 % identity

NCBI Description Z.mays mRNA for cysteine proteinase, See1

Seq. No. 300204

Seq. ID LIB3180-028-P2-M2-C3

Method BLASTX NCBI GI q3549667 BLAST score 188 1.0e-14 E value 68 Match length 60 % identity

NCBI Description (AL031394) Arabidopsis dynamin-like protein ADL2

[Arabidopsis thaliana]

Seq. No. 300205

LIB3180-028-P2-M2-D11 Seq. ID

Method BLASTX g2760349 NCBI GI BLAST score 362 E value 1.0e-34 Match length 87 % identity 17

(U84969) ubiquitin [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                   300206
                  LIB3180-028-P2-M2-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417745
BLAST score
                  219
                  6.0e-18
E value
Match length
                  83
                  57
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >qi 170773 (L11872)
                   S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]
Seq. No.
                   300207
                  LIB3180-028-P2-M2-F9
Seq. ID
Method
                  BLASTN
                  a168425
NCBI GI
                   82
BLAST score
E value
                  1.0e-38
                   106
Match length
% identity
                   94
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds
                   300208
Seq. No.
Seq. ID
                  LIB3180-028-P2-M2-H8
Method
                  BLASTX
                   q4138179
NCBI GI
                   268
BLAST score
                   4.0e-24
E value
Match length
                   64
% identity
                   81
                  (AJ223969) elongation factor 1 alpha subunit [Malus
NCBI Description
                   domestica]
Seq. No.
                   300209
Seq. ID
                   LIB3180-029-P2-M2-C4
Method
                   BLASTN
NCBI GI
                   g168482
BLAST score
                   80
E value
                   3.0e-37
Match length
                   184
% identity
                   86
NCBI Description Corn starch branching enzyme II mRNA, complete cds
Seq. No.
                   300210
                   LIB3180-029-P2-M2-F10
Seq. ID
Method
                   BLASTN
                   g3318612
NCBI GI
                   53
BLAST score
                   3.0e-21
E value
Match length
                   69
                   94
% identity
                   Zea mays mRNA for mitochondrial phosphate transporter,
NCBI Description
                   complete cds
```

Method BLASTX



NCBI GI q2642159 BLAST score 159 1.0e-10 E value Match length 53 % identity NCBI Description (AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi 3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana] Seq. No. Seq. ID LIB3180-030-P2-M2-B11 Method BLASTX NCBI GI q129171 BLAST score 221 E value 6.0e-18 Match length 81 % identity 65 OPAQUE-2 REGULATORY PROTEIN >gi 22388 emb CAA33550_ NCBI Description (X15544) opaque-2 protein [Zea mays] Seq. No. 300213 Seq. ID LIB3180-030-P2-M2-B4 Method BLASTX q2104712 NCBI GI 486 BLAST score 3.0e-49 E value 115 Match length % identity (U95180) endosperm specific protein [Zea mays] NCBI Description 300214 Seq. No. Seq. ID LIB3180-030-P2-M2-F4 Method BLASTX NCBI GI q1076748 209 BLAST score 6.0e-17 E value 65 Match length % identity 62 major intrinsic protein - rice >gi_440869_dbj_BAA04257_ NCBI Description (D17443) major intrinsic protein [Oryza sativa] Seq. No. 300215 Seq. ID LIB3180-030-P2-M2-G3 BLASTX Method NCBI GI g3281846 BLAST score 267 1.0e-23 E value 70 Match length

76 % identity

NCBI Description (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No. 300216

Seq. ID LIB3180-031-P2-M2-A11

BLASTX Method NCBI GI q2435522 BLAST score 192



E value 9.0e-15
Match length 70
% identity 54

NCBI Description (AF024504) contains similarity to other AMP-binding enzymes

[Arabidopsis thaliana]

Seq. No. 300217

Seq. ID LIB3180-031-P2-M2-C1

Method BLASTN
NCBI GI g340933
BLAST score 35
E value 1.0e-10
Match length 87
% identity 85

NCBI Description Zea mays 10-kDa zein gene, complete cds

Seq. No. 300218

Seq. ID LIB3180-031-P2-M2-C5

Method BLASTN
NCBI GI g2282583
BLAST score 65
E value 2.0e-28
Match length 113
% identity 89

NCBI Description Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete

cds

Seq. No. 300219

Seq. ID LIB3180-031-P2-M2-D12

Method BLASTN
NCBI GI g257040
BLAST score 167
E value 3.0e-89
Match length 187
% identity 97

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 300220

Seq. ID LIB3180-031-P2-M2-F2

Method BLASTN
NCBI GI g2286152
BLAST score 72
E value 2.0e-32
Match length 88
% identity 95

NCBI Description Zea mays cytoplasmic malate dehydrogenase mRNA, complete

cds

Seq. No. 300221

Seq. ID LIB3180-031-P2-M2-F3

Method BLASTN
NCBI GI g2909845
BLAST score 92
E value 2.0e-44
Match length 122
% identity 93

NCBI Description Zea mays (S)-adenosyl-L-methionine:delta 24-sterol



methyltransferase mRNA, complete cds

```
300222
Seq. No.
Seq. ID
                  LIB3180-031-P2-M2-F7
Method
                  BLASTX
                  g282994
NCBI GI
BLAST score
                  212
E value
                  1.0e-17
                  45
Match length
% identity
                  82
                  Sip1 protein - barley >gi 167100 (M77475) seed imbibition
NCBI Description
                  protein [Hordeum vulgare]
                  300223
Seq. No.
Seq. ID
                  LIB3180-031-P2-M2-G8
Method
                  BLASTN
NCBI GI
                  g2257755
BLAST score
                  51
                  4.0e-20
E value
                  95
Match length
% identity
                  88
NCBI Description
                  Zea mays nucleolar histone deacetylase HD2-p39 mRNA,
                  complete cds
                  300224
Seq. No.
Seq. ID
                  LIB3180-032-P2-M2-C11
Method
                  BLASTX
NCBI GI
                  q1710551
BLAST score
                  281
                  3.0e-25
E value
                  51
Match length
                  100
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L39 >qi 1177369 emb CAA64728
                   (X95458) ribosomal protein L39 [Zea mays]
                  300225
Seq. No.
Seq. ID
                  LIB3180-033-P2-M2-B2
Method
                  BLASTN
NCBI GI
                  q435456
BLAST score
                  34
                  4.0e-10
E value
Match length
                  85
                  85
% identity
NCBI Description
                  Proso millet gene for aspartate aminotransferase, complete
                  cds
                  300226
Seq. No.
Seq. ID
                  LIB3180-033-P2-M2-B5
                  BLASTX
Method
                  g3132825
NCBI GI
BLAST score
                  212
E value
                  2.0e-17
Match length
                  45
% identity
                  93
NCBI Description
                  (AF063403) putative cytosine-5 DNA methyltransferase [Zea
```

mays]

Seq. No.

Seq. ID

300232

LIB3180-034-P2-M2-B9



```
Seq. No.
                  300227
Seq. ID
                  LIB3180-033-P2-M2-C7
Method
                  BLASTX
NCBI GI
                  g2967456
BLAST score
                  182
E value
                  5.0e-14
Match length
                  50
                  74
% identity
NCBI Description (AB012048) sulfate transporter [Arabidopsis thaliana]
Seq. No.
                  300228
Seq. ID
                  LIB3180-033-P2-M2-D1
Method
                  BLASTN
NCBI GI
                  g257807
BLAST score
                  57
                  1.0e-23
E value
Match length
                   61
% identity
                  98
                  cyppdkZml=orthophosphate dikinase {5'region} [maize,
NCBI Description
                  Genomic, 895 nt]
Seq. No.
                   300229
Seq. ID
                  LIB3180-033-P2-M2-G10
Method
                  BLASTX
NCBI GI
                  q3334349
BLAST score
                  174
                   6.0e-13
E value
Match length
                  79
% identity
                   49
                  GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)
NCBI Description
                  >gi 2564215_emb_CAA05162 (AJ002062) glycyl-tRNA synthetase
                   [Arabidopsis thaliana]
                   300230
Seq. No.
Seq. ID
                  LIB3180-033-P2-M2-G6
Method
                  BLASTX
                   q3334349
NCBI GI
                   193
BLAST score
                   1.0e-19
E value
Match length
                   85
                   59
% identity
                  GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)
NCBI Description
                   >gi 2564215 emb CAA05162 (AJ002062) glycyl-tRNA synthetase
                   [Arabidopsis thaliana]
Seq. No.
                   300231
Seq. ID
                   LIB3180-034-P2-M2-A3
Method
                  BLASTN
NCBI GI
                   q13918
                   75
BLAST score
E value
                   1.0e-34
Match length
                   115
                   91
% identity
NCBI Description Maize mitochondrial DNA for 5kB alpha-R1 repeat
```

NCBI GI



```
Method
                  BLASTN
                  q1495231
NCBI GI
BLAST score
                  41
                  2.0e-14
E value
                  79
Match length
                  87
% identity
NCBI Description Z.mays mRNA for 22kD zein protein
Seq. No.
                  300233
Seq. ID
                  LIB3180-034-P2-M2-E3
Method
                  BLASTX
NCBI GI
                  q4581164
BLAST score
                  261
E value
                  3.0e-23
Match length
                  74
                  65
% identity
NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]
                  300234
Seq. No.
Seq. ID
                  LIB3180-034-P2-M2-E7
Method
                  BLASTN
NCBI GI
                  q1184775
BLAST score
                  47
E value
                  8.0e-18
                  83
Match length
                  89
% identity
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4
NCBI Description
                  (gpc4) mRNA, complete cds
Seq. No.
                  300235
Seq. ID
                  LIB3180-034-P2-M2-F1
Method
                  BLASTX
NCBI GI
                  g136063
BLAST score
                  159
E value
                  2.0e-11
Match length
                  50
% identity
                  66
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >qi 68426 pir ISZMT triose-phosphate isomerase (EC
                  5.3.1.1) - maize >gi 168647 (L00371) triosephosphate
                  isomerase 1 [Zea mays] >gi 217974 dbj BAA00009 (D00012)
                  triosephosphate isomerase [Zea mays]
Seq. No.
                  300236
                  LIB3180-034-P2-M2-H12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22544
BLAST score
                  144
                  2.0e-75
E value
                  176
Match length
                  95
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                  300237
Seq. No.
Seq. ID
                  LIB3180-035-P2-M2-A2
                  BLASTX
Method
```

42261

g2511535



```
298
BLAST score
                  4.0e-44
E value
                  106
Match length
                  86
% identity
                  (AF008122) alpha-tubulin 3 [Eleusine indica]
NCBI Description
                  300238
Seq. No.
                  LIB3180-035-P2-M2-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q82720
                   252
BLAST score
E value
                   6.0e-45
Match length
                   115
% identity
                   87
                  regulatory protein O2 - maize >gi 22384 emb CAA34614_
NCBI Description
                   (X16618) O2 protein (AA 1-460) [Zea mays]
                   300239
Seq. No.
                  LIB3180-035-P2-M2-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1532210
BLAST score
                   269
E value
                   7.0e-43
Match length
                   136
                   67
% identity
                  (U68268) cyclophilin A [Trypanosoma congolense]
NCBI Description
Seq. No.
                   300240
                   LIB3180-035-P2-M2-G1
Seq. ID
Method
                   BLASTN
                   g902524
NCBI GI
                   37
BLAST score
E value
                   2.0e-11
Match length
                   121
% identity
                   83
                   Zea mays clone MubG10 ubiquitin fusion protein gene,
NCBI Description
                   complete cds
                   300241
Seq. No.
Seq. ID
                   LIB3180-035-P2-M2-G12
                   BLASTN
Method
                   g575730
NCBI GI
BLAST score
                   45
                   3.0e-16
E value
                   65
Match length
                   92
% identity
NCBI Description Z.mays mRNA for transmembrane protein
                   300242
Seq. No.
                   LIB3180-035-P2-M2-H1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22516
BLAST score
                   235
                   1.0e-129
E value
                   318
Match length
                   94
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
```



300243

LIB3180-036-P2-M2-A11

Seq. No.

Seq. ID

```
Method
                  BLASTX
NCBI GI
                  g3924596
BLAST score
                  265
                  2.0e-23
E value
Match length
                  78
% identity
                  71
NCBI Description
                  (AF069442) putative phospho-ser/thr phosphatase
                  [Arabidopsis thaliana]
Seq. No.
                  300244
                  LIB3180-036-P2-M2-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q300265
BLAST score
                  316
E value
                  4.0e-29
Match length
                  89
                  73
% identity
                  HSP68=68 kda heat-stress DnaK homolog [Lycopersicon
NCBI Description
                  peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]
Seq. No.
                  300245
                  LIB3180-036-P2-M2-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q169818
BLAST score
                  43
E value
                  5.0e-15
Match length
                  171
% identity
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                  300246
Seq. ID
                  LIB3180-036-P2-M2-E2
Method
                  BLASTX
NCBI GI
                  q3559805
BLAST score
                  614
E value
                  4.0e-64
Match length
                  134
% identity
                  78
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                  thaliana]
                  300247
Seq. No.
Seq. ID
                  LIB3180-036-P2-M2-E8
Method
                  BLASTX
NCBI GI
                  g1762130
BLAST score
                  235
E value
                  1.0e-19
Match length
                  66
                  77
% identity
                  (U46136) chaperonin-60 beta subunit [Solanum tuberosum]
NCBI Description
                  300248
Seq. No.
Seq. ID
                  LIB3180-036-P2-M2-F1
Method
                  BLASTX
```



NCBI GI a584706 BLAST score 211 8.0e-17 E value Match length 58 78 % identity ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A) NCBI Description >gi 2130066 pir JC5124 aspartate transaminase (EC 2.6.1.1), cytoplasmic - rice >gi 287298 dbj BAA03504_ (D14673) aspartate aminotransferase [Oryza sativa] Seq. No. 300249 Seq. ID LIB3180-036-P2-M2-F10 Method BLASTN NCBI GI q14395 BLAST score 177 E value 7.0e-95 302 Match length % identity 94 NCBI Description T.aestivum mitochondrion fMet, 18S, 5S repeat unit DNA 300250 Seq. No. LIB3180-036-P2-M2-F8 Seq. ID Method BLASTX NCBI GI q4490330 377 BLAST score 1.0e-36 E value 75 Match length 92 % identity (AL035656) splicing factor-like protein [Arabidopsis NCBI Description thaliana] Seq. No. 300251 LIB3180-036-P2-M2-F9 Seq. ID Method BLASTX NCBI GI q585084 BLAST score 170 E value 4.0e-12 Match length 43 % identity 77 ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) NCBI Description >qi 543383 pir S40780 translation elongation factor G, mitochondrial - rat >gi_310102 (L14684) elongation factor G [Rattus norvegicus] 300252 Seq. No. Seq. ID LIB3180-036-P2-M2-G10 Method BLASTX g3789911 NCBI GI 194 BLAST score

Method BLASTX
NCBI GI g3789911
BLAST score 194
E value 8.0e-15
Match length 81
% identity 48

NCBI Description (AF081802) developmental protein DG1118 [Dictyostelium

discoideum]

Seq. No. 300253

Seq. ID LIB3180-036-P2-M2-G6



```
Method
                  BLASTX
                  q16073
NCBI GI
BLAST score
                  422
E value
                  1.0e-41
Match length
                  134
% identity
                  68
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
Seq. No.
Seq. ID
                  LIB3180-036-P2-M2-H3
Method
                  BLASTN
NCBI GI
                  q625147
BLAST score
                  153
E value
                  1.0e-80
                  296
Match length
% identity
                  94
                  Zea mays protein disulfide isomerase (pdi) mRNA, complete
NCBI Description
Seq. No.
                  300255
Seq. ID
                  LIB3180-037-P2-M2-A10
Method
                  BLASTX
NCBI GI
                  q168691
BLAST score
                  325
E value
                  3.0e-30
Match length
                  101
% identity
                  63
                  (M29628) zein [Zea mays]
NCBI Description
Seq. No.
                  300256
Seq. ID
                  LIB3180-037-P2-M2-A9
Method
                  BLASTX
NCBI GI
                  g2494073
BLAST score
                  139
E value
                  9.0e-09
Match length
                  46
% identity
                  BETAINE-ALDEHYDE DEHYDROGENASE (BADH)
NCBI Description
                  >qi 2144333 pir S71413 betaine-aldehyde dehydrogenase (EC
                  1.2.1.8) precursor - barley >gi 927643 dbj_BAA05466
                   (D26448) betaine aldehyde dehydrogenase [Hordeum vulgare]
                  300257
Seq. No.
Seq. ID
                  LIB3180-037-P2-M2-D9
Method
                  BLASTX
NCBI GI
                  g168691
BLAST score
                  302
E value
                  1.0e-27
                  110
Match length
                  59
% identity
NCBI Description
                  (M29628) zein [Zea mays]
                  300258
Seq. No.
Seq. ID
                  LIB3180-037-P2-M2-F6
Method
                  BLASTX
```

42265

g1174448

145

NCBI GI BLAST score



```
E value
                  4.0e-09
Match length
                  42
% identity
                  71
                  TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR
NCBI Description
                   (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)
                   (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative
                   [Arabidopsis thaliana]
                  300259
Seq. No.
                  LIB3180-037-P2-M2-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220523
BLAST score
                  312
E value
                  1.0e-28
                  98
Match length
                  58
% identity
NCBI Description (AL035356) putative alliin lyase [Arabidopsis thaliana]
Seq. No.
                  300260
                  LIB3180-038-P2-M2-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4558460
BLAST score
                  419
E value
                  3.0e-41
Match length
                  81
% identity
                  100
                  (AF073775) replication origin activator ROA2 [Zea mays]
NCBI Description
                  300261
Seq. No.
                  LIB3180-038-P2-M2-E2
Seq. ID
                  BLASTX
Method
                   q417154
NCBI GI
BLAST score
                   350
E value
                   3.0e-33
                  113
Match length
% identity
                   63
                  HEAT SHOCK PROTEIN 82 >gi 100685_pir__S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                   300262
                   LIB3180-038-P2-M2-F10
Seq. ID
Method
                  BLASTX
                   g1658313
NCBI GI
BLAST score
                   442
E value
                   4.0e-44
Match length
                   97
% identity
                   46
                  (Y08987) osr40g2 [Oryza sativa]
NCBI Description
```

Seq. No. 300263

Seq. ID LIB3180-038-P2-M2-G12

Method BLASTX
NCBI GI g168586
BLAST score 484
E value 7.0e-49

Match length

% identity

100

NCBI Description (AF059484) actin [Gossypium hirsutum]



```
Match length
                  85
% identity
                  (M58656) pyruvate, orthophosphate dikinase [Zea mays]
NCBI Description
                  300264
Seq. No.
                  LIB3180-038-P2-M2-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4033424
                  295
BLAST score
E value
                  9.0e-27
Match length
                  89
% identity
                  72
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                  PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
                   300265
Seq. No.
Seq. ID
                  LIB3180-039-P2-M2-A10
Method
                  BLASTX
NCBI GI
                   g419803
BLAST score
                   211
E value
                   4.0e-17
Match length
                  80
% identity
                   50
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
Seq. No.
                   300266
                   LIB3180-039-P2-M2-A7
Seq. ID
Method
                  BLASTX
                   g4321782
NCBI GI
BLAST score
                   291
E value
                   2.0e-26
Match length
                   85
% identity
                   62
NCBI Description (AF061178) arsenical resistance ATPase [Mus musculus]
                   300267
Seq. No.
                   LIB3180-039-P2-M2-F3
Seq. ID
                   BLASTN
Method
                   g22514
NCBI GI
                   121
BLAST score
                   7.0e-62
E value
                   153
Match length
                   95
% identity
                  Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
NCBI Description
                   300268
Seq. No.
Seq. ID
                   LIB3180-039-P2-M2-G2
                   BLASTX
Method
                   g3420239
NCBI GI
                   267
BLAST score
                   2.0e-23
E value
                   50
```



Seq. No. 300269 Seq. ID LIB3180-039-P2-M2-G5 Method BLASTX NCBI GI g1174613 BLAST score 344 E value 2.0e-32 Match length 80 84 % identity NCBI Description

26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_ (D17788) rice homologue of Tat binding protein [Oryza

sativa]

Seq. No. 300270

Seq. ID LIB3180-039-P2-M2-H4

Method BLASTX NCBI GI q113621 BLAST score 190 2.0e-14 E value 60 Match length % identity 68

FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME NCBI Description

> >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 300271

LIB3180-040-P2-M2-A12 Seq. ID

Method BLASTN NCBI GI q625147 BLAST score 49 E value 1.0e-18 Match length 69 % identity 93

NCBI Description Zea mays protein disulfide isomerase (pdi) mRNA, complete

300272 Seq. No.

Seq. ID LIB3180-040-P2-M2-C12

Method BLASTN NCBI GI g2832242 BLAST score 42 2.0e-14 E value Match length 78 % identity 88

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 300273

Seq. ID LIB3180-040-P2-M2-D8

Method BLASTX NCBI GI g1184776 BLAST score 233 E value 1.0e-37 Match length 91 % identity 91



```
NCBI Description
                  (U45857) cytosolic qlyceroldehyde-3-phosphate dehydrogenase
                  GAPC4 [Zea mays]
Seq. No.
                  300274
Seq. ID
                  LIB3180-040-P2-M2-E5
Method
                  BLASTX
NCBI GI
                  q4115936
BLAST score
                  258
E value
                  2.0e-22
Match length
                  83
% identity
                  65
NCBI Description (AF118223) No definition line found [Arabidopsis thaliana]
Seq. No.
                  300275
Seq. ID
                  LIB3180-040-P2-M2-H10
Method
                  BLASTX
NCBI GI
                  g3935152
BLAST score
                  258
E value
                  2.0e-22
Match length
                  84
                  58
% identity
NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana]
Seq. No.
                  300276
Seq. ID
                  LIB3180-040-P2-M2-H11
Method
                  BLASTX
NCBI GI
                  q2833378
BLAST score
                  187
E value
                  2.0e-14
Match length
                  87
                  43
% identity
NCBI Description
                  HEXOKINASE >gi 619928 (U18754) hexokinase [Arabidopsis
                  thaliana] >gi 1582383 prf 2118367A hexokinase [Arabidopsis
                  thaliana]
                  300277
Seq. No.
Seq. ID
                  LIB3180-041-P2-M2-C11
Method
                  BLASTN
NCBI GI
                  g22516
BLAST score
                  279
                  1.0e-156
E value
                  370
Match length
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                  300278
Seq. No.
Seq. ID
                  LIB3180-041-P2-M2-D3
Method
                  BLASTX
NCBI GI
                  q1771780
BLAST score
                  444
                  3.0e-44
E value
                  96
Match length
```

Seq. No. 300279

% identity

Seq. ID LIB3180-041-P2-M2-E11

93

NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]



```
Method
                  BLASTN
NCBI GI
                  q168704
BLAST score
                  102
                  1.0e-50
E value
                  122
Match length
% identity
                  96
NCBI Description Zea mays zein protein gene, complete cds
                  300280
Seq. No.
Seq. ID
                  LIB3180-041-P2-M2-G5
Method
                  BLASTX
NCBI GI
                  q543867
BLAST score
                  163
E value
                  2.0e-11
Match length
                  76
% identity
                  57
NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor - sweet potato
                  >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit
                  [Ipomoea batatas]
Seq. No.
                  300281
Seq. ID
                  LIB3180-042-P2-M2-A6
Method
                  BLASTN
NCBI GI
                  q22516
BLAST score
                  152
E value
                  4.0e-80
                  268
Match length
% identity
                  89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.
                  300282
Seq. ID
                  LIB3180-042-P2-M2-A7
Method
                  BLASTX
NCBI GI
                  g141615
BLAST score
                  266
E value
                  2.0e-23
Match length
                  72
                  78
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
NCBI Description
                  >gi 22536 emb CAA24727 (V01480) zein protein 3 [Zea mays]
Seq. No.
                  300283
Seq. ID
                  LIB3180-042-P2-M2-B3
Method
                  BLASTN
NCBI GI
                  g168484
BLAST score
                  183
                  1.0e-98
E value
                  243
Match length
                  94
% identity
```

NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 300284

Seq. ID LIB3180-042-P2-M2-C12

Method BLASTN NCBI GI g22292



```
BLAST score
E value
                  1.0e-10
Match length
                  59
                  90
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
Seq. No.
                  300285
                  LIB3180-042-P2-M2-D10
Seq. ID
Method
                  BLASTX
                  q141608
NCBI GI
BLAST score
                  225
E value
                  9.0e-20
Match length
                  119
% identity
                  52
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943_pir_ S15655
NCBI Description
                  zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                  zein [Zea mays]
                  300286
Seq. No.
                  LIB3180-042-P2-M2-E1
Seq. ID
Method
                  BLASTN
                  q1495231
NCBI GI
BLAST score
                  89
E value
                  2.0e-42
Match length
                  154
% identity
                  88
NCBI Description Z.mays mRNA for 22kD zein protein
                  300287
Seq. No.
                  LIB3180-042-P2-M2-F2
Seq. ID
                  BLASTX
Method
                  q1169911
NCBI GI
BLAST score
                  279
E value
                  5.0e-25
                   65
Match length
% identity
                  85
                  1,4-ALPHA-GLUCAN BRANCHING ENZYME IIB PRECURSOR (STARCH
NCBI Description
                  BRANCHING ENZYME IIB) (Q-ENZYME) >gi_168483 (L08065) starch
                  branching enzyme II [Zea mays]
                   300288
Seq. No.
                   LIB3180-042-P2-M2-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g72307
                   267
BLAST score
                   3.0e-23
E value
Match length
                   91
% identity
                   65
                  22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   300289
Seq. No.
```

Seq. ID LIB3180-042-P2-M2-H5

BLASTX Method g2257756 NCBI GI BLAST score 247 5.0e-21 E value



Match length 96 % identity 56

NCBI Description (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays] >gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea

mays]

Seq. No. 300290

Seq. ID LIB3180-042-P2-M2-H7

Method BLASTX
NCBI GI g3850583
BLAST score 262
E value 8.0e-23
Match length 106
% identity 53

NCBI Description (AC005278) Contains similarity to transcription initiation

factor IIE, alpha subunit gb X63468 from Homo sapiens.

[Arabidopsis thaliana]

Seq. No. 300291

Seq. ID LIB3180-042-P2-M2-H8

Method BLASTX
NCBI GI g2653558
BLAST score 344
E value 1.0e-32
Match length 102
% identity 69

NCBI Description (D50679) ferredoxin-sulfite reductase precursor [Zea mays]

Seq. No. 300292

Seq. ID LIB3180-043-P2-M2-B6

Method BLASTX
NCBI GI g1184774
BLAST score 211
E value 2.0e-17
Match length 47
% identity 89

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 300293

Seq. ID LIB3180-043-P2-M2-B7

Method BLASTX
NCBI GI g141597
BLAST score 248
E value 2.0e-28
Match length 100
% identity 75

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)

>gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
>gi 22545 emb CAA24728 (V01481) reading frame zein [2]

[Zea mays]

Seq. No. 300294

Seq. ID LIB3180-043-P2-M2-C10

Method BLASTX
NCBI GI g2507349
BLAST score 193



```
E value
                   8.0e-15
                   113
Match length
% identity
                   37
                   DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE (B150)
NCBI Description
                   (RNA POLYMERASE II SUBUNIT 2) >gi 82997_pir__A25884
                   DNA-directed RNA polymerase (EC 2.7.7.6) II 140K chain -
                   yeast (Saccharomyces cerevisiae) >gi 1293711 (U55020) Rpb2p
                   polymerase [Saccharomyces cerevisiae]
                   >gi 1420379 emb CAA99357 (Z75059) ORF YOR151c
                   [Saccharomyces cerevisiae]
Seq. No.
                   300295
Seq. ID
                   LIB3180-043-P2-M2-C7
Method
                   BLASTN
NCBI GI
                   q1184773
BLAST score
                   67
E value
                   2.0e-29
Match length
                   191
                   85
% identity
NCBI Description
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3
                   (gpc3) mRNA, complete cds
Seq. No.
                   300296
Seq. ID
                   LIB3180-043-P2-M2-D10
Method
                   BLASTX
NCBI GI
                   q730450
BLAST score
                   341
E value
                   3.0e - 32
                   99
Match length
% identity
                   68
                   60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
NCBI Description
                   >gi_480649_pir__S37134 cold-induced protein BnC24B - rape
>gi_398922_emb_CAA80343_ (Z22620) cold induced protein
                   (BnC24B) [Brassica napus]
                   300297
Seq. No.
Seq. ID
                   LIB3180-043-P2-M2-D3
                   BLASTX
Method
NCBI GI
                   g141602
                   239
BLAST score
                   2.0e-20
E value
Match length
                   61
                   84
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
NCBI Description
                   >gi 82658 pir A22831 19K zein precursor (clone M6) - maize
                   >gi_22538_emb_CAA26294 (X02450) zein precursor [Zea mays]
Seq. No.
                   300298
Seq. ID
                   LIB3180-043-P2-M2-G6
Method
                   BLASTX
NCBI GI
                   g2369714
```

BLAST score 272 2.0e-24 E value 79 Match length 67 % identity

(Z97178) elongation factor 2 [Beta vulgaris] NCBI Description



Seq. No.

300299

```
Seq. ID
                  LIB3180-043-P2-M2-H10
                  BLASTX
Method
NCBI GI
                  g2244772
BLAST score
                  259
                  8.0e-23
E value
                  77
Match length
% identity
                   60
NCBI Description
                  (Z97335) transport protein [Arabidopsis thaliana]
Seq. No.
                  300300
Seq. ID
                  LIB3180-044-P2-M2-A1
Method
                  BLASTX
NCBI GI
                  q1313907
BLAST score
                  140
E value
                  8.0e-09
Match length
                  82
% identity
                   46
NCBI Description
                  (D84507) CDPK-related protein kinase [Zea mays]
Seq. No.
                  300301
Seq. ID
                  LIB3180-044-P2-M2-C3
Method
                  BLASTX
NCBI GI
                  q1184776
BLAST score
                  215
E value
                  9.0e-18
                  59
Match length
                  75
% identity
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
Seq. No.
                  300302
Seq. ID
                  LIB3180-044-P2-M2-C5
Method
                  BLASTX
NCBI GI
                  g1545871
BLAST score
                   427
E value
                  2.0e-42
                  91
Match length
                  91
% identity
                  (U66607) cyclin type B-like [Zea mays] >qi 1545873 (U66608)
NCBI Description
                  cyclin type B-like [Zea mays]
                  300303
Seq. No.
Seq. ID
                  LIB3180-044-P2-M2-D2
                  BLASTN
Method
                  g1737491
NCBI GI
BLAST score
                  35
E value
                  2.0e-10
Match length
                  63
% identity
                  89
NCBI Description
                  Triticum aestivum poly(A)-binding protein (wheatpab) mRNA,
                  complete cds
Seq. No.
                  300304
                  LIB3180-044-P2-M2-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1184776
```



```
BLAST score
                  2.0e-41
E value
Match length
                  90
% identity
                   91
NCBI Description
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                  GAPC4 [Zea mays]
Seq. No.
                   300305
                  LIB3180-044-P2-M2-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141616
BLAST score
                  208
E value
                   9.0e-17
Match length
                   61
% identity
                  ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                  >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
Seq. No.
                   300306
Seq. ID
                  LIB3180-044-P2-M2-F12
Method
                  BLASTX
NCBI GI
                   g118104
BLAST score
                   362
E value
                   1.0e-34
Match length
                  79
                   91
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                   >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
Seq. No.
                   300307
Seq. ID
                   LIB3180-044-P2-M2-G7
Method
                  BLASTN
                   q3694806
NCBI GI
BLAST score
                   38
                   3.0e-12
E value
Match length
                   78
                   87
% identity
                  Zea mays alanine aminotransferase (alt) gene, complete cds
NCBI Description
Seq. No.
                   300308
Seq. ID
                  LIB3180-045-P2-M2-A6
                  BLASTX
Method
NCBI GI
                   g118104
BLAST score
                   376
                   3.0e-36
E value
```

Match length 102 73 % identity

PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) NCBI Description

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

>gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -

maize >gi 168461 (M55021) cyclophilin [Zea mays]

>gi $82914\overline{8}$ emb CAA48638 (X68678) cyclophilin [Zea mays]

300309 Seq. No.



```
LIB3180-045-P2-M2-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4204859
BLAST score
                  415
E value
                  8.0e-41
Match length
                  104
% identity
                  (U55859) heat shock protein 80 [Triticum aestivum]
NCBI Description
Seq. No.
                  300310
Seq. ID
                  LIB3180-045-P2-M2-F7
Method
                  BLASTX
NCBI GI
                  q3063473
                  315
BLAST score
                  3.0e-29
E value
                  105
Match length
% identity
                  63
NCBI Description (AC003981) F22013.35 [Arabidopsis thaliana]
                  300311
Seq. No.
                  LIB3180-045-P2-M2-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g547683
BLAST score
                  141
                  5.0e-09
E value
                  41
Match length
% identity
                  71
                  HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat
NCBI Description
                  shock cognate protein 80 [Solanum lycopersicum]
                  >gi_445601_prf__1909348A heat shock protein hsp80
                   [Lycopersicon esculentum]
Seq. No.
                  300312
Seq. ID
                  LIB3180-046-P2-M2-B4
Method
                  BLASTX
                  q2224641
NCBI GI
BLAST score
                  237
E value
                  7.0e-20
Match length
                  109
% identity
                   40
NCBI Description (AB002348) KIAA0350 [Homo sapiens]
                  300313
Seq. No.
Seq. ID
                  LIB3180-046-P2-M2-D11
                  BLASTN
Method
                  q4733890
NCBI GI
BLAST score
                   46
E value
                   4.0e-17
                  106
Match length
% identity
                  86
                  Zea mays unconventional myosin heavy chain (MYO1) mRNA,
NCBI Description
                  partial cds
Seq. No.
                   300314
Seq. ID
                  LIB3180-046-P2-M2-D3
```

42276

BLASTX

g2827711

Method NCBI GI



```
BLAST score
                   2.0e-31
E value
                  107
Match length
% identity
                   65
                   (AL021684) oxoglutarate dehydrogenase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   300315
                   LIB3180-046-P2-M2-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1184776
BLAST score
                   270
E value
                   7.0e-24
Match length
                   80
                   70
% identity
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC4 [Zea mays]
                   300316
Seq. No.
                   LIB3180-046-P2-M2-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1346432
BLAST score
                   210
E value
                   6.0e-17
                   72
Match length
                   58
% identity
                   LEGUMAIN PRECURSOR (ASPARAGINYL ENDOPEPTIDASE)
NCBI Description
                   >qi 1076483 pir JX0344 legumain (EC 3.4.22.34) precursor -
                   jack bean >qi 499294 dbj BAA06596_ (D31787) asparaginyl
                   endopeptidase (Legumain) [Canavalia ensiformis]
                   300317
Seq. No.
Seq. ID
                   LIB3180-047-P2-A6
Method
                   BLASTN
NCBI GI
                   g22326
BLAST score
                   56
                   8.0e-23
E value
                   92
Match length
% identity
                   90
                   Z.mays gene for Hageman factor inhibitor
NCBI Description
                   300318
Seq. No.
Seq. ID
                   LIB3180-047-P2-C2
Method
                   BLASTN
                   g1532162
NCBI GI
                   34
BLAST score
                   9.0e-10
E value
Match length
                   50
                   31
% identity
```

Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, NCBI Description AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14

genes, partial cds, AT.I.24-7, ascorbate peroxidase

(ATHAPX1), EF-lalpha-A1, -A2 and -A3 (EF-lalpha) and AT.I

300319 Seq. No.

Seq. ID LIB3180-047-P2-D5

Method BLASTN



```
NCBI GI
                  g22344
BLAST score
                  42
                  2.0e-14
E value
                  82
Match length
% identity
                  89
NCBI Description Maize gene for heat shock protein 70 exon 1 (clone 9508)
Seq. No.
                  300320
                  LIB3180-047-P2-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4581111
BLAST score
                  152
E value
                  7.0e-10
Match length
                  140
                  29
% identity
                  (AC005825) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                  300321
Seq. No.
                  LIB3180-047-P2-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3757521
BLAST score
                  153
E value
                  3.0e-10
                   67
Match length
                   48
% identity
                  (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   300322
Seq. ID
                  LIB3180-047-P2-G2
Method
                  BLASTN
NCBI GI
                   g22099
BLAST score
                   39
                   4.0e-13
E value
Match length
                   67
                   90
% identity
NCBI Description Z.mays 27kDa zein locus DNA
Seq. No.
                   300323
Seq. ID
                   LIB3180-048-P2-A2
Method
                   BLASTX
NCBI GI
                   g4249382
BLAST score
                   234
E value
                   8.0e-20
Match length
                   64
                   67
% identity
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
                   300324
Seq. No.
Seq. ID
                   LIB3180-048-P2-B11
                   BLASTN
Method
NCBI GI
                   g4096785
BLAST score
                   52
```

2.0e-20

88

E value Match length



```
% identity
                  Zea mays NADP-malic enzyme root isoform mRNA, complete cds
NCBI Description
Seq. No.
                  300325
Seq. ID
                  LIB3180-048-P2-C10
Method
                  BLASTX
NCBI GI
                  g118104
BLAST score
                  237
E value
                  2.0e-33
                  88
Match length
                  77
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi_168461 (M55021) cyclophilin [Zea mays]
                  >gi 82914\overline{8} emb CAA48638 (X68678) cyclophilin [Zea mays]
                  300326
Seq. No.
Seq. ID
                  LIB3180-048-P2-C5
                  BLASTN
Method
NCBI GI
                  g6598604
BLAST score
                  37
                  2.0e-11
E value
Match length
                  65
                  89
% identity
                  Arabidopsis thaliana chromosome II BAC F11A3 genomic
NCBI Description
                  sequence, complete sequence
                  300327
Seq. No.
Seq. ID
                  LIB3180-048-P2-D8
                  BLASTX
Method
NCBI GI
                  g2738248
BLAST score
                  304
                  4.0e-28
E value
                  88
Match length
                  66
% identity
NCBI Description
                  (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
                  300328
Seq. No.
Seq. ID
                  LIB3180-048-P2-E10
Method
                  BLASTN
NCBI GI
                  q168652
                  124
BLAST score
                  3.0e-63
E value
Match length
                  128
% identity
NCBI Description
                  Maize amyloplast-specific transit protein (waxy; wx+
                  locus), complete cds
Seq. No.
                  300329
Seq. ID
                  LIB3180-048-P2-E6
```

Method BLASTX NCBI GI q625509 BLAST score 443 E value 3.0e-44 Match length 94

Seq. ID



```
% identity
NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment)
Seq. No.
                  300330
Seq. ID
                  LIB3180-048-P2-E7
Method
                  BLASTN
NCBI GI
                  g556685
BLAST score
                  114
                  3.0e-57
E value
Match length
                  129
% identity
                  98
NCBI Description Z.mays mRNA for ADP-ribosylation factor
Seq. No.
                  300331
Seq. ID
                  LIB3180-048-P2-F1
Method
                  BLASTX
NCBI GI
                  g2282584
BLAST score
                  148
E value
                  6.0e-10
Match length
                  40
% identity
                  78
NCBI Description
                  (U76259) elongation factor 1-alpha [Zea mays]
Seq. No.
                  300332
Seq. ID
                  LIB3180-048-P2-F3
Method
                  BLASTX
NCBI GI
                  q542125
BLAST score
                  212
                  2.0e-17
E value
Match length
                  55
                  76
% identity
                  translation elongation factor eEF-1 alpha chain - barley
NCBI Description
                  >gi_396134_emb_CAA80666_ (Z23130) protein synthesis
                  elongation factor-1 alpha [Hordeum vulgare]
Seq. No.
                  300333
Seq. ID
                  LIB3180-048-P2-G3
Method
                  BLASTX
NCBI GI
                  q1903034
BLAST score
                  201
E value
                  6.0e-16
                  68
Match length
% identity
                  50
NCBI Description
                  (X94625) amp-binding protein [Brassica napus]
                  300334
Seq. No.
Seq. ID
                  LIB3180-048-P2-G7
Method
                  BLASTX
NCBI GI
                  g168586
BLAST score
                  302
E value
                  5.0e-28
                  74
Match length
% identity
                  81
NCBI Description (M58656) pyruvate, orthophosphate dikinase [Zea mays]
                  300335
Seq. No.
```

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LIB3180-048-P2-H6

```
Method
                  BLASTX
NCBI GI
                  g3057120
BLAST score
                  492
E value
                  4.0e-50
Match length
                  90
                  98
% identity
NCBI Description (AF023159) starch synthase DULL1 [Zea mays]
Seq. No.
                  300336
Seq. ID
                  LIB3180-049-P2-M1-A4
Method
                  BLASTX
```

NCBI GI g20559
BLAST score 602
E value 1.0e-62
Match length 127
% identity 94

NCBI Description (X13301) hsp70 (AA 6 - 651) [Petunia x hybrida]

 Seq. No.
 300337

 Seq. ID
 LIB3180-049-P2-M1-B2

 Method
 BLASTX

NCBI GI g3914006
BLAST score 313
E value 5.0e-29
Match length 65
% identity 97

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1816588

(U85495) LON2 [Zea mays]

Seq. No. 300338

Seq. ID LIB3180-049-P2-M1-B9

Method BLASTX
NCBI GI g551288
BLAST score 345
E value 2.0e-32
Match length 82
% identity 82

NCBI Description (Z33611) phosphoglycerate mutase [Zea mays]

Seq. No. 300339

Seq. ID LIB3180-049-P2-M1-D12

Method BLASTN
NCBI GI g940880
BLAST score 54
E value 2.0e-21
Match length 146
% identity 85

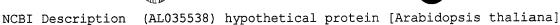
NCBI Description Z.mays zag2 gene

Seq. No. 300340

Seq. ID LIB3180-049-P2-M1-D2

Method BLASTX
NCBI GI g4467124
BLAST score 241
E value 2.0e-20
Match length 136
% identity 37





Seq. ID LIB3180-049-P2-M1-D5

Method BLASTX
NCBI GI g3608171
BLAST score 475
E value 7.0e-60
Match length 139
% identity 86

NCBI Description (D86306) proton-translocating inorganic pyrophosphatase

[Cucurbita moschata]

Seq. No. 300342

Seq. ID LIB3180-049-P2-M1-E1

Method BLASTX
NCBI GI g67155
BLAST score 240
E value 2.0e-20
Match length 119
% identity 56

NCBI Description pyruvate, orthophosphate dikinase (EC 2.7.9.1) precursor -

maize

Seq. No. 300343

Seq. ID LIB3180-049-P2-M1-H11

Method BLASTX
NCBI GI g2288999
BLAST score 194
E value 9.0e-23
Match length 82
% identity 65

NCBI Description (AC002335) electron transfer flavoprotein ubiquinone

oxidoreductase isolog [Arabidopsis thaliana]

Seq. No. 300344

Seq. ID LIB3180-049-P2-M1-H2

Method BLASTX
NCBI GI g1184776
BLAST score 442
E value 6.0e-44
Match length 88
% identity 95

NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC4 [Zea mays]

Seq. No. 300345

Seq. ID LIB3180-049-P2-M1-H4

Method BLASTX
NCBI GI 94512667
BLAST score 572
E value 4.0e-66
Match length 137
% identity 86

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 300346



```
LIB3180-049-P2-M1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1184774
BLAST score
                  155
                  2.0e-10
E value
                  43
Match length
% identity
                  (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC3 [Zea mays]
Seq. No.
                  300347
Seq. ID
                  LIB3180-050-P2-M1-A9
Method
                  BLASTX
NCBI GI
                  q3510253
BLAST score
                  194
                  2.0e-15
E value
                  63
Match length
% identity
                  57
NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]
                  300348
Seq. No.
                  LIB3180-050-P2-M1-C1
Seq. ID
Method
                  BLASTX
                  q3309243
NCBI GI
                  169
BLAST score
                  2.0e-12
E value
Match length
                  41
                  78
% identity
                   (AF073507) aconitase-iron regulated protein 1 [Citrus
NCBI Description
Seq. No.
                   300349
                  LIB3180-050-P2-M1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                   q416150
BLAST score
                  79
                  8.0e-37
E value
Match length
                   115
% identity
                   92
NCBI Description Zea mays beta-8 tubulin (tub8) mRNA, complete cds
                   300350
Seq. No.
                   LIB3180-050-P2-M1-E5
Seq. ID
Method
                  BLASTX
                   g3152581
NCBI GI
                   247
BLAST score
E value
                   3.0e-21
Match length
                   69
% identity
                   65
                   (AC002986) Similar to E. coli sulfurtransferase (rhodanese)
NCBI Description
                   gb AE00338. ESTs gb T03984, gb T03983 and gb W43228 come
                   from this gene. [Arabidopsis thaliana]
                   300351
```

Seq. ID LIB3180-050-P2-M1-F1

BLASTX Method NCBI GI g1723436

NCBI GI

E value

BLAST score



```
BLAST score
E value
                   4.0e-26
                  106
Match length
% identity
                   58
                  HYPOTHETICAL 119.9 KD PROTEIN C56F8.03 IN CHROMOSOME I
NCBI Description
                  >gi 1204225 emb CAA93574 (Z69728) unknown
                   [Schizosaccharomyces pombe]
Seq. No.
                  300352
Seq. ID
                  LIB3180-051-P2-M1-A1
Method
                  BLASTX
NCBI GI
                  g1184774
BLAST score
                  370
E value
                  2.0e-35
Match length
                  88
% identity
                  84
NCBI Description
                  (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                  GAPC3 [Zea mays]
Seq. No.
                   300353
Seq. ID
                  LIB3180-051-P2-M1-A2
Method
                  BLASTX
NCBI GI
                  q4406769
BLAST score
                   247
E value
                   4.0e-21
Match length
                  84
% identity
NCBI Description
                  (AC006836) putative translin [Arabidopsis thaliana]
                   300354
Seq. No.
                  LIB3180-051-P2-M1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q82695
                   326
BLAST score
E value
                   1.0e-30
                   72
Match length
                   93
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) 3 -
NCBI Description
                  maize (fragment) >gi 293887 (L13431)
                   glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
                   300355
Seq. No.
Seq. ID
                  LIB3180-051-P2-M1-D9
Method
                  BLASTX
NCBI GI
                   g22216
BLAST score
                   184
                   9.0e-14
E value
                  81
Match length
% identity
                   52
                  (X55722) 22kD zein [Zea mays]
NCBI Description
Seq. No.
                   300356
                  LIB3180-052-P2-M1-C3
Seq. ID
Method
                  BLASTX
```

g3915826

290 2.0e-26



57

% identity

```
Match length
                  71
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L5
                  300357
Seq. No.
Seq. ID
                  LIB3180-052-P2-M1-C6
Method
                  BLASTX
NCBI GI
                  g4091008
BLAST score
                  214
E value
                  3.0e-17
Match length
                  87
% identity
                  55
                  (AF040700) methionyl-tRNA synthetase [Oryza sativa]
NCBI Description
Seq. No.
                  300358
Seq. ID
                  LIB3180-052-P2-M1-D10
Method
                  BLASTN
NCBI GI
                  g4206307
BLAST score
                  36
E value
                  9.0e-11
Match length
                  108
% identity
                  84
NCBI Description Zea mays retrotransposon Cinful-2
Seq. No.
                  300359
Seq. ID
                  LIB3180-052-P2-M1-E12
Method
                  BLASTX
NCBI GI
                  q4585966
BLAST score
                  156
E value
                  2.0e-10
Match length
                  70
% identity
                  54
NCBI Description
                   (AC005287) Putative dihyrdolipoamide acetyltransferase
                   [Arabidopsis thaliana]
                  300360
Seq. No.
Seq. ID
                  LIB3180-052-P2-M1-F6
Method
                  BLASTX
NCBI GI
                  g135398
BLAST score
                  313
                  5.0e-29
E value
                  58
Match length
% identity
                  98
                  TUBULIN ALPHA-1 CHAIN >gi 82731 pir S15773 tubulin alpha-1
NCBI Description
                  chain - maize >gi 22147 emb CAA33734 (X15704)
                  alpha1-tubulin [Zea mays]
Seq. No.
                  300361
                  LIB3180-052-P2-M1-G11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3452091
BLAST score
                  268
E value
                  1.0e-23
                  86
Match length
```

NCBI Description (AJ004899) rudimentary enhancer [Glycine max]



```
Seq. No.
                  300362
                  LIB3180-052-P2-M1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3318615
BLAST score
                  212
E value
                  3.0e-17
Match length
                  46
                  91
% identity
                  (AB016065) mitochondrial phosphate transporter [Oryza
NCBI Description
Seq. No.
                  300363
Seq. ID
                  LIB3180-052-P2-M1-G3
Method
                  BLASTX
NCBI GI
                  q168586
                  433
BLAST score
                  7.0e-43
E value
Match length
                  138
% identity
                  69
                  (M58656) pyruvate, orthophosphate dikinase [Zea mays]
NCBI Description
                  300364
Seq. No.
                  LIB3180-052-P2-M1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4263722
BLAST score
                  411
                  3.0e-40
E value
Match length
                  131
                  60
% identity
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
                  300365
Seq. No.
                  LIB3180-053-P2-M1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914557
BLAST score
                   322
E value
                   8.0e-30
Match length
                  77
                   84
% identity
                  RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED
NCBI Description
                   PROTEIN) >qi 1155265 (U40219) possible apospory-associated
                  protein [Pennisetum ciliare]
Seq. No.
                   300366
                  LIB3180-053-P2-M1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2827080
BLAST score
                   157
E value
                   8.0e-11
Match length
                   63
% identity
                  (AF020271) malate dehydrogenase precursor [Medicago sativa]
NCBI Description
```

Seq. ID LIB3180-053-P2-M1-C5

Method BLASTX NCBI GI g3511285



```
BLAST score
E value
                  7.0e-19 ·
                  62
Match length
% identity
                  68
                  (AF081534) cellulose synthase [Populus alba x Populus
NCBI Description
                  300368
Seq. No.
                  LIB3180-053-P2-M1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g260041
BLAST score
                  45
E value
                  2.0e-16
Match length
                  73
% identity
                  90
NCBI Description Sh2=shrunken-2 locus [maize, mRNA Partial, 1867 nt]
                  300369
Seq. No.
                  LIB3180-053-P2-M1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g463151
BLAST score
                  119
E value
                  1.0e-60
Match length
                  159
% identity
                  94
NCBI Description Zea mays high sulfur zein gene, complete cds
                  300370
Seq. No.
Seq. ID
                  LIB3180-053-P2-M1-D7
Method
                  BLASTX
                  q730125
NCBI GI
BLAST score
                   426
                   1.0e-46
E value
Match length
                   122
% identity
                  NADPH-CYTOCHROME P450 REDUCTASE >gi 322739 pir S31502
NCBI Description
                  NADPH--ferrihemoprotein reductase (\overline{EC}\ 1.6.\overline{2}.4) - Madagascar
                   periwinkle >qi 18139 emb CAA49446 (X69791)
                   NADPH--ferrihemoprotein reductase [Catharanthus roseus]
Seq. No.
                   300371
Seq. ID
                  LIB3180-054-P2-M1-A3
Method
                  BLASTX
NCBI GI
                   g464707
BLAST score
                   263
                   4.0e-23
E value
Match length
                   66
                   76
% identity
                  40S RIBOSOMAL PROTEIN S18 >qi 480908 pir S37496 ribosomal
NCBI Description
                   protein S18.A - Arabidopsis thaliana
                   >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                   [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >gi 2505871 emb CAA72909 (Y12227) ribosomal protein S18A
```



[Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

```
300372
Seq. No.
                   LIB3180-054-P2-M1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2370312
BLAST score
                   457
E value
                   1.0e-45
                   102
Match length
% identity
                   79
                   (AJ000995) DnaJ-like protein [Medicago sativa] >gi_3202020
NCBI Description
                   (AF069507) DnaJ-like protein MsJ1 [Medicago sativa]
                   300373
Seq. No.
                   LIB3180-054-P2-M1-F3
Seq. ID
                   BLASTX
Method
                   q4008159
NCBI GI
BLAST score
                   156
E value
                   8.0e-11
                   57
Match length
% identity
                   61
                  (AB015601) DnaJ homolog [Salix gilgiana]
NCBI Description
Seq. No.
                   300374
                   LIB3180-054-P2-M1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2735841
BLAST score
                   241
E value
                   2.0e-20
Match length
                   116
% identity
                   42
                   (AF010283) No definition line found [Sorghum bicolor]
NCBI Description
Seq. No.
                   300375
                   LIB3180-055-P2-M1-A10
Seq. ID
Method
                   BLASTX
                   g1143864
NCBI GI
BLAST score
                   320
E value
                   7.0e-30
                   98
Match length
% identity
                   63
                   (U28047) beta glucosidase [Oryza sativa]
NCBI Description
                   300376
Seq. No.
Seq. ID
                   LIB3180-055-P2-M1-B6
Method
                   BLASTN
                   q949979
NCBI GI
BLAST score
                   128
                   5.0e-66
E value
                   184
Match length
```

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92

NCBI Description Z.mays Glossy2 locus DNA

% identity

% identity

NCBI Description

```
300377
Seq. No.
                  LIB3180-055-P2-M1-D10
Seq. ID
Method
                  BLASTX
                  g1076746
NCBI GI
BLAST score
                  518
                  7.0e-53
E value
Match length
                  101
                  97
% identity
NCBI Description
                  heat shock protein 70 - rice (fragment)
                  >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                  [Oryza sativa]
                  300378
Seq. No.
                  LIB3180-055-P2-M1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g126896
BLAST score
                  271
E value
                  5.0e-24
Match length
                  108
% identity
NCBI Description
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
                  >gi_319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37)
                  precursor, mitochondrial - watermelon
                  >gi 18297 emb CAA35239 (X17362) precursor protein (AA -27
                  to 320) [Citrullus lanatus]
Seq. No.
                  300379
                  LIB3180-057-P2-M1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22336
                  59
BLAST score
E value
                  5.0e-25
Match length
                  63
% identity
                  98
                  Maize mRNA for an 18kDa heat shock protein
NCBI Description
                  300380
Seq. No.
                  LIB3180-058-P2-M1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4587584
BLAST score
                  153
                  1.0e-10
E value
Match length
                  50
% identity
                  62
                  (AC007232) unknown protein [Arabidopsis thaliana]
NCBI Description
                  300381
Seq. No.
Seq. ID
                  LIB3180-058-P2-M1-F12
                  BLASTX
Method
                  q3560533
NCBI GI
BLAST score
                  202
                  2.0e-16
E value
                  51
Match length
                  76
```

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[Oryza sativa]

(AF042333) 24-methylene lophenol C24(1)methyltransferase

Seq. ID

Method NCBI GI

```
Seq. No.
                  300382
Seq. ID
                  LIB3180-058-P2-M1-H1
Method
                  BLASTX
NCBI GI
                  g520582
BLAST score
                  164
E value
                  2.0e-11
Match length
                  52
                  62
% identity
NCBI Description (D37796) Ids3 [Hordeum vulgare]
Seq. No.
                  300383
Seq. ID
                  LIB3180-059-P2-M1-A10
Method
                  BLASTN
NCBI GI
                  q1184775
BLAST score
                  78
                  5.0e-36
E value
Match length
                  138
                  89
% identity
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4
NCBI Description
                  (gpc4) mRNA, complete cds
Seq. No.
                  300384
Seq. ID
                  LIB3180-059-P2-M1-A11
Method
                  BLASTX
NCBI GI
                  q4454480
BLAST score
                  153
E value
                  1.0e-10
Match length
                  37
                  76
% identity
                  (AC006234) putative (1-4)-beta-mannan endohydrolase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  300385
Seq. ID
                  LIB3180-059-P2-M1-B3
Method
                  BLASTX
NCBI GI
                  g2668744
BLAST score
                  243
E value
                  7.0e-21
Match length
                  54
% identity
                  83
NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]
Seq. No.
                  300386
Seq. ID
                  LIB3180-059-P2-M1-E1
Method
                  BLASTX
NCBI GI
                  q4415996
BLAST score
                  212
                  3.0e-17
E value
Match length
                  61
% identity
                  66
                  (AF059290) beta-tubulin 4 [Eleusine indica]
NCBI Description
Seq. No.
                  300387
```

42290

LIB3180-059-P2-M1-E2

BLASTN

g1037129



```
BLAST score
                  2.0e-14
E value
                  84
Match length
                  90
% identity
                  (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
Seq. No.
                  300388
Seq. ID
                  LIB3180-059-P2-M1-F10
                  BLASTN
Method
NCBI GI
                  g2642323
                  91
BLAST score
                  1.0e-43
E value
Match length
                  131
% identity
                  91
NCBI Description Zea mays profilin (PRO4) mRNA, complete cds
                  300389
Seq. No.
Seq. ID
                  LIB3180-059-P2-M1-H2
Method
                  BLASTX
NCBI GI
                  g2244971
BLAST score
                  229
                  6.0e-19
E value
                  52
Match length
                  77
% identity
NCBI Description (297340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  300390
Seq. ID
                  LIB3180-060-P2-M1-A1
                  BLASTX
Method
NCBI GI
                  g559713
BLAST score
                  237
E value
                  4.0e-20
Match length
                  86
% identity
                  55
                  (D38552) The half39 protein is related to cyclophilin.
NCBI Description
                  [Homo sapiens]
                  300391
Seq. No.
Seq. ID
                  LIB3180-060-P2-M1-A4
Method
                  BLASTN
NCBI GI
                  g168584
BLAST score
                  79
E value
                  4.0e-37
Match length
                  95
% identity
                  96
NCBI Description Corn pyruvate, orthophosphate dikinase gene, exons 2-19
Seq. No.
                  300392
                  LIB3180-060-P2-M1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22138
BLAST score
                  60
                  2.0e-25
E value
Match length
                  131
% identity
                  87
NCBI Description Z.mays gene for acetohydroxyacid synthase (AHAS108)
```

NCBI GI

BLAST score



```
Seq. No.
                   300393
Seq. ID
                  LIB3180-060-P2-M1-H6
Method
                  BLASTN
NCBI GI
                   q536891
BLAST score
                   36
E value
                   5.0e-11
Match length
                   60
% identity
                  90
NCBI Description Wheat mRNA for protein H2A, complete cds, clone wcH2A-4
Seq. No.
                   300394
Seq. ID
                  LIB3180-061-P2-M1-A1
Method
                  BLASTX
NCBI GI
                  a3393067
BLAST score
                   314
E value
                   5.0e-29
Match length
                  87
                  72
% identity
NCBI Description
                  (AJ001117) sucrose synthase type I [Triticum sp.]
Seq. No.
                   300395
Seq. ID
                  LIB3180-061-P2-M1-A10
Method
                  BLASTX
NCBI GI
                  q2829871
BLAST score
                  227
                  8.0e-19
E value
Match length
                  112
% identity
                   43
NCBI Description
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   300396
Seq. ID
                  LIB3180-061-P2-M1-A9
Method
                  BLASTX
NCBI GI
                  g2194142
BLAST score
                  331
E value
                   6.0e-31
Match length
                  131
% identity
                   47
                   (AC002062) ESTs gb N38288, gb T43486, gb AA395242 come from
NCBI Description
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  300397
Seq. ID
                  LIB3180-061-P2-M1-B11
Method
                  BLASTN
NCBI GI
                  g260041
BLAST score
                  40
E value
                  2.0e-13
Match length
                  67
                  90
% identity
                  Sh2=shrunken-2 locus [maize, mRNA Partial, 1867 nt]
NCBI Description
Seq. No.
                  300398
Seq. ID
                  LIB3180-061-P2-M1-B2
Method
                  BLASTX
```

42292

g1370603



```
E value
                  9.0e-27
Match length
                  92
                  66
% identity
                  (X98245) annexin p35 [Zea mays]
NCBI Description
                  300399
Seq. No.
                  LIB3180-061-P2-M1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119355
BLAST score
                  289
                  5.0e-26
E value
                  57
Match length
                  100
% identity
NCBI Description
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                  >gi 100869 pir S16257 phosphopyruvate hydratase (EC
                  4.2.1.11) - maize >gi 22273 emb CAA39454 (X55981) enolase
                  [Zea mays]
Seq. No.
                  300400
Seq. ID
                  LIB3180-061-P2-M1-D3
Method
                  BLASTN
NCBI GI
                  g168673
BLAST score
                  61
E value
                  1.0e-25
Match length
                  73
                  96
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
                  300401
Seq. No.
                  LIB3180-061-P2-M1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g231654
BLAST score
                  310
E value
                  2.0e-28
                  79
Match length
% identity
                  81
                  BRITTLE-1 PROTEIN PRECURSOR >gi_82676_pir__JQ1459 Bt1
NCBI Description
                  protein precursor - maize >gi_168426 (M79333) brittle-1
                  protein [Zea mays]
Seq. No.
                  300402
                  LIB3180-061-P2-M1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22516
BLAST score
                  100
                  5.0e-49
E value
                  176
Match length
% identity
                  89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.
                  300403
Seq. ID
                  LIB3180-061-P2-M1-F3
Method
                  BLASTN
NCBI GI
                  g248336
BLAST score
                  72
```

42293

2.0e-32

E value

NCBI Description



```
Match length
                  124
                  31
% identity
NCBI Description polyubiquitin [maize, Genomic, 3841 nt]
                  300404
Seq. No.
                  LIB3180-061-P2-M1-G1
Seq. ID
                  BLASTX
Method
                  g131773
NCBI GI
BLAST score
                  448
                  1.0e-44
E value
                  122
Match length
                  76
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                  >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
                  maize
                   300405
Seq. No.
                  LIB3180-061-P2-M1-H2
Seq. ID
                   BLASTX
Method
                   q2668742
NCBI GI
BLAST score
                   365
                   4.0e-35
E value
                  86
Match length
                   87
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   300406
Seq. No.
                   LIB3180-061-P2-M1-H7
Seq. ID
                   BLASTX
Method
                   g421855
NCBI GI
BLAST score
                   264
                   4.0e-23
E value
                   78
Match length
                   59
% identity
                  alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana
NCBI Description
                   (fragment)
                   300407
Seq. No.
                   LIB3180-062-P2-M1-A2
Seq. ID
Method
                   BLASTX
                   q1658313
NCBI GI
                   172
BLAST score
                   3.0e-25
E value
                   79
Match length
                   44
% identity
                   (Y08987) osr40g2 [Oryza sativa]
NCBI Description
                   300408
Seq. No.
                   LIB3180-062-P2-M1-C8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2688830
BLAST score
                   177
                   3.0e-13
E value
                   45
Match length
                   80
% identity
```

(AF000952) putative sugar transporter [Prunus armeniaca]



```
300409
Seq. No.
Seq. ID
                  LIB3180-062-P2-M1-D9
Method
                  BLASTX
NCBI GI
                  g4210330
BLAST score
                  261
                  7.0e-23
E value
Match length
                  93
% identity
                  56
NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, El subunit
                  [Arabidopsis thaliana]
                  300410
Seq. No.
                  LIB3180-062-P2-M1-E1
Seq. ID
Method
                  BLASTN
                  g3057119
NCBI GI
                  246
BLAST score
                  1.0e-136
E value
                  298
Match length
                  96
% identity
NCBI Description Zea mays starch synthase DULL1 (dull1) mRNA, complete cds
                  300411
Seq. No.
                  LIB3180-062-P2-M1-G4
Seq. ID
Method
                  BLASTX
                  g3694807
NCBI GI
BLAST score
                  386
                  2.0e-37
E value
                  87
Match length
                  86
% identity
NCBI Description (AF055898) alanine aminotransferase [Zea mays]
                  300412
Seq. No.
                  LIB3181-001-P1-M1-B1
Seq. ID
Method
                  BLASTN
                  g168698
NCBI GI
BLAST score
                   63
E value
                   5.0e-27
Match length
                  151
% identity
                   85
NCBI Description Z.mays zein mRNA, complete cds
                   300413
Seq. No.
                  LIB3181-001-P1-M1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2827524
BLAST score
                   168
E value
                   3.0e-12
Match length
                   54
% identity
                   59
```

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 300414

Seq. ID LIB3181-001-P1-M1-C7

Method BLASTN
NCBI GI g413792
BLAST score 47
E value 2.0e-17



```
Match length
                  83
% identity
NCBI Description Cloning vector lambda EMBL3 SP6/T7, left arm
                  300415
Seq. No.
Seq. ID
                  LIB3181-001-P1-M1-C9
Method
                  BLASTN
NCBI GI
                  g168694
BLAST score
                  120
E value
                  4.0e-61
Match length
                  128
% identity
                  98
NCBI Description Maize gamma zein mRNA, partial cds
Seq. No.
                  300416
Seq. ID
                  LIB3181-001-P1-M1-D3
Method
                  BLASTX
NCBI GI
                  q567893
BLAST score
                  224
E value
                  2.0e-18
Match length
                  75
% identity
                  56
NCBI Description
                  (L37382) beta-galactosidase-complementation protein
                  [Cloning vector]
Seq. No.
                  300417
Seq. ID
                  LIB3181-001-P1-M1-G8
Method
                  BLASTX
NCBI GI
                  q141605
BLAST score
                  228
                  5.0e-19
E value
                  73
Match length
% identity
                  68
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  300418
Seq. ID
                  LIB3181-002-P1-M1-B10
                  BLASTX
Method
                  g3298548
NCBI GI
BLAST score
                  386
E value
                  2.0e-37
                  109
Match length
% identity
                  72
NCBI Description
                  (AC004681) putative spliceosomal protein [Arabidopsis
                  thaliana]
Seq. No.
                  300419
Seq. ID
                  LIB3181-002-P1-M1-B5
Method
                  BLASTN
```

NCBI GI g168484
BLAST score 77
E value 1.0e-35
Match length 157
% identity 87

NCBI Description Maize endosperm glutelin-2 gene, complete cds

300425



```
Seq. No.
                  300420
Seq. ID
                  LIB3181-002-P1-M1-C1
Method
                  BLASTN
                  g22524
NCBI GI
BLAST score
                  110
                  4.0e-55
E value
Match length
                  194
                  90
% identity
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)
                  300421
Seq. No.
Seq. ID
                  LIB3181-002-P1-M1-C2
Method
                  BLASTX
NCBI GI
                  g168699
BLAST score
                  214
                  2.0e-17
E value
Match length
                  67
                  69
% identity
NCBI Description (M60836) zein [Zea mays]
                  300422
Seq. No.
                  LIB3181-002-P1-M1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174526
BLAST score
                  352
                  2.0e-33
E value
                  98
Match length
                  67
% identity
NCBI Description
                  LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)
                  >gi_1074993_pir__D64110 lysine--tRNA ligase (EC 6.1.1.6) -
                  Haemophilus influenzae (strain Rd KW20) >gi_1574141
                   (U32800) lysyl-tRNA synthetase (lysU) [Haemophilus
                  influenzae Rd]
Seq. No.
                  300423
Seq. ID
                  LIB3181-002-P1-M1-E5
Method
                  BLASTX
                  q4204294
NCBI GI
BLAST score
                  314
                  5.0e-29
E value
                  90
Match length
                  76
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  300424
Seq. ID
                  LIB3181-002-P1-M1-F5
Method
                  BLASTN
NCBI GI
                  q168696
BLAST score
                  83
E value
                  7.0e-39
Match length
                  103
% identity
                  95
NCBI Description Z.mays zein mRNA, 3' end
```



Seq. ID LIB3181-003-P1-M1-A12

Method BLASTX
NCBI GI g4504165
BLAST score 220
E value 1.0e-21
Match length 79
% identity 62

NCBI Description gelsolin (amyloidosis, Finnish type)

>gi 121116 sp P06396 GELS HUMAN GELSOLIN PRECURSOR, PLASMA

(ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL)
>gi_71649_pir__FAHUP gelsolin precursor, plasma - human
>gi_736249_emb_CAA28000_ (X04412) plasma gelsolin [Homo
sapiens] >gi_225304_prf__1211330A gelsolin [Homo sapiens]

Seq. No. 300426

Seq. ID LIB3181-003-P1-M1-B1

Method BLASTN NCBI GI g22514 BLAST score 141 E value 2.0e-73 Match length 365 % identity 85

NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)

Seq. No. 300427

Seq. ID LIB3181-003-P1-M1-B11

Method BLASTN
NCBI GI g4038570
BLAST score 174
E value 4.0e-93
Match length 291
% identity 89

NCBI Description Human DNA sequence from clone 51J12 on chromosome 6q26-27.

Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain

RNA Binding proteins) and zebrafish ZKQ-1 (Qu

Seq. No. 300428

Seq. ID LIB3181-003-P1-M1-B6

Method BLASTN
NCBI GI g1684789
BLAST score 62
E value 3.0e-26
Match length 294
% identity 81

NCBI Description Human epithelial membrane protein (CL-20) mRNA, complete

cds

Seq. No. 300429

Seq. ID LIB3181-003-P1-M1-B7

Method BLASTX
NCBI GI g3335226
BLAST score 403
E value 3.0e-39
Match length 119
% identity 65

NCBI Description (AF077374) small proline-rich protein [Homo sapiens]



```
300430
Seq. No.
                   LIB3181-003-P1-M1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3293537
                   142
BLAST score
                   7.0e-09
E value
Match length
                   79
                   38
% identity
                   (AF071059) zinc finger RNA binding protein [Mus musculus]
NCBI Description
                   300431
Seq. No.
                   LIB3181-003-P1-M1-C12
Seq. ID
Method
                   BLASTX
                   g4504165
NCBI GI
                    421
BLAST score
                    1.0e-41
E value
                    103
Match length
                    84
% identity
                   gelsolin (amyloidosis, Finnish type)
NCBI Description
                    >gi 121116_sp_P06396_GELS_HUMAN GELSOLIN PRECURSOR, PLASMA
                    (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL)
                    >gi_71649_pir__FAHUP gelsolin precursor, plasma - human
                    >gi_736249 emb_CAA28000 (X04412) plasma gelsolin [Homo
sapiens] >gi_225304_prf__1211330A gelsolin [Homo sapiens]
                    300432
Seq. No.
                    LIB3181-003-P1-M1-C5
Seq. ID
                    BLASTX
Method
                    g346219
NCBI GI
BLAST score
                    257
                    1.0e-22
E value
                    74
Match length
                    70
% identity
NCBI Description keratin K4a - human (fragment)
                    300433
Seq. No.
                    LIB3181-003-P1-M1-D10
Seq. ID
Method
                    BLASTN
                    q180222
NCBI GI
BLAST score
                    35
E value
                    4.0e-10
Match length
                    125
                    82
% identity
NCBI Description Human carcinoembryonic antigen mRNA (CEA), complete cds
                    300434
Seq. No.
                    LIB3181-003-P1-M1-D4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g224507
BLAST score
                    270
                    9.0e-24
E value
Match length
                    97
                    61
% identity
```

300435

NCBI Description zein Al [Zea mays]

Seq. No.

Match length

% identity

65

63



```
LIB3181-003-P1-M1-E10
Seq. ID
Method
                  BLASTX
                  g2224565
NCBI GI
                  712
BLAST score
                  2.0e-75
E value
                  138
Match length
                  96
% identity
NCBI Description (AB002310) KIAA0312 [Homo sapiens]
                  300436
Seq. No.
                  LIB3181-003-P1-M1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22288
BLAST score
                  107
                  4.0e-53
E value
                  131
Match length
                  95
% identity
NCBI Description Maize mRNA fragment for endosperm glutelin-2
                  300437
Seq. No.
                  LIB3181-003-P1-M1-F10
Seq. ID
                  BLASTX
Method
                  g2118384
NCBI GI
                  170
BLAST score
E value
                  5.0e-13
                  109
Match length
                  50
% identity
NCBI Description squamous cell carcinoma antigen 2 - human
                  300438
Seq. No.
                  LIB3181-003-P1-M1-F4
Seq. ID
                  BLASTX
Method
                  g16073
NCBI GI
BLAST score
                  293
                  1.0e-26
E value
Match length
                  67
                  88
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                  300439
Seq. No.
                  LIB3181-003-P1-M1-F7
Seq. ID
                  BLASTX
Method
                  q168691
NCBI GI
                   238
BLAST score
E value
                   5.0e-20
                   89
Match length
                   56
% identity
NCBI Description (M29628) zein [Zea mays]
                   300440
Seq. No.
                   LIB3181-003-P1-M1-G10
Seq. ID
Method
                  BLASTX
                   q2137308
NCBI GI
BLAST score
                   186
E value
                   3.0e-14
```



NCBI Description G protein beta subuit like - mouse >gi_475012_dbj_BAA06185_ (D29802) G protein beta subuit like [Mus musculus]

Seq. No. 300441

Seq. ID LIB3181-003-P1-M1-G8

Method BLASTN
NCBI GI g3777595
BLAST score 71

BLAST score 71 E value 1.0e-31 Match length 119

Match length 119 % identity 90

NCBI Description Homo sapiens TACC2 protein (TACC2) mRNA, partial cds

Seq. No. 300442

Seq. ID LIB3181-003-P1-M1-H1

Method BLASTX
NCBI GI g3763845
BLAST score 220
E value 1.0e-19
Match length 84
% identity 61

NCBI Description (AB018375) early nodulin [Oryza sativa]

>gi_3763847_dbj_BAA33814_ (AB018376) early nodulin [Oryza

sativa]

Seq. No. 300443

Seq. ID LIB3181-003-P1-M1-H10

Method BLASTN
NCBI GI g3551833
BLAST score 45
E value 3.0e-16
Match length 127
% identity 84

NCBI Description Homo sapiens clone 24 diacylglycerol kinase alpha (DAGK1)

mRNA, complete cds

Seq. No. 300444

Seq. ID LIB3181-004-P1-M1-B12

Method BLASTN
NCBI GI g531832
BLAST score 37
E value 2.0e-11
Match length 137
% identity 82

NCBI Description Cloning vector pSport2, complete sequence

Seq. No. 300445

Seq. ID LIB3181-004-P1-M1-B3

Method BLASTX
NCBI GI g2244732
BLAST score 225
E value 9.0e-19
Match length 55
% identity 69

NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No. 300446

```
LIB3181-004-P1-M1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q16073
                  365
BLAST score
                  6.0e-35
E value
                  127
Match length
                  61
% identity
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                  300447
Seq. No.
                  LIB3181-004-P1-M1-D1
Seq. ID
Method
                  BLASTN
                  q168663
NCBI GI
BLAST score
                  56
E value
                  6.0e-23
                  68
Match length
                  96
% identity
NCBI Description Maize sulfur-rich zein protein of Mr 15,000, complete cds
                  300448
Seq. No.
                  LIB3181-004-P1-M1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82660
BLAST score
                  168
E value
                  5.0e-12
                  60
Match length
                  62
% identity
NCBI Description
                  19K zein precursor (clone ZG31A) - maize (fragment)
                  >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
Seq. No.
                  300449
                  LIB3181-004-P1-M1-G3
Seq. ID
                  BLASTN
Method
NCBI GI
                  q22524
BLAST score
                  161
E value
                  2.0e-85
Match length
                  320
                  89
% identity
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)
                  300450
Seq. No.
                  LIB3181-006-P1-K2-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168681
BLAST score
                  119
                  3.0e-60
E value
Match length
                  235
                  89
% identity
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                  >gi 270686 gb I03333_ Sequence 8 from Patent US
```

Seq. ID LIB3181-006-P1-K2-E4

Method BLASTX
NCBI GI g3482913
BLAST score 249
E value 1.0e-21



Match length % identity 57

(AC003970) Similar to MtN21, gi 2598575, Megicago NCBI Description

truncatula nodulation induced gene [Arabidopsis thaliana]

300452 Seq. No.

Seq. ID LIB3181-006-P1-K2-F5

Method BLASTX g141609 NCBI GI 182 BLAST score E value 5.0e-14 Match length 56 % identity 71

ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir__S15656 zein, 19K - maize >gi_22448_emb_CAA41543_ (X58700) 19 kDa NCBI Description

zein [Zea mays]

300453 Seq. No.

LIB3181-007-P1-K2-D6 Seq. ID

Method BLASTX g168691 NCBI GI BLAST score 280 6.0e-25 E value Match length 80 % identity 70

NCBI Description (M29628) zein [Zea mays]

300454 Seq. No.

LIB3181-007-P1-K2-F10 Seq. ID

Method BLASTX NCBI GI g100940 304 BLAST score 1.0e-27 E value Match length 125 % identity 54

NCBI Description zein zA1 - maize

300455 Seq. No.

LIB3181-007-P1-K2-H3 Seq. ID

Method BLASTX NCBI GI g1709990 BLAST score 155 E value 1.0e-10 Match length 45 % identity 64

NCBI Description 60S RIBOSOMAL PROTEIN L35A

Seq. No. 300456

LIB3181-007-P1-M1-C4 Seq. ID

Method BLASTX NCBI GI g2832247 BLAST score 186 E value 6.0e-14Match length 111 % identity 43

NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]



```
Seq. No.
                  LIB3181-007-P1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2506328
BLAST score
                  314
E value
                  6.0e-29
Match length
                  97
                  64
% identity
                  CYTOCHROME C >gi 1235929 (L77113) cytochrome c [Helianthus
NCBI Description
                  annuus]
Seq. No.
                  300458
Seq. ID
                  LIB3181-007-P1-M1-E5
Method
                  BLASTN
NCBI GI
                  q168673
BLAST score
                  41
E value
                  9.0e-14
Match length
                  41
                  100
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
                  300459
Seq. No.
Seq. ID
                  LIB3181-007-P1-M1-G5
Method
                  BLASTN
                  q168673
NCBI GI
                  78
BLAST score
                  7.0e-36
E value
                  187
Match length
% identity
                  84
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
                  300460
Seq. No.
                  LIB3181-008-P1-K2-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q168699
BLAST score
                  226
E value
                  1.0e-18
Match length
                   60
                  83
% identity
NCBI Description (M60836) zein [Zea mays]
Seq. No.
                  300461
                  LIB3181-008-P1-K2-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3924594
BLAST score
                  289
E value
                   7.0e-26
Match length
                   80
% identity
                   65
                   (AF069442) putative ribonucleoprotein [Arabidopsis
NCBI Description
                   thaliana] >gi 4262139 gb AAD14439 (AC005275) putative
                   ribonucleoprotein [Arabidopsis thaliana]
```

Seq. ID LIB3181-008-P1-K2-C6

Method BLASTN NCBI GI g22544

BLAST score

E value

510 8.0e-52



```
BLAST score
E value
                  3.0e-41
                  200
Match length
                  87
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                  300463
Seq. No.
                  LIB3181-008-P1-M1-B12
Seq. ID
Method
                  BLASTX
                  g168699
NCBI GI
BLAST score
                  258
E value
                  2.0e-22
Match length
                  106
% identity
                  58
NCBI Description (M60836) zein [Zea mays]
                  300464
Seq. No.
                  LIB3181-008-P1-M1-D6
Seq. ID
Method
                  BLASTX
                  g1710530
NCBI GI
BLAST score
                  162
                  1.0e-11
E value
Match length
                  43
                  74
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir __S71256
                  ribosomal protein L27a - Arabidopsis thaliana
                  >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                  L27a [Arabidopsis thaliana]
Seq. No.
                  300465
                  LIB3181-009-P1-K2-A10
Seq. ID
Method
                  BLASTX
                  g168701
NCBI GI
BLAST score
                  169
                  1.0e-23
E value
Match length
                  127
% identity
                  59
NCBI Description
                  (M60837) zein [Zea mays]
Seq. No.
                  300466
                  LIB3181-009-P1-K2-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2131417
BLAST score
                  165
E value
                  2.0e-11
Match length
                  129
                  29
% identity
NCBI Description
                  hypothetical protein YDR291w - yeast (Saccharomyces
                  cerevisiae) >gi 1230655 (U51031) Ydr291wp [Saccharomyces
                  cerevisiae]
Seq. No.
                  300467
Seq. ID
                  LIB3181-009-P1-K2-C3
Method
                  BLASTX
NCBI GI
                  g2529340
```



```
Match length
% identity
                  81
                  (L81162) homologue; putative [Zea mays]
NCBI Description
                   300468
Seq. No.
Seq. ID
                  LIB3181-009-P1-K2-F6
Method
                  BLASTN
                   q1617473
NCBI GI
                  118
BLAST score
                  1.0e-59
E value
Match length
                  202
% identity
                   99
NCBI Description Z.mays mRNA for Rb1 protein
                   300469
Seq. No.
Seq. ID
                   LIB3181-009-P1-K2-H8
                   BLASTX
Method
NCBI GI
                   g72307
                   371
BLAST score
                   1.0e-35
E value
Match length
                   127
                   65
% identity
                   22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   300470
Seq. No.
Seq. ID
                   LIB3181-010-P1-K2-D5
                   BLASTN
Method
NCBI GI
                   g168673
                   161
BLAST score
                   2.0e-85
E value
                   240
Match length
                   95
% identity
                  Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
NCBI Description
                   300471
Seq. No.
                   LIB3181-010-P1-K2-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2791516
                   208
BLAST score
                   4.0e-17
E value
                   58
Match length
% identity
                   66
                   (AL021246) hypothetical protein Rv2476c [Mycobacterium
NCBI Description
                   tuberculosis]
                   300472
Seq. No.
                   LIB3181-010-P1-M1-F3
Seq. ID
```

BLASTN Method g168673 NCBI GI 39 BLAST score 1.0e-12 E value 83 Match length 87 % identity

NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

300473 Seq. No.



```
LIB3181-011-P1-K2-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168579
                  41
BLAST score
                  6.0e-14
E value
Match length
                  112
% identity
NCBI Description Maize pyruvate, orthophosphate dikinase mRNA, complete cds
                  300474
Seq. No.
                  LIB3181-011-P1-K2-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141605
BLAST score
                  482
                  1.0e-48
E value
Match length
                  111
                  88
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
                  300475
Seq. No.
                  LIB3181-011-P1-K2-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1698548
BLAST score
                  260
                  2.0e-22
E value
                  104
Match length
                  58
% identity
NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]
                  300476
Seq. No.
                  LIB3181-011-P1-K2-B3
Seq. ID
Method
                  BLASTN
                   g2832242
NCBI GI
BLAST score
                   141
E value
                   2.0e-73
                   293
Match length
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                   300477
Seq. No.
                   LIB3181-011-P1-K2-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115786
BLAST score
                   169
                   2.0e-12
E value
Match length
                   61
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB) (LHCP) >gi 82680 pir A29119 chlorophyll a/b-binding
                   protein - maize >gi 22357 emb CAA68451 (Y00379) LHCP [Zea
                   mays]
Seq. No.
                   300478
                   LIB3181-011-P1-K2-G6
Seq. ID
```

42307

BLASTX

Method

Seq. ID

Method



```
NCBI GI
                  q3953466
BLAST score
                  186
                  7.0e-22
E value
Match length
                  89
% identity
                  (AC002328) F20N2.11 [Arabidopsis thaliana]
NCBI Description
                  300479
Seq. No.
                  LIB3181-011-P1-M1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g224508
BLAST score
                  172
E value
                  2.0e-12
                  50
Match length
                  68
% identity
                  zein A20 [Zea mays]
NCBI Description
                  300480
Seq. No.
                  LIB3181-013-P1-K2-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3449334
BLAST score
                  186
E value
                  1.0e-100
Match length
                  316
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYH9, complete sequence [Arabidopsis thaliana]
                   300481
Seq. No.
                  LIB3181-013-P1-K2-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4490717
BLAST score
                   76
E value
                   6.0e-35
Match length
                   96
% identity
                   95
                  Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
NCBI Description
                  project)
Seq. No.
                   300482
Seq. ID
                   LIB3181-013-P1-K2-A9
Method
                   BLASTX
                   g1170040
NCBI GI
BLAST score
                   426
                   3.0e-42
E value
                   96
Match length
% identity
                   89
                  GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE)
NCBI Description
                   >gi 451198 dbj BAA03137 (D14049) glutathione reductase
                   precursor [Arabidopsis thaliana] >gi_1944448_dbj_BAA19653_
                   (D89620) glutathione reductase precursor [Arabidopsis
                   thaliana] >gi 740576 prf 2005376A glutathione reductase
                   [Arabidopsis thaliana]
                   300483
Seq. No.
```

42308

LIB3181-013-P1-K2-C12

BLASTX



```
NCBI GI
                  q3915847
BLAST score
                  455
E value
                  2.0e-45
Match length
                  105
% identity
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
                  300484
Seq. No.
Seq. ID
                  LIB3181-013-P1-K2-D12
Method
                  BLASTX
NCBI GI
                  q1769905
BLAST score
                  259
E value
                  1.0e-22
Match length
                  106
% identity
                  54
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  300485
Seq. ID
                  LIB3181-013-P1-K2-D3
Method
                  BLASTX
NCBI GI
                  q4049341
BLAST score
                  439
                  2.0e-43
E value
Match length
                  126
% identity
                  69
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                  300486
Seq. No.
                  LIB3181-013-P1-K2-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2829792
BLAST score
                  261
E value
                  5.0e-23
Match length
                  86
% identity
                  57
NCBI Description
                  SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS I)
                  >gi_1781353_emb_CAA71442 (Y10416) soluble starch
                   (bacterial glycogen) synthase [Solanum tuberosum]
Seq. No.
                  300487
Seq. ID
                  LIB3181-013-P1-K2-H12
Method
                  BLASTX
NCBI GI
                  g3377797
BLAST score
                  352
E value
                  1.0e-33
Match length
                  85
% identity
                  82
NCBI Description
                  (AF075597) Similar to 60S ribosome protein L19; coded for
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
```

R90691 [Ara Seq. No. 300488

Seq. ID LIB3181-013-P1-K2-H8

H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

BLAST score

E value

260

7.0e-23



```
Method
                   BLASTX
NCBI GI
                   q2829899
BLAST score
                   220
E value
                   3.0e-18
Match length
                   70
% identity
                   57
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp_AJ001449_2465015 and major#latex protein,
                   gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                   300489
Seq. ID
                   LIB3181-014-P1-K2-A10
Method
                  BLASTX
NCBI GI
                   q168586
BLAST score
                   382
E value
                   4.0e-37
Match length
                   98
% identity
                   74
NCBI Description
                  (M58656) pyruvate, orthophosphate dikinase [Zea mays]
Seq. No.
                   300490
Seq. ID
                  LIB3181-014-P1-K2-A4
Method
                  BLASTX
NCBI GI
                   g2130065
BLAST score
                   149
E value
                   9.0e-10
Match length
                   64
                   56
% identity
NCBI Description
                  alpha-globulin precursor - rice >gi 1783206 dbj BAA09308
                   (D50643) 26 kDa globulin [Oryza satīva]
Seq. No.
                   300491
Seq. ID
                  LIB3181-014-P1-K2-E10
Method
                  BLASTN
NCBI GI
                   g22326
BLAST score
                   78
                   6.0e-36
E value
                   142
Match length
% identity
                   89
NCBI Description Z.mays gene for Hageman factor inhibitor
Seq. No.
                   300492
Seq. ID
                  LIB3181-014-P1-K2-E11
Method
                  BLASTN
NCBI GI
                  g532622
BLAST score
                  77
                  3.0e-35
E value
Match length
                  185
% identity
                  85
NCBI Description
                  Zea mays lipase (LIP) mRNA, complete cds
Seq. No.
                  300493
Seq. ID
                  LIB3181-014-P1-K2-E4
Method
                  BLASTX
NCBI GI
                  g2832243
```

NCBI Description



```
Match length
% identity
                  59
NCBI Description
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
                  300494
Seq. No.
                  LIB3181-014-P1-K2-F6
Seq. ID
Method
                  BLASTX
                  q16073
NCBI GI
BLAST score
                  223
                  3.0e-18
E value
Match length
                  113
% identity
                  50
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                  300495
Seq. No.
                  LIB3181-014-P1-K2-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g141600
BLAST score
                   333
                   4.0e-31
E value
Match length
                  123
                   59
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
                  >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
Seq. No.
                   300496
                  LIB3181-014-P1-K2-H9
Seq. ID
Method
                  BLASTN
                   g531828
NCBI GI
BLAST score
                   39
E value
                   2.0e-12
                  131
Match length
% identity
                   82
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                   300497
Seq. ID
                   LIB3181-014-P1-M1-C9
Method
                  BLASTX
NCBI GI
                   q531829
BLAST score
                   140
                   5.0e-09
E value
                   71
Match length
% identity
                   45
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                   300498
Seq. No.
Seq. ID
                  LIB3181-014-P1-M1-H1
Method
                  BLASTX
NCBI GI
                   q141617
                   318
BLAST score
                   2.0e-29
E value
Match length
                   115
% identity
                   58
```

42311

>gi 100941 pir S12140 zein Zc1 - maize

ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)



>gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666 (M16460) 16-kDa zein protein [Zea mays]

 Seq. No.
 300499

 Seq. ID
 LIB3182-001-P1-M1-E5

 Method
 BLASTX

 NCBI GI
 g82659

BLAST score 141
E value 8.0e-09
Match length 57
% identity 53

NCBI Description 19K zein precursor (clone Z4) - maize

>gi 4388702 emb CAA24719 (V01472) zein [Zea mays]

Seq. No. 300500

Seq. ID LIB3182-001-P1-M1-F12

Method BLASTX
NCBI GI g141606
BLAST score 300
E value 2.0e-27
Match length 90
% identity 68

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)

>gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No. 300501

Seq. ID LIB3182-001-P1-M1-H5

Method BLASTX
NCBI GI g1707924
BLAST score 537
E value 4.0e-55
Match length 110
% identity 93

NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 1

PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE

EXECORDOR (ADE GEOCOSE SINIMAE) (ADE GEOCOSE

PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) (SHRUNKEN-2) >gi_1947182 (M81603) shrunken-2 [Zea mays] >gi_444329_prf__1906378A ADP glucose

pyrophosphorylase [Zea mays]

Seq. No. 300502

Seq. ID LIB3182-002-P1-M1-C11

Method BLASTX
NCBI GI g511870
BLAST score 206
E value 2.0e-16
Match length 36
% identity 100

NCBI Description (M23537) zein protein [Zea mays]

Seq. No. 300503

Seq. ID LIB3182-002-P1-M1-C4

Method BLASTX NCBI GI g141606 BLAST score 319



```
E value 1.0e-29
Match length 107
% identity 63
```

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)

>gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No. 300504

Seq. ID LIB3182-002-P1-M1-D11

Method BLASTX
NCBI GI g3868758
BLAST score 144
E value 1.0e-18
Match length 96
% identity 56

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 300505

Seq. ID LIB3182-002-P1-M1-D3

Method BLASTN
NCBI GI g168681
BLAST score 59
E value 1.0e-24
Match length 203
% identity 82

NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.

>gi_270686 gb I03333 Sequence 8 from Patent US

Seq. No. 300506

Seq. ID LIB3182-002-P1-M1-E10

Method BLASTX
NCBI GI g1184774
BLAST score 442
E value 4.0e-44
Match length 84
% identity 100

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 300507

Seq. ID LIB3182-002-P1-M1-G3

Method BLASTX
NCBI GI g141600
BLAST score 144
E value 3.0e-09
Match length 66
% identity 58

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)

>gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 300508

Seq. ID LIB3182-004-P2-M1-A9

Method BLASTX
NCBI GI g141607
BLAST score 257
E value 3.0e-22

BLAST score

% identity

E value Match length 323 4.0e-30

94

69



```
Match length
                   66
                  77
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
NCBI Description
                  >gi 22521 emb CAA24718 (V01471) zein [Zea mays] >gi 168672
                   (J01244) zein 19 kd protein (partial) [Zea mays]
Seq. No.
                  300509
Seq. ID
                  LIB3182-004-P2-M1-B4
Method
                  BLASTX
NCBI GI
                  q224508
BLAST score
                  348
E value
                  8.0e-33
Match length
                  129
                   60
% identity
NCBI Description zein A20 [Zea mays]
                  300510
Seq. No.
Seq. ID
                  LIB3182-004-P2-M1-E1
Method
                  BLASTX
NCBI GI
                  g2832243
BLAST score
                  218
E value
                  1.0e-17
Match length
                  127
% identity
                  46
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                   300511
Seq. No.
Seq. ID
                  LIB3182-004-P2-M1-E8
Method
                  BLASTX
NCBI GI
                   g121631
BLAST score
                   242
E value
                   2.0e-20
Match length
                   74
% identity
                   64
                  GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR
NCBI Description
                   >gi_72323_pir__KNNT2S glycine-rich protein 2 - wood tobacco
                   >gi 19743 emb CAA42622 (X60007) nsGRP-2 [Nicotiana
                   sylvestris]
                   300512
Seq. No.
Seq. ID
                   LIB3182-004-P2-M1-F10
Method
                   BLASTX
                   g224509
NCBI GI
BLAST score
                   386
                   3.0e-37
E value
Match length
                   138
% identity
                   64
NCBI Description
                  zein E19 [Zea mays]
                   300513
Seq. No.
Seq. ID
                   LIB3182-005-P2-M1-B8
Method
                   BLASTX
NCBI GI
                   g419803
```



```
zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
                  300514
Seq. No.
                  LIB3182-005-P2-M1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168673
BLAST score
                  80
                  5.0e-37
E value
Match length
                  303
% identity
                  84
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
Seq. No.
                  300515
                  LIB3182-005-P2-M1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  94
                  2.0e-45
E value
                  274
Match length
                  43
% identity
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
Seq. No.
                  300516
                  LIB3182-005-P2-M1-E11
Seq. ID
Method
                  BLASTX
                  g3885334
NCBI GI
BLAST score
                  354
E value
                  1.0e-40
Match length
                  108
                  82
% identity
NCBI Description (AC005623) putative argonaute protein [Arabidopsis
                  thaliana]
Seq. No.
                  300517
Seq. ID
                  LIB3182-005-P2-M1-H12
Method
                  BLASTN
                  g2832242
NCBI GI
BLAST score
                  60
E value
                  3.0e-25
Match length
                  144
% identity
                  44
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                  300518
Seq. No.
                  LIB3182-006-P2-M1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q22216
BLAST score
                  223
```

E value 2.0e-18 Match length 92 % identity 55

NCBI Description (X55722) 22kD zein [Zea mays]

300519 Seq. No.

LIB3182-008-P2-M1-B10 Seq. ID



```
Method
                  BLASTN
NCBI GI
                  q1212995
BLAST score
                  35
                  3.0e-10
E value
                  71
Match length
                  87
% identity
NCBI Description H.vulgare mRNA for UDP-glucose pyrophosphorylase
                  300520
Seq. No.
                  LIB3182-008-P2-M1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22544
BLAST score
                  82
                  3.0e-38
E value
                  167
Match length
                  94
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                  300521
Seq. No.
                  LIB3182-008-P2-M1-E5
Seq. ID
Method
                  BLASTX
                  q141612
NCBI GI
BLAST score
                  146
E value
                  2.0e-09
Match length
                  36
% identity
                  83
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)
NCBI Description
                  >gi_72306_pir__ZIZMC2 22K zein precursor (clone cZ22C2) -
                  maize (fragment) >qi 168688 (M12141) 22 kDa zein protein
                   [Zea mays]
                   300522
Seq. No.
                  LIB3182-008-P2-M1-H3
Seq. ID
Method
                  BLASTN
                   g22544
NCBI GI
BLAST score
                   113
E value
                   1.0e-56
Match length
                   217
                   89
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
Seq. No.
                   300523
                   LIB3182-009-P2-M1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141605
BLAST score
                   202
E value
                   4.0e-16
Match length
                   73
% identity
                   62
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
```

Seq. ID LIB3182-009-P2-M1-A10

BLASTN Method NCBI GI g1314396



```
BLAST score
                  7.0e-85
E value
Match length
                  221
                  92
% identity
NCBI Description Zea mays ssp. mays USDA PI 515436 ITS1, 5.8S rRNA, ITS2
                  300525
Seq. No.
                  LIB3182-009-P2-M1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141605
BLAST score
                  303
                  6.0e-37
E value
Match length
                  120
% identity
                  70
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
```

maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 300526 LIB3182-009-P2-M1-B1 Seq. ID Method BLASTX

NCBI GI g141606 BLAST score 211 E value 7.0e-17 Match length 78 62 % identity

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1) NCBI Description

>gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

300527 Seq. No.

LIB3182-009-P2-M1-B4 Seq. ID

Method BLASTX NCBI GI q1279640 229 BLAST score E value 4.0e-19 Match length 101 % identity 49

(X92204) NAM [Petunia x hybrida] NCBI Description

Seq. No. 300528

LIB3182-009-P2-M1-D1 Seq. ID

Method BLASTX g2832247 NCBI GI BLAST score 236 8.0e-20 E value 92 Match length 59 % identity

NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 300529

LIB3182-009-P2-M1-E10 Seq. ID

BLASTX Method NCBI GI g168695 BLAST score 157 E value 4.0e-11 Match length 48



```
% identity
                  (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                  zein gamma [Zea mays]
                  300530
Seq. No.
                  LIB3182-009-P2-M1-E2
Seq. ID
Method
                  BLASTX
                  g1084457
NCBI GI
BLAST score
                  168
                  5.0e-12
E value
                  62
Match length
                  55
% identity
NCBI Description elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_
                  (D23674) elongation factor 1 beta [Oryza sativa]
                  300531
Seq. No.
                  LIB3182-009-P2-M1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g508545
                  213
BLAST score
                  3.0e-17
E value
                  71
Match length
                  63
% identity
NCBI Description (L34340) zein [Zea mays]
                  300532
Seq. No.
                  LIB3182-009-P2-M1-F11
Seq. ID
                  BLASTX
Method
                  q141600
NCBI GI
BLAST score
                  354
                  2.0e-38
E value
                  111
Match length
                  80
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                  >gi 72315_pir ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
                   300533
Seq. No.
                  LIB3182-009-P2-M1-G1
Seq. ID
Method
                  BLASTX
                  q141610
NCBI GI
                   177
BLAST score
                   6.0e-13
E value
                   84
Match length
% identity
                   51
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)
                   300534
Seq. No.
                   LIB3182-009-P2-M1-H11
```

Seq. ID

Method BLASTN q168700 NCBI GI 38 BLAST score 3.0e-12 E value 77 Match length 87 % identity

NCBI Description Z.mays zein mRNA, complete cds



```
300535
Seq. No.
                  LIB3182-009-P2-M1-H6
Seq. ID
                  BLASTX
Method
                  g22216
NCBI GI
BLAST score
                  142
                  2.0e-11
E value
                  78
Match length
                  59
% identity
NCBI Description (X55722) 22kD zein [Zea mays]
                  300536
Seq. No.
                  LIB3182-010-P2-M1-E2
Seq. ID
Method
                  BLASTX
                  q4336434
NCBI GI
BLAST score
                   311
                   1.0e-28
E value
Match length
                   114
                   53
% identity
                   (AF092431) nodule-enhanced protein phosphatase type 2C
NCBI Description
                   [Lotus japonicus]
Seq. No.
                   300537
Seq. ID
                   LIB3182-010-P2-M1-E6
Method
                   BLASTX
NCBI GI
                   g82654
BLAST score
                   221
                   2.0e-20
E value
Match length
                   83
% identity
                   65
                   10K zein precursor - maize >gi_22541_emb_CAA30409_ (X07535)
NCBI Description
                   10kDa zein (AA 1 - 150) [Zea mays]
Seq. No.
                   300538
Seq. ID
                   LIB3182-010-P2-M1-F2
Method
                   BLASTX
                   q82660
NCBI GI
BLAST score
                   183
                   2.0e-22
E value
                   83
Match length
                   75
% identity
                   19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                   >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
                   300539
Seq. No.
                   LIB3182-010-P2-M1-H1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22219
BLAST score
                   111
                   9.0e-56
E value
                   178
Match length
                   92
% identity
NCBI Description Z.mays ZSF4C2 gene for 22 kD zein
Seq. No.
                   300540
Seq. ID
                   LIB3182-012-P2-M1-B4
                   BLASTN
Method
```

42319

g168484

NCBI GI

% identity

90



```
BLAST score
                  1.0e-178
E value
                  360
Match length
                  97
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                  300541
Seq. No.
                  LIB3182-012-P2-M1-B5
Seq. ID
                  BLASTN
Method
                  g22531
NCBI GI
BLAST score
                  68
                  2.0e-30
E value
                  120
Match length
% identity
                  89
                  Zea mays mRNA encoding a zein (clone pZ22.1)
NCBI Description
                  >gi_270688_gb_I03336_ Sequence 10 from Patent US 4885357
                  >gi_270741_gb_I03273_ Sequence 2 from Patent US
                  300542
Seq. No.
                  LIB3182-012-P2-M1-B6
Seq. ID
                  BLASTN
Method
                  g168652
NCBI GI
                  100
BLAST score
                  5.0e-49
E value
Match length
                  108
                  98
% identity
NCBI Description Maize amyloplast-specific transit protein (waxy; wx+
                  locus), complete cds
                  300543
Seq. No.
                  LIB3182-012-P2-M1-B9
Seq. ID
                  BLASTX
Method
                  g22216
NCBI GI
BLAST score
                  247
E value
                  1.0e-32
                  111
Match length
                  70
% identity
                  (X55722) 22kD zein [Zea mays]
NCBI Description
                   300544
Seq. No.
                  LIB3182-012-P2-M1-D12
Seq. ID
Method
                  BLASTX
                  g16073
NCBI GI
                   364
BLAST score
E value
                   9.0e-35
Match length
                   116
% identity
                   69
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
Seq. No.
                   300545
Seq. ID
                   LIB3182-012-P2-M1-F1
Method
                   BLASTN
NCBI GI
                   q22528
BLAST score
                   50
E value
                   4.0e-19
Match length
                   82
```



```
NCBI Description Zea mays mRNA encoding a zein (clone A20)
                  300546
Seq. No.
                  LIB3182-012-P2-M1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832243
BLAST score
                  386
                  2.0e-37
E value
Match length
                  121
                  70
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                  300547
Seq. No.
                  LIB3182-013-P2-M1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q629861
BLAST score
                  173
                  1.0e-12
E value
                  76
Match length
                  54
% identity
                  zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
NCBI Description
                  zein Zdl (19 kDa zein) [Zea mays]
                                                                              1
Seq. No.
                  300548
                  LIB3182-014-P2-M1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q22216
BLAST score
                  176
                  2.0e-27
E value
Match length
                  92
                  74
% identity
NCBI Description
                  (X55722) 22kD zein [Zea mays]
Seq. No.
                  300549
Seq. ID
                  LIB3182-014-P2-M1-A5
Method
                  BLASTN
NCBI GI
                  g16072
                  107
BLAST score
                  2.0e-53
E value
                  220
Match length
% identity
                  87
NCBI Description Acetabularia mediterranea zein gene
Seq. No.
                  300550
                  LIB3182-014-P2-M1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141597
BLAST score
                  241
                  2.0e-20
E value
Match length
                  126
% identity
                  46
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >qi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize
                  >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
```

[Zea mays]



78

% identity

NCBI Description

```
LIB3182-014-P2-M1-C1
Seq. ID
Method
                    BLASTX
                    g121472
NCBI GI
                     280
BLAST score
                     6.0e-25
E value
                     105
Match length
% identity
                    GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                     (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi_72326_pir__ZMZM19 glutelin_2 precursor (clone pME119) -
maize >gi_22289 emb CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517 emb_CAA37594_ (X53514) zein Zc2 [Zea
                     mays] >gi_1684\overline{8}5 (M1\overline{6}066) gluteli\overline{n}-2 [Zea mays]
                     300552
Seq. No.
                     LIB3182-014-P2-M1-C4
Seq. ID
                     BLASTX
Method
                     g2832247
NCBI GI
BLAST score
                     374
                     6.0e-36
E value
                     120
Match length
                     68
% identity
                    (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
Seq. No.
                     300553
                     LIB3182-014-P2-M1-E12
Seq. ID
                     BLASTN
Method
                     q168704
NCBI GI
BLAST score
                     118
                     8.0e-60
E value
                     118
Match length
                     100
% identity
NCBI Description Zea mays zein protein gene, complete cds
                     300554
Seq. No.
                     LIB3182-014-P2-M1-G3
Seq. ID
Method
                     BLASTX
                     g141612
NCBI GI
BLAST score
                     411
E value
                     3.0e-40
                     136
Match length
% identity
                     ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)
NCBI Description
                     >gi 72306 pir_ZIZMC2 22K zein precursor (clone cZ22C2) -
                     maize (fragment) >gi_168688 (M12141) 22 kDa zein protein
                     [Zea mays]
                     300555
Seq. No.
Seq. ID
                     LIB3182-014-P2-M1-H7
                     BLASTX
Method
NCBI GI
                     q16073
BLAST score
                     272
                     2.0e-24
E value
Match length
                     71
```

42322

(X59526) zein protein [Acetabularia mediterranea]

BLAST score

Match length

E value

189

8.0e-24



```
300556
Seq. No.
                  LIB3182-015-P2-M1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22514
BLAST score
                  320
                  1.0e-180
E value
                  339
Match length
                  99
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                  300557
Seq. No.
                  LIB3182-015-P2-M1-C10
Seq. ID
                  BLASTN
Method
                  g2832242
NCBI GI
BLAST score
                  49
                  6.0e-19
E value
                  73
Match length
                  10
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  300558
                  LIB3182-015-P2-M1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g168701
BLAST score
                  196
E value
                  2.0e-15
Match length
                  81
% identity
                   60
NCBI Description
                  (M60837) zein [Zea mays]
Seq. No.
                  300559
                  LIB3182-015-P2-M1-C3
Seq. ID
Method
                  BLASTN
                   g340933
NCBI GI
BLAST score
                  84
                   5.0e-40
E value
Match length
                   112
                   95
% identity
NCBI Description Zea mays 10-kDa zein gene, complete cds
Seq. No.
                   300560
                  LIB3182-015-P2-M1-H5
Seq. ID
Method
                  BLASTN
                   g168694
NCBI GI
BLAST score
                   164
E value
                   2.0e-87
Match length
                   196
% identity
                   96
NCBI Description Maize gamma zein mRNA, partial cds
Seq. No.
                   300561
Seq. ID
                   LIB3182-016-P2-M1-A2
Method
                   BLASTX
NCBI GI
                   q629861
```

```
% identity
                  zein Zd1, 19K - maize >qi 535020 emb CAA47639 (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
                   300562
Seq. No.
Seq. ID
                   LIB3182-016-P2-M1-B6
Method
                   BLASTX
NCBI GI
                   g141617
BLAST score
                   260
                   2.0e-22
E value
Match length
                   130
% identity
NCBI Description
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
                  >gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
                   >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
Seq. No.
                   300563
                   LIB3182-016-P2-M1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141613
BLAST score
                   140
E value
                   9.0e-09
Match length
                   63
% identity
                   52
                   ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                   >gi_72305_pir_ZIZM21 22K zein precursor (clone pZ22.1) -
                   maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]
Seq. No.
                   300564
Seq. ID
                   LIB3182-016-P2-M1-C5
Method
                   BLASTX
NCBI GI
                   g2832243
BLAST score
                   171
E value
                   3.0e-12
Match length
                   94
% identity
                   45
NCBI Description
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
                   300565
Seq. No.
Seq. ID
                   LIB3182-016-P2-M1-C8
Method
                   BLASTX
NCBI GI
                   g16073
BLAST score
                   408
E value
                   6.0e-40
Match length
                   124
% identity
                   69
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   300566
Seq. No.
```

Seq. ID LIB3182-016-P2-M1-D6

BLASTX Method NCBI GI g141615 BLAST score 218 7.0e-18 E value Match length 70

```
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
NCBI Description
                  >gi 22536 emb CAA24727_ (V01480) zein protein 3 [Zea mays]
                  300567
Seq. No.
                  LIB3182-016-P2-M1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g508545
BLAST score
                  161
                  1.0e-18
E value
                  64
Match length
                  81
% identity
NCBI Description (L34340) zein [Zea mays]
                  300568
Seq. No.
                  LIB3182-016-P2-M1-D8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g22447
BLAST score
                  95
                  4.0e-46
E value
                  163
Match length
                  89
% identity
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein
                  300569
Seq. No.
                  LIB3279-003-P1-K1-B10
Seq. ID
                  BLASTN
Method
                  g473602
NCBI GI
BLAST score
                  151
E value
                  2.0e-79
                  276
Match length
                   88
% identity
NCBI Description Zea mays W-22 histone H2A mRNA, complete cds
                   300570
Seq. No.
                  LIB3279-003-P1-K1-B5
Seq. ID
Method
                   BLASTX
                   q4559339
NCBI GI
BLAST score
                   363
E value
                   1.0e-34
                   96
Match length
                   74
% identity
                   (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                   thaliana]
                   300571
Seq. No.
                   LIB3279-003-P1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3047086
BLAST score
                   193
E value
                   1.0e-14
Match length
                   122
% identity
                   33
```

NCBI Description

42325

(AF058914) similar to reverse transcriptase (Pfam:

transcript fact.hmm, score: 72.31) [Arabidopsis thaliana]



```
LIB3279-003-P1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g585338
                  260
BLAST score
                  1.0e-22
E value
Match length
                  80
% identity
                  ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                  >gi 391879 dbj BAA01181 (D10335) adenylate kinase-b [Oryza
Seq. No.
                  300573
                  LIB3279-003-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3868758
BLAST score
                  254
E value
                  3.0e-33
Match length
                  128
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                  300574
Seq. ID
                  LIB3279-003-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q3004564
BLAST score
                  501
E value
                  6.0e-51
Match length
                  111
% identity
                  80
                   (AC003673) putative receptor Ser/Thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  300575
Seq. ID
                  LIB3279-004-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2500497
BLAST score
                  326
E value
                  2.0e-30
Match length
                  80
                  82
% identity
                  40S RIBOSOMAL PROTEIN S21 >gi 1419372 emb CAA67225
NCBI Description
                   (X98656) ribosomal protein S21 [Zea mays]
                  300576
Seq. No.
Seq. ID
                  LIB3279-004-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1170029
BLAST score
                  498
                  2.0e-50
E value
Match length
                  105
                  90
% identity
```

GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) NCBI Description (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)

>gi_100581_pir__A35789 glutamate-1-semialdehyde

2,1-aminomutase (EC 5.4.3.8) - barley >gi_506383 (M31545) glutamate 1-semialdehyde aminotransferase [Hordeum vulgare]

Seq. ID

Method



```
Seq. No.
Seq. ID
                  LIB3279-004-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q3080420
BLAST score
                  168
E value
                  7.0e-12
Match length
                  113
% identity
                   40
NCBI Description
                  (AL022604) putative sugar transporter protein [Arabidopsis
Seq. No.
                  300578
Seq. ID
                  LIB3279-004-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q135398
BLAST score
                  372
E value
                  4.0e-36
Match length
                  85
% identity
                  84
NCBI Description
                  TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1
                  chain - maize >gi_22147_emb_CAA33734_ (X15704)
                  alphal-tubulin [Zea mays]
Seq. No.
                   300579
Seq. ID
                  LIB3279-004-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  q4585620
BLAST score
                  41
E value
                  7.0e-14
Match length
                  117
% identity
NCBI Description Zea mays hmgi/y gene, exons 1-2
                  300580
Seq. No.
Seq. ID
                  LIB3279-004-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  g984755
BLAST score
                   46
E value
                  8.0e-17
Match length
                  118
% identity
                  85
NCBI Description O.sativa mRNA for chilling-inducible protein
                  300581
Seq. No.
Seq. ID
                  LIB3279-004-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q399854
BLAST score
                  212
E value
                  5.0e-17
                  90
Match length
                  58
% identity
                  HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize
NCBI Description
                  >gi 22325 emb CAA40565 (X57313) H2B histone [Zea mays]
                  300582
Seq. No.
```

42327

LIB3279-005-P1-K1-A7

BLASTX



```
q3551245
NCBI GI
BLAST score
                       348
                       5.0e-33
E value
Match length
                       76
                       86
% identity
NCBI Description (AB012702) P40-like protein [Daucus carota]
Seq. No.
                       300583
                      LIB3279-005-P1-K1-B7
Seq. ID
Method
                      BLASTX
NCBI GI
                      g729671
BLAST score
                       150
E value
                       9.0e-10
Match length
                       95
                       41
% identity
NCBI Description HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]
                       300584
Seq. No.
                      LIB3279-005-P1-K1-D2
Seq. ID
                      BLASTX
Method
                       g2245125
NCBI GI
                       159
BLAST score
                       8.0e-11
E value
Match length
                       52
% identity
                       58
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
                       300585
Seq. No.
                       LIB3279-005-P1-K1-D5
Seq. ID
Method
                       BLASTX
NCBI GI
                       g417103
BLAST score
                       442
                       4.0e-44
E value
Match length
                       92
                       97
% identity
                       HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone
NCBI Description
                       H3.3-like protein - Arabidopsis thaliana
                       >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
                       (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460)
                       histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157 emb_CAA58445 (X83422)
                       histone H3 variant H3.3 [Lycopersicon esculentum]
                       >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]
                       >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana
                       tabacum] >qi 3885890 (AF093633) histone H3 [Oryza sativa]
                       >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
                       coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone
                       H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_
                       (AL035708) Histon H3 [Arabidopsis thaliana]
```

Seq. ID LIB3279-005-P1-K1-D6

Seq. ID

300591

LIB3279-006-P1-K1-D4



```
BLASTX
Method
                    g4006877
NCBI GI
BLAST score
                    230
                    5.0e-19
E value
                    77
Match length
                    61
% identity
NCBI Description (Z99707) RNA-binding like protein [Arabidopsis thaliana]
                    300587
Seq. No.
                    LIB3279-005-P1-K1-F6
Seq. ID
                    BLASTX
Method
                    g135399
NCBI GI
BLAST score
                    415
E value
                    1.0e-40
                    139
Match length
% identity
                    61
                    TUBULIN ALPHA-1 CHAIN >gi_100716_pir___S20758 tubulin
NCBI Description
                    alpha-1 chain - rice >gi_20379_emb_CAA77988 (Z11931) alpha 1 tubulin [Oryza sativa] >gi_1136124_emb_CAA62918 (X91808)
                    alfa-tubulin [Oryza sativa]
                    300588
Seq. No.
                    LIB3279-005-P1-K1-G9
Seq. ID
                    BLASTX
Method
                    g3885884
NCBI GI
                    148
BLAST score
                     1.0e-09
E value
                     62
Match length
                     50
% identity
                    (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
                     300589
Seq. No.
                     LIB3279-005-P1-K1-H9
Seq. ID
                     BLASTX
Method
                     g729762
NCBI GI
                     141
BLAST score
                     7.0e-12
E value
Match length
                     57
                     68
% identity
                     17.0 KD CLASS II HEAT SHOCK PROTEIN (HSP 18)
NCBI Description
                     >gi_477225_pir_A48425 heat shock protein HSP18 - maize >gi_300079_bbs_130952 (S59777) HSP18=18 kda heat shock
                     protein [Zea mays, Oh43, clone cMHSP18-1, Peptide, 154 aa]
                     [Zea mays]
                     300590
Seq. No.
                     LIB3279-006-P1-K1-D12
Seq. ID
                     BLASTX
Method
NCBI GI
                     g2245038
                     254
BLAST score
E value
                     7.0e-22
                     130
Match length
 % identity
                    (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```



Method BLASTX
NCBI GI g498707
BLAST score 329
E value 1.0e-30
Match length 133
% identity 52

NCBI Description (X78422) HYP1 [Arabidopsis thaliana]

Seq. No. 300592

Seq. ID LIB3279-006-P1-K1-D6

Method BLASTN
NCBI GI g3341647
BLAST score 45
E value 3.0e-16
Match length 109
% identity 94

NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase

Seq. No. 300593

Seq. ID LIB3279-006-P1-K1-E6

Method BLASTX
NCBI GI g3063455
BLAST score 276
E value 2.0e-24
Match length 71
% identity 68

NCBI Description (AC003981) F22013.17 [Arabidopsis thaliana]

Seq. No. 300594

Seq. ID LIB3279-006-P1-K1-F10

Method BLASTX
NCBI GI g1363492
BLAST score 292
E value 2.0e-26
Match length 116
% identity 54

NCBI Description outer envelope membrane protein OEP75 precursor - garden

pea >gi_576507 (L36858) outer membrane protein [Pisum
sativum] >gi_633607 emb_CAA58720 (X83767) chloroplastic
outer envelope membrane protein (OEP75) [Pisum sativum]

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Seq. No. 300595

Seq. ID LIB3279-007-P1-K1-A9

Method BLASTX
NCBI GI g2654088
BLAST score 207
E value 2.0e-16
Match length 123
% identity 35

NCBI Description (AF033118) potassium transporter [Arabidopsis thaliana]

>gi_2688979 (AF029876) high-affinity potassium transporter;
AtKUP1p [Arabidopsis thaliana] >gi_3150413 (AC004165)
high-affinity potassium transporter (AtKUP1) [Arabidopsis thaliana] >gi_3420045 (AC004680) high-affinity potassium

transporter (AtKUP1) [Arabidopsis thaliana]

Seq. No. 300596

```
LIB3279-007-P1-K1-C1
Seq. ID
Method
                  BLASTN
                  q312180
NCBI GI
BLAST score
                  40
                  3.0e-13
E value
                  100
Match length
                  85
% identity
NCBI Description Z.mays GapC4 gene
                  300597
Seq. No.
                  LIB3279-007-P1-K1-E4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2673906
BLAST score
                  526
                  9.0e-54
E value
                  139
Match length
                  76
% identity
                  (AC002561) putative DNA polymerase delta small subunit
NCBI Description
                   [Arabidopsis thaliana]
                  300598
Seq. No.
                  LIB3279-007-P1-K1-H7
Seq. ID
                  BLASTX
Method
                  g4559333
NCBI GI
BLAST score
                  154
                   3.0e-10
E value
Match length
                  120
                   28
% identity
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]
                   300599
Seq. No.
                   LIB3279-008-P1-K1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4580515
BLAST score
                   218
E value
                   3.0e-18
                   62
Match length
% identity
                   60
NCBI Description (AF036301) scarecrow-like 3 [Arabidopsis thaliana]
                   300600
Seq. No.
                   LIB3279-008-P1-K1-F11
Seq. ID
                   BLASTN
Method
                   g473602
NCBI GI
BLAST score
                   51
                   7.0e-20
E value
                   107
Match length
                   87
% identity
NCBI Description Zea mays W-22 histone H2A mRNA, complete cds
```

Seq. ID LIB3279-008-P1-K1-F5

Method BLASTX
NCBI GI g2262111
BLAST score 248
E value 3.0e-21
Match length 82

% identity



```
% identity
                     (AC002343) ribitol dehydrogenase isolog [Arabidopsis
  NCBI Description
                     thaliana]
                     300602
   Seq. No.
                     LIB3279-008-P1-K1-F8
   Seq. ID
                     BLASTX
  Method
  NCBI GI
                     g2262143
                     301
  BLAST score
                     2.0e-27
E value
                     93
  Match length
                     61
   % identity
                    (AC002330) putative serine/threonine protein kinase
  NCBI Description
                     [Arabidopsis thaliana]
                     300603
   Seq. No.
                     LIB3279-008-P1-K1-G11
   Seq. ID
                     BLASTX
   Method
                     g2443857
   NCBI GI
                     147
  BLAST score
                     3.0e-09
   E value
   Match length
                     40
                     72
   % identity
   NCBI Description (U79961) vacuolar sorting receptor homolog [Zea mays]
                     300604
   Seq. No.
                     LIB3279-008-P1-K1-H6
   Seq. ID
                     BLASTX
   Method
                     g3914020
   NCBI GI
                     262
   BLAST score
                     8.0e-23
   E value
                     137
   Match length
                     42
   % identity
                     (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
   NCBI Description
                      (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                     >gi_1561641_emb_CAA69388_ (Y08211) mandelonitrile lyase
                      [Prunus dulcis]
                     300605
   Seq. No.
                     LIB3279-009-P1-K1-A4
   Seq. ID
   Method
                     BLASTX
                     q2660669
   NCBI GI
                     164
   BLAST score
   E value
                     2.0e-11
   Match length
                     51
                     57
   % identity
                     (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis
   NCBI Description
                     thaliana]
                      300606
   Seq. No.
   Seq. ID
                      LIB3279-009-P1-K1-C4
                     BLASTX
   Method
                     q1703201
   NCBI GI
   BLAST score
                      235
   E value
                      9.0e-20
   Match length
                      67
```

Seq. ID

Method



```
PROTEIN KINASE AFC3 >gi_601791 (U16178) protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   300607
Seq. No.
                  LIB3279-009-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1806283
                  161
BLAST score
                  2.0e-11
E value
Match length
                   48
                  73
% identity
NCBI Description (Z79637) Histone H4 homologue [Sesbania rostrata]
                   300608
Seq. No.
                  LIB3279-009-P1-K1-E6
Seq. ID
                  BLASTX
Method
                   q553073
NCBI GI
BLAST score
                   233
                   9.0e-20
E value
                   78
Match length
                   60
% identity
NCBI Description (M94481) reverse transcriptase [Zea mays]
Seq. No.
                   300609
                   LIB3279-009-P1-K1-F1
Seq. ID
Method
                   BLASTX
                   g3176726
NCBI GI
BLAST score
                   294
                   6.0e-27
E value
Match length
                   82
                   70
% identity
NCBI Description
                  (AC002392) putative serine proteinase [Arabidopsis
                   thaliana]
                   300610
Seq. No.
                   LIB3279-009-P1-K1-F7
Seq. ID
Method
                   BLASTX
                   q1076678
NCBI GI
                   319
BLAST score
E value
                   6.0e-30
                   68
Match length
% identity
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.
                   300611
                   LIB3279-009-P1-K1-G4
Seq. ID
Method
                   BLASTX
                   q4512696
NCBI GI
BLAST score
                   195
                   4.0e-15
E value
Match length
                   64
% identity
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   300612
```

42333

LIB3279-009-P1-K1-G8

BLASTX

% identity



```
g283051
NCBI GI
                  160
BLAST score
                  3.0e-11
E value
                  57
Match length
                  61
% identity
                  RNA-directed DNA polymerase (EC 2.7.7.49) - maize
NCBI Description
                  transposon (fragment)
                  300613
Seq. No.
                  LIB3279-009-P1-K1-H9
Seq. ID
                  BLASTX
Method
                  g2828279
NCBI GI
                  170
BLAST score
                  3.0e-12
E value
Match length
                   41
                  73
% identity
NCBI Description (AL021687) hypothetical protein [Arabidopsis thaliana]
                   300614
Seq. No.
                   LIB3279-010-P1-K1-C4
Seq. ID
Method
                   BLASTX
                   g2213594
NCBI GI
                   240
BLAST score
                   2.0e-20
E value
                   103
Match length
% identity
                   45
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.
                   300615
                   LIB3279-010-P1-K1-E12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1711036
                   205
BLAST score
                   3.0e-16
E value
                   63
Match length
                   71
% identity
                   (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum
NCBI Description
                   sativum]
                   300616
Seq. No.
                   LIB3279-011-P1-K1-A2
Seq. ID
                   BLASTX
Method
                   g4589961
NCBI GI
                   321
BLAST score
                   1.0e-29
E value
                   150
Match length
% identity
                   47
                   (AC007169) unknown protein [Arabidopsis thaliana]
NCBI Description
                   300617
Seq. No.
                   LIB3279-011-P1-K1-A4
Seq. ID
Method
                   BLASTX
                   g4314388
NCBI GI
                   531
BLAST score
                   2.0e-54
E value
                   126
Match length
                   77
```

Method

BLASTX



```
NCBI Description (AC006232) hypothetical protein [Arabidopsis thaliana]
                  300618
Seq. No.
                  LIB3279-011-P1-K1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3451071
                  273
BLAST score
                  2.0e-24
E value
                  87
Match length
% identity
                  67
NCBI Description (AL031326) beta adaptin - like protein [Arabidopsis
                  thaliana]
                  300619
Seq. No.
                  LIB3279-011-P1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2982266
BLAST score
                  381
                   9.0e-37
E value
                   83
Match length
% identity
NCBI Description (AF051216) probable fibrillarin [Picea mariana]
                   300620
Seq. No.
                   LIB3279-011-P1-K1-D1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q577824
                   49
BLAST score
                   1.0e-18
E value
Match length
                   104
                   87
% identity
NCBI Description Z.mays gene for H2B histone (gH2B3)
                   300621
 Seq. No.
                   LIB3279-011-P1-K1-D3
 Seq. ID
                   BLASTN
 Method
                   g886400
 NCBI GI
                   40
 BLAST score
                   2.0e-13
 E value
                   52
 Match length
                   94
 % identity
 NCBI Description Oryza sativa MADS-box protein (MADS2) mRNA, complete cds
                   300622
 Seq. No.
                   LIB3279-011-P1-K1-F11
 Seq. ID
                   BLASTX
 Method
                   g4455300
 NCBI GI
                   179
 BLAST score
                   3.0e-13
 E value
                   69
 Match length
                   49
 % identity
                   (AL035528) putative pectate lyase All (fragment)
 NCBI Description
                   [Arabidopsis thaliana]
                   300623
 Seq. No.
                   LIB3279-011-P1-K1-G6
 Seq. ID
```



```
g2498077
   NCBI GI
BLAST score
                      296
                      5.0e-27
   E value
                      81
   Match length
    % identity
                      NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
   NCBI Description
                      (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase
                      [Saccharum officinarum]
                      300624
    Seq. No.
                      LIB3279-011-P1-K1-H2
    Seq. ID
                      BLASTX
   Method
                      q3913804
    NCBI GI
    BLAST score
                      236
                      7.0e-20
    E value
    Match length
                      60
    % identity
    NCBI Description HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone
                      [Zea mays]
                      300625
    Seq. No.
                      LIB3279-011-P1-K1-H6
    Seq. ID
                      BLASTX
    Method
                      g121974
    NCBI GI
                      343
    BLAST score
                      2.0e-32
    E value
    Match length
                      71
                      97
    % identity
    NCBI Description HISTONE H2A.2.1 >gi_70710_pir__HSWT2A histone H2A.2 - wheat
                      300626
    Seq. No.
                      LIB3279-011-P1-K1-H7
    Seq. ID
                      BLASTX
    Method
                      g1703380
    NCBI GI
                      442
    BLAST score
                      6.0e-44
    E value
                      100
    Match length
                      87
    % identity
    NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)
                      ADP-ribosylation factor [Oryza sativa]
                       300627
    Seq. No.
                      LIB3279-012-P1-K1-A10
    Seq. ID
                      BLASTX
    Method
                       g3461835
    NCBI GI
                       262
    BLAST score
                       7.0e-23
    E value
                       83
    Match length
    % identity
                       (AC005315) putative protein kinase [Arabidopsis thaliana]
    NCBI Description
                       >gi 3927840 (AC005727) putative protein kinase [Arabidopsis
                       thaliana]
                       300628
    Seq. No.
                       LIB3279-012-P1-K1-C10
    Seq. ID
    Method
                       BLASTX
```

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g1550814

NCBI GI



BLAST score E value 5.0e-16 Match length 51 % identity NCBI Description (Y07959) 60S acidic ribosomal protein P0 [Zea mays] Seq. No. 300629 LIB3279-012-P1-K1-E10 Seq. ID Method BLASTX NCBI GI g131772 BLAST score 375 4.0e-36 E value 94 Match length 82 % identity NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) maize 300630 Seq. No. LIB3279-012-P1-K1-E11 Seq. ID Method BLASTX NCBI GI g1173027 BLAST score 167 E value 4.0e-12 Match length 52 % identity 60 60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal NCBI Description protein L31 [Nicotiana glutinosa] Seq. No. 300631 Seq. ID LIB3279-012-P1-K1-F10 Method BLASTX NCBI GI g399854 BLAST score 144 3.0e-09 E value Match length 57 58 % identity HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize NCBI Description >gi 22325 emb CAA40565 (X57313) H2B histone [Zea mays] 300632 Seq. No. Seq. ID LIB3279-012-P1-K1-F4 Method BLASTN NCBI GI g22324 BLAST score 111 E value 1.0e-55 Match length 207 % identity 88

NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No. 300633

Seq. ID LIB3279-012-P1-K1-F7

Method BLASTX
NCBI GI g4585908
BLAST score 181
E value 2.0e-13
Match length 92

NCBI Description



```
% identity
                  (ACO06298) putative lysosomal acid lipase [Arabidopsis
NCBI Description
                  thaliana]
                  300634
Seq. No.
                  LIB3279-012-P1-K1-G2
Seq. ID
                  BLASTN
Method
                  q459267
NCBI GI
                  131
BLAST score
                  1.0e-67
E value
                  155
Match length
                  97
% identity
NCBI Description Z.mays gene for HMG protein
                  300635
Seq. No.
                  LIB3279-012-P1-K1-G6
Seq. ID
                  BLASTN
Method
                  q3452287
NCBI GI
                  58
BLAST score
                  7.0e-24
E value
                  148
Match length
                  91
% identity
NCBI Description Zea mays retrotransposon Fourf 3' LTR, partial sequence
                  300636
Seq. No.
                  LIB3279-013-P1-K1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1723958
BLAST score
                   325
                   3.0e-30
E value
                   135
Match length
% identity
                   51
NCBI Description PUTATIVE KINESIN-LIKE PROTEIN YGL216W
                   >gi_2131622_pir__S64238 hypothetical protein YGL216w -
                   yeast (Saccharomyces cerevisiae) >gi_1322862_emb_CAA96933_
                   (Z72739) ORF YGL216w [Saccharomyces cerevisiae]
                   300637
Seq. No.
                   LIB3279-013-P1-K1-C11
Seq. ID
                   BLASTX
Method
                   g2832625
NCBI GI
                   205
BLAST score
                   4.0e-16
E value
                   79
Match length
                   54
% identity
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
                   300638
Seq. No.
                   LIB3279-013-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q728882
BLAST score
                   258
                   2.0e-23
E value
                   114
Match length
                   61
% identity
                   ADP-RIBOSYLATION FACTOR 3 >gi_541846_pir__S41938
```

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ADP-ribosylation factor 3 - Arabidopsis thaliana



300639

>gi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3 [Arabidopsis thaliana]

Seq. No. LIB3279-013-P1-K1-H3 Seq. ID Method BLASTX g122022 NCBI GI BLAST score 338 1.0e-31 E value 93 Match length 76

% identity HISTONE H2B >gi 283025_pir__S22323 histone H2B - wheat NCBI Description >gi_21801_emb_CAA42530_ (X $\overline{59}873$) histone H2B [Triticum

aestivum]

300640 Seq. No.

LIB3279-014-P1-K1-A9 Seq. ID

BLASTX Method g3608485 NCBI GI 292 BLAST score 1.0e-42 E value 101 Match length 88 % identity

(AF088915) proteasome beta subunit [Petunia x hybrida] NCBI Description

300641 Seq. No.

LIB3279-014-P1-K1-C9 Seq. ID

BLASTX Method g3023713 NCBI GI BLAST score 178 3.0e-13 E value 58 Match length 66 % identity

ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) NCBI Description

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372

(U09450) enolase [Oryza sativa]

300642 Seq. No.

LIB3279-014-P1-K1-D12 Seq. ID

Method BLASTX q133867 NCBI GI 198 BLAST score 1.0e-15 E value 70 Match length % identity 63

40S RIBOSOMAL PROTEIN S11 >gi_82722 pir__S16577 ribosomal NCBI Description

protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)

ribosomal protein S11 [Zea mays]

300643 Seq. No.

LIB3279-014-P1-K1-D8 Seq. ID

Method BLASTN NCBI GI g168492 BLAST score 149 E value 3.0e-78 Match length 221 % identity 92

Seq. ID Method

BLASTN



```
NCBI Description Corn histone H3 (H3C3) gene, complete cds
                  300644
Seq. No.
                  LIB3279-014-P1-K1-E9
Seq. ID
                  BLASTX
Method
                  g1519253
NCBI GI
BLAST score
                  262
                  7.0e-23
E value
                  85
Match length
                  64
% identity
NCBI Description (U65958) GF14-d protein [Oryza sativa]
                  300645
Seq. No.
                  LIB3279-015-P1-K1-C4
Seq. ID
                  BLASTX
Method
                  g2865394
NCBI GI
                  365
BLAST score
                  7.0e-35
E value
                  133
Match length
                  49
% identity
NCBI Description (AF036949) basic leucine zipper protein [Zea mays]
                  300646
Seq. No.
                  LIB3279-015-P1-K1-C6
Seq. ID
Method
                  BLASTX
                  g2129635
NCBI GI
BLAST score
                  440
                  1.0e-43
E value
                  145
Match length
                   58
% identity
                  light repressible receptor protein kinase - Arabidopsis
NCBI Description
                   thaliana >gi 1321686 emb CAA66376 (X97774) light
                   repressible receptor protein kinase [Arabidopsis thaliana]
                   300647
Seq. No.
                   LIB3279-015-P1-K1-E5
Seq. ID
Method
                   BLASTN
                   q22483
NCBI GI
                   58
BLAST score
E value
                   6.0e-24
Match length
                   146
                   86
% identity
NCBI Description Z.mays RNA for superoxide dismutase Sod4
                   300648
Seq. No.
                   LIB3279-016-P1-K1-A3
Seq. ID
                   BLASTN
Method
                   q22121
NCBI GI
BLAST score
                   214
                   1.0e-117
E value
Match length
                   218
                   100
% identity
NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1F)
                   300649
Seq. No.
                   LIB3279-016-P1-K1-C4
```



```
g22243
NCBI GI
BLAST score
                  44
                  1.0e-15
E value
Match length
                  88
% identity
                  88
                  Zea mays Cin1 repeat from Cin1 middle repetitive family
NCBI Description
                  300650
Seq. No.
                  LIB3279-016-P1-K1-C8
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
                  8.0e-11
E value
                  48
Match length
% identity
                  67
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  300651
Seq. No.
                  LIB3279-016-P1-K1-C9
Seq. ID
                  BLASTX
Method
                  q3355468
NCBI GI
BLAST score
                  156
                   6.0e-12
E value
                   109
Match length
% identity
                   42
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                   thaliana]
                   300652
Seq. No.
                   LIB3279-016-P1-K1-H5
Seq. ID
                   BLASTX
Method
                   g498931
NCBI GI
                   289
BLAST score
                   7.0e-26
E value
                   94
Match length
                   64
% identity
                   (Z12825) ORF167; homologous to reverse transcriptases from
NCBI Description
                   retroviral-like transposons TNT 1-94 from tobacco and COPIA
                   from Drosophila [Beta vulgaris]
                   300653
Seq. No.
                   LIB3279-016-P1-K1-H8
Seq. ID
                   BLASTX
Method
                   q118104
NCBI GI
BLAST score
                   610
                   1.0e-63
E value
                   131
Match length
% identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi_168461 (M55021) cyclophilin [Zea mays]
                   >qi 829\overline{148} emb CAA48638 (X68678) cyclophilin [Zea mays]
```

Seq. ID LIB3279-017-P1-K1-A1

Method BLASTX



NCBI GI g2315449 BLAST score 253 E value 9.0e-22 Match length 109 % identity 44

NCBI Description (AF016448) similar to Saccharomyces cerevisiae nuclear protein SNF7 (SP:P39929)in one region and the chromosome

segregation protein SMC2 (SP:P38989) in another

[Caenorhabditis elegans]

Seq. No. 300655

Seq. ID LIB3279-017-P1-K1-D5

Method BLASTX
NCBI GI g3080398
BLAST score 238
E value 4.0e-25
Match length 142
% identity 34

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 300656

Seq. ID LIB3279-017-P1-K1-D9

Method BLASTX
NCBI GI g4455255
BLAST score 176
E value 1.0e-12
Match length 69
% identity 58

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 300657

Seq. ID LIB3279-017-P1-K1-E6

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300658

Seq. ID LIB3279-017-P1-K1-F8

Method BLASTX
NCBI GI g2982435
BLAST score 215
E value 2.0e-17
Match length 89
% identity 56

NCBI Description (AL022224) retrotransposon like protein (fragment)

[Arabidopsis thaliana]

Seq. No. 300659

Seq. ID LIB3279-017-P1-K1-G5

Method BLASTX
NCBI GI g2245012
BLAST score 217
E value 1.0e-17



```
Match length 131
% identity 43
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No. 300660
Seq. ID LIB3279-018-P1-K1-A8
```

Method BLASTX
NCBI GI g3915131
BLAST score 158
E value 4.0e-11
Match length 50
% identity 60

NCBI Description THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1) >gi 426442 dbj_BAA04864_ (D21836) thioredoxin h [Oryza

sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza

sativa]

 Seq. No.
 300661

 Seq. ID
 LIB3279-018-P1-K1-B6

 Method
 BLASTX

 NCBI GI
 g576886

 BLAST score
 311

 E value
 4.0e-29

Match length 59 % identity 97

NCBI Description (L37750) kaurene synthase A [Zea mays]

Seq. No. 300662

Seq. ID LIB3279-018-P1-K1-C10

Method BLASTX
NCBI GI g544125
BLAST score 153
E value 2.0e-10
Match length 42
% identity 64

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

>gi 81651 pir S22496 peptidylprolyl isomerase (EC 5.2.1.8)

- Arabidopsis thaliana >gi_16248_emb_CAA45161_ (X63616)

cyclophorin-like protein [Arabidopsis thaliana]

Seq. No. 300663

Seq. ID LIB3279-018-P1-K1-D10

Method BLASTX
NCBI GI g728826
BLAST score 209
E value 6.0e-17
Match length 90
% identity 49

NCBI Description ALDO-KETO REDUCTASE >gi_155867 (M93122) aldo-keto reductase

[Babesia bovis]

Seq. No. 300664

Seq. ID LIB3279-018-P1-K1-E2

Method BLASTX NCBI GI g3096949



```
BLAST score
                  3.0e-31
E value
Match length
                  91
                  66
% identity
                  (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                  [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic
                  nucleotide-gated cation channel [Arabidopsis thaliana]
                  300665
Seq. No.
                  LIB3279-018-P1-K1-E9
Seq. ID
                  BLASTX
Method
                  g1078813
NCBI GI
BLAST score
                  163
                  2.0e-11
E value
                  53
Match length
                  21
% identity
                  polyubiquitin - Euplotes eurystomus (SGC9) >gi_159038
NCBI Description
                   (M57231) ubiquitin [Euplotes eurystomus]
                  300666
Seq. No.
                  LIB3279-049-P1-K1-C4
Seq. ID
                  BLASTX
Method
                  g231573
NCBI GI
                  298
BLAST score
                  7.0e-31
E value
                  100
Match length
                  71
% identity
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                   >gi_99970_pir__S24757 asparaginase (EC 3.5.1.1) -
                   narrow-leaved blue lupine >gi_19135_emb_CAA43099_ (X60691)
                   developing seed L-asparaginase [Lupinus angustifolius]
                   300667
Seq. No.
                   LIB3279-049-P1-K1-D9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3334133
BLAST score
                   155
                   1.0e-10
E value
                   87
Match length
                   44
% identity
                   CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi_1432145
NCBI Description
                   (U61231) cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   300668
Seq. ID
                   LIB3279-050-P1-K1-A3
                   BLASTN
Method
                   q2832242
NCBI GI
                   71
BLAST score
E value
                   1.0e-31
Match length
                   266
% identity
                   87
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
```

Seq. ID LIB3279-050-P1-K1-C1

Method BLASTX NCBI GI g3860277

Match length

126



```
BLAST score
                  4.0e-17
E value
                  50
Match length
                  92
% identity
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
                   300670
Seq. No.
                  LIB3279-050-P1-K1-G5
Seq. ID
                  BLASTX
Method
                   g1917019
NCBI GI
                   155
BLAST score
                   3.0e-13
E value
                   63
Match length
                   70
% identity
                   (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
NCBI Description
Seq. No.
                   300671
                   LIB3279-051-P1-K1-A4
Seq. ID
                   BLASTX
Method
                   g2668742
NCBI GI
                   267
BLAST score
                   4.0e-25
E value
                   79
Match length
                   81
% identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   300672
Seq. No.
                   LIB3279-051-P1-K1-C10
Seq. ID
                   BLASTN
Method
                   g575425
NCBI GI
                   65
BLAST score
                   4.0e-28
E value
                   129
Match length
                   88
 % identity
                   Z.mays mRNA for sugar-starvation induced protein
NCBI Description
                   300673
 Seq. No.
                   LIB3279-051-P1-K1-C7
 Seq. ID
                   BLASTX
 Method
                   q462229
 NCBI GI
                   271
 BLAST score
                   5.0e-24
 E value
                   91
 Match length
                   58
 % identity
                   HISTONE H2A.1 >gi_542442 pir S41471 histone H2A.1 -
 NCBI Description
                    Tetrahymena thermophila (SGC5) >gi_310870 (L18892) histone
                   H2A.1 [Tetrahymena thermophila]
                    300674
 Seq. No.
                    LIB3279-051-P1-K1-D7
 Seq. ID
                    BLASTX
 Method
                    q1172553
 NCBI GI
                    289
 BLAST score
                    1.0e-31
 E value
```



```
% identity
NCBI Description OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
                  (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                  >qi 456672 emb CAA54788_ (X77733) voltage dependent anion
                  channel (VDAC) [Triticum aestivum]
                  300675
Seq. No.
                  LIB3279-051-P1-K1-F1
Seq. ID
                  BLASTX
Method
                  g131773
NCBI GI
                  222
BLAST score
                  3.0e-21
E value
                  82
Match length
                  74
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                  >gi 82724 pir_B30097 ribosomal protein S14 (clone MCH2) -
                  maize
                  300676
Seq. No.
                  LIB3279-051-P1-K1-F9
Seq. ID
                  BLASTX
Method
                  g1865677
NCBI GI
                  254
BLAST score
                  5.0e-22
E value
                  86
Match length
                  62
% identity
                  (Y08568) trehalose-6-phosphate synthase [Arabidopsis
NCBI Description
                  thaliana]
                   300677
Seq. No.
                  LIB3279-052-P1-K1-A2
Seq. ID
                  BLASTX
Method
                   g2668742
NCBI GI
                   298
BLAST score
                   3.0e-27
E value
                   73
Match length
                   78
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   300678
Seq. No.
                   LIB3279-052-P1-K1-A8
Seq. ID
                   BLASTX
Method
                   g2191169
NCBI GI
BLAST score
                   199
                   6.0e-20
E value
Match length
                   94
                   54
% identity
                   (AF007270) Similar to shaggy related protein kinase.
NCBI Description
                   Belongs to the CDC2/CDKX subfamily [Arabidopsis thaliana]
Seq. No.
                   300679
                   LIB3279-052-P1-K1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3128168
BLAST score
                   415
```

42346

3.0e-45

131

E value Match length



% identity (AC004521) putative carboxyl-terminal peptidase NCBI Description [Arabidopsis thaliana] 300680 Seq. No. LIB3279-052-P1-K1-F2 Seq. ID BLASTX Method q409007 NCBI GI BLAST score 247 4.0e-21 E value 74 Match length 68 % identity BBI-M-Bowman-Birk trypsin inhibitor-related protein [Zea NCBI Description mays=corn, Peptide, 102 aa] >gi_447268_prf__1914141A trypsin inhibitor-related protein [Zea mays] 300681 Seq. No. LIB3279-052-P1-K1-G12 Seq. ID Method BLASTX g112994 NCBI GI BLAST score 262 4.0e-23 E value Match length 60 % identity 85 GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN NCBI Description >gi 82685 pir__S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564) ABA-inducible gene protein [Zea mays] >gi 226091 prf 1410284A abscisic acid inducible gene [Zea mays] 300682 Seq. No. LIB3279-053-P1-K1-A12 Seq. ID BLASTX Method g2961346 NCBI GI BLAST score 333 3.0e-31 E value 73 Match length % identity 75 (AL022140) pectinesterase like protein [Arabidopsis NCBI Description thaliana] 300683 Seq. No. LIB3279-053-P1-K1-F7 Seq. ID BLASTX Method NCBI GI g2765837 BLAST score 168 7.0e-12 E value 41 Match length % identity 76 (Z96936) NAP16kDa protein [Arabidopsis thaliana] NCBI Description

Seq. No. 300684

Seq. ID LIB3279-053-P1-K1-G1

Method BLASTN
NCBI GI g1546918
BLAST score 63



```
5.0e-27
E value
                  71
Match length
                  97
% identity
                  Z.mays mRNA for translation initiation factor 5A
NCBI Description
                  300685
Seq. No.
                  LIB3279-053-P1-K1-G5
Seq. ID
Method
                  BLASTX
                  g2190547
NCBI GI
                  298
BLAST score
                  4.0e-27
E value
                  114
Match length
                  66
% identity
                  (AC001229) ESTs
NCBI Description
                  gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb_AA404382 come
                  from this gene. [Arabidopsis thaliana]
                  300686
Seq. No.
                  LIB3279-054-P1-K1-B1
Seq. ID
                  BLASTX
Method
                  g2982289
NCBI GI
                  162
BLAST score
                  1.0e-11
E value
                  75
Match length
                  56
% identity
                  (AF051229) 60S ribosomal protein L17 [Picea mariana]
NCBI Description
                  300687
Seq. No.
                  LIB3279-054-P1-K1-D6
Seq. ID
                  BLASTX
Method
                  g1346251
NCBI GI
                  260
BLAST score
                   1.0e-22
E value
                   73
Match length
                   77
% identity
                  HISTONE H2B.4 >gi_577819_emb_CAA49585_ (X69961) H2B histone
NCBI Description
                   [Zea mays]
                   300688
Seq. No.
                   LIB3279-054-P1-K1-E7
Seq. ID
Method
                   BLASTX
                   q2829889
NCBI GI
                   175
BLAST score
E value
                   1.0e-12
Match length
                   61
% identity
                   64
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   300689
Seq. No.
                   LIB3279-054-P1-K1-F7
Seq. ID
Method
                   BLASTX
                   q4091010
NCBI GI
```

42348

NCBI Description (AF042275) anther-specific protein [Oryza sativa]

161

69

52

5.0e-11

BLAST score

Match length % identity

E value

Method

NCBI GI

BLAST score

BLASTN

40

g498642

```
Seq. No.
                  300690
                  LIB3279-055-P1-K1-A1
Seq. ID
Method
                  BLASTX
                  g2245394
NCBI GI
BLAST score
                  168
E value
                  7.0e-12
Match length
                  43
                  63
% identity
NCBI Description (U89771) ARF1-binding protein [Arabidopsis thaliana]
                  300691
Seq. No.
                  LIB3279-055-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2344899
                  184
BLAST score
                  1.0e-13
E value
Match length
                  68
% identity
                  50
                  (AC002388) unknown protein [Arabidopsis thaliana]
NCBI Description
                  300692
Seq. No.
                  LIB3279-055-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132849
                  189
BLAST score
                  2.0e-14
E value
                  54
Match length
                  69
% identity
                  60S RIBOSOMAL PROTEIN L2 >gi 20001 emb CAA44362.1 (X62500)
NCBI Description
                  60S ribosomal protein L2 [Nicotiana tabacum]
                   300693
Seq. No.
Seq. ID
                  LIB3279-055-P1-K1-D12
Method
                  BLASTX
NCBI GI
                   q1143864
BLAST score
                   222
E value
                   2.0e-18
Match length
                   70
% identity
                   60
NCBI Description
                  (U28047) beta glucosidase [Oryza sativa]
Seq. No.
                   300694
Seq. ID
                   LIB3279-055-P1-K1-H6
Method
                   BLASTN
NCBI GI
                   q473604
BLAST score
                   113
E value
                   6.0e-57
Match length
                   164
                   93
% identity
NCBI Description Zea mays W-22 histone H2B mRNA, complete cds
                   300695
Seq. No.
Seq. ID
                   LIB3279-057-P1-K1-A1
```



```
2.0e-13
E value
Match length
                  60
% identity
                  92
                  Zea mays G-box binding factor 1 (GBF1) mRNA, complete cds
NCBI Description
                  300696
Seq. No.
                  LIB3279-057-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4371282
BLAST score
                . 305
                  6.0e-28
E value
                  99
Match length
% identity
                  67
                  (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                  thaliana]
                  300697
Seq. No.
                  LIB3279-057-P1-K1-B9
Seq. ID
Method
                  BLASTX
                  g1815681
NCBI GI
                  189
BLAST score
                  2.0e-14
E value
Match length
                  35
                  94
% identity
NCBI Description (U85246) expansin [Oryza sativa]
                  300698
Seq. No.
                  LIB3279-057-P1-K1-C11
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2623247
BLAST score
                  99
                  2.0e-48
E value
                  135
Match length
                  93
% identity
NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds
Seq. No.
                  300699
                  LIB3279-057-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3292820
BLAST score
                  158
E value
                  1.0e-10
                  83
Match length
                   42
% identity
                   (AL031018) putative MADS Box / AGL protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   300700
                  LIB3279-057-P1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244952
BLAST score
                   163
                   6.0e-19
E value
Match length
                   103
% identity
                   51
                   (Z97340) strong similarity to ZK688.3 protein -
NCBI Description
                   Caenorhabditis elegans [Arabidopsis thaliana]
```

Method

NCBI GI

BLASTX

g4469009



```
300701
Seq. No.
Seq. ID
                  LIB3279-057-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q3894393
BLAST score
                  158
E value
                  1.0e-10
Match length
                  130
% identity
                  33
NCBI Description (AF053998) Hcr2-5D [Lycopersicon esculentum]
Seq. No.
                  300702
Seq. ID
                  LIB3279-057-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g4455309
BLAST score
                  272
                  5.0e-24
E value
Match length
                  71
% identity
                  72
NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]
                  300703
Seq. No.
                  LIB3279-059-P1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4234859
BLAST score
                  53
                  5.0e-21
E value
Match length
                  61
% identity
                  97
NCBI Description
                 Zea mays copia-like retrotransposon Stl-14 leader region,
                  partial sequence
Seq. No.
                  300704
Seq. ID
                  LIB3279-059-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q629846
BLAST score
                  233
                  2.0e-19
E value
Match length
                  49
                  88
% identity
NCBI Description initiator-binding protein - maize >gi_483444 emb_CAA55693_
                  (X79086) initiator-binding protein [Zea mays]
Seq. No.
                  300705
Seq. ID
                  LIB3279-059-P1-K1-C9
Method
                  BLASTN
                  g2062705
NCBI GI
BLAST score
                  35
E value
                  2.0e-10
                  35
Match length
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  300706
                  LIB3279-059-P1-K1-F3
Seq. ID
```

BLAST score

E value

305 6.0e-28



```
BLAST score
E value
                  4.0e-18
Match length
                  99
                  54
% identity
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  300707
                  LIB3279-059-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123270
BLAST score
                  215
E value
                  1.0e-21
Match length
                  67
                  80
% identity
                  40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)
NCBI Description
                  >gi_2463335_emb_CAA75242_ (Y15009) ribosomal protein S4
                  [Oryza sativa]
Seq. No.
                  300708
                  LIB3279-059-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1870700
BLAST score
                  227
                  4.0e-19
E value
Match length
                  60
% identity
                  75
                  (U84116) cleavage stage histone H3 [Psammechinus miliaris]
NCBI Description
Seq. No.
                  300709
                  LIB3279-060-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3201541
BLAST score
                  292
E value
                  2.0e-26
Match length
                  111
% identity
                  (AJ005077) TCTR2 protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  300710
                  LIB3279-060-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g728777
BLAST score
                  238
E value
                  5.0e-20
Match length
                   61
                  70
% identity
                  ACTIVATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD
NCBI Description
                  SUBUNIT) (A1 36 KD SUBUNIT) (RF-C 36 KD SUBUNIT) (RFC36)
                  >qi 1498257 (L07540) replication factor C, 36-kDa subunit
                   [Homo sapiens]
                   300711
Seq. No.
                  LIB3279-060-P1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832672
```



```
Match length
% identity
                  76
                  (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
                  300712
Seq. No.
Seq. ID
                  LIB3279-060-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q445612
                  231
BLAST score
                  3.0e-19
E value
Match length
                  56
% identity
                  79
NCBI Description ribosomal protein S19 [Solanum tuberosum]
                  300713
Seq. No.
                  LIB3279-060-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171429
BLAST score
                  337
E value
                  1.0e-31
Match length
                  90
                  68
% identity
                  (U44028) CKC [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  300714
                  LIB3279-060-P1-K1-F7
Seq. ID
Method
                  BLASTN
                  q1657766
NCBI GI
BLAST score
                   39
                  2.0e-12
E value
                   55
Match length
                   95
% identity
                  Zea mays retrotransposon Opie-2 5' LTR, primer binding
NCBI Description
                   site, gag gene, pol gene, complete cds, polypurine tract
                  and 3' LTR
Seq. No.
                   300715
                  LIB3279-060-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3738304
BLAST score
                   263
E value
                   6.0e-23
                   80
Match length
                   60
% identity
NCBI Description
                   (AC005309) hypothetical protein [Arabidopsis thaliana]
                   300716
Seq. No.
Seq. ID
                   LIB36-001-Q1-E1-C6
Method
                   BLASTX
NCBI GI
                   g1084479
BLAST score
                   262
```

E value 9.0e-23 53 Match length 98 % identity

H+-transporting ATP synthase (EC 3.6.1.34) delta chain -NCBI Description maize (fragment) >gi_311237_emb_CAA46804_ (X66005)

H(+)-transporting ATP synthase [Zea mays]



85

Match length

NCBI Description

% identity

```
300717
Seq. No.
                  LIB36-001-Q1-E1-D2
Seq. ID
Method
                  BLASTX
                  g3021506
NCBI GI
                  538
BLAST score
                  1.0e-63
E value
                  138
Match length
                  92
% identity
                  (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana
NCBI Description
                  tabacum]
                  300718
Seq. No.
                  LIB36-001-Q1-E1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172818
BLAST score
                  172
                  8.0e-13
E value
                  48
Match length
                  73
% identity
                  40S RIBOSOMAL PROTEIN S16 >gi 538428 (L36313) ribosomal
NCBI Description
                  protein S16 [Oryza sativa] >gi_1096552_prf__2111468A
                  ribosomal protein S16 [Oryza sativa]
Seq. No.
                  300719
                  LIB36-001-Q1-E1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3789952
BLAST score
                  517
                  1.0e-52
E value
                  129
Match length
% identity
                  80
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   300720
Seq. No.
                  LIB36-002-Q1-E1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4191348
                   557
BLAST score
E value
                   2.0e-57
Match length
                   125
                   85
% identity
                   (AF087661) NADH-ubiquinone oxidoreductase 42 kDa subunit
NCBI Description
                   [Homo sapiens]
                   300721
Seq. No.
                   LIB36-002-Q1-E1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3093334
BLAST score
                   37
E value
                   8.0e-12
```

lymphoma (clone h12-22)

Homo sapiens mRNA from HIV-associated non-Hodgkin's



```
300722
Seq. No.
                  LIB36-003-Q1-E1-B5
Seq. ID
                  BLASTX
Method
                  g3810596
NCBI GI
                  337
BLAST score
                  1.0e-31
E value
                  105
Match length
                  56
% identity
                  (AC005398) reverse-transcriptase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  300723
Seq. No.
                  LIB36-003-Q1-E1-D3
Seq. ID
                  BLASTN
Method
                  g3420038
NCBI GI
                  56
BLAST score
                   6.0e-23
E value
                   165
Match length
                   43
% identity
                  Zea mays gypsy/Ty3-type retrotransposon Tekay, complete
NCBI Description
                   sequence
                   300724
Seq. No.
                   LIB36-004-Q1-E1-A1
Seq. ID
                   BLASTN
Method
                   q3821780
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   300725
Seq. No.
                   LIB36-004-Q1-E1-C12
Seq. ID
                   BLASTX
Method
                   g1171579
NCBI GI
                   207
BLAST score
                   2.0e-16
E value
Match length
                   69
% identity
                   55
NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]
                   300726
Seq. No.
                   LIB36-004-Q1-E1-D9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2191161
BLAST score
                   147
                   2.0e-09
E value
                   56
Match length
                   61
% identity
                   (AF007270) contains similarity to B. subtilus flagellar
NCBI Description
                   biosynthesis protein FLHA (SW:P35620) [Arabidopsis
                   thaliana]
```

Seq. ID LIB36-004-Q1-E1-F5

Method BLASTN

```
g2062705
NCBI GI
BLAST score
                  36
E value
                  7.0e-11
Match length
                  36
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  300728
Seq. No.
                  LIB36-004-Q1-E1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4240035
                  397
BLAST score
                  1.0e-38
E value
Match length
                  112
% identity
                  70
NCBI Description (AB018588) ZmGR1b [Zea mays]
                  300729
Seq. No.
Seq. ID
                  LIB36-005-Q1-E1-D11
                  BLASTX
Method
NCBI GI
                  g168586
BLAST score
                  170
E value
                  4.0e-12
Match length
                  95
% identity
                  48
NCBI Description (M58656) pyruvate, orthophosphate dikinase [Zea mays]
Seq. No.
                  300730
Seq. ID
                  LIB36-005-Q1-E1-D6
                  BLASTX
                  g3193330
```

Method BLASTX
NCBI GI g3193330
BLAST score 172
E value 3.0e-12
Match length 73
% identity 42

NCBI Description (AF069299) contains similarity to Medicago sativa corC

(GB:L22305) [Arabidopsis thaliana]

Seq. No. 300731

Seq. ID LIB36-006-Q1-E1-D9

Method BLASTX
NCBI GI g120670
BLAST score 404
E value 1.0e-39
Match length 77
% identity 100

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 100879 pir S06879 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12) C - maize

>gi 295853 emb CAA33620 (X15596) GAPDH [Zea mays]

Seq. No. 300732

Seq. ID LIB36-006-Q1-E1-E8

Method BLASTX
NCBI GI g126737
BLAST score 151
E value 3.0e-20



```
Match length
                  70
% identity
                  MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)
NCBI Description
                   (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)
                  >gi_65939_pir__DEZMMX malate dehydrogenase
                   (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40)
                  precursor, chloroplast - maize >gi_168528 (J05130)
                  NADP-dependent malic enzyme (EC 1.1.1.40) [Zea mays]
                  300733
Seq. No.
                  LIB36-006-Q1-E1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  218
                  9.0e-18
E value
                  80
Match length
                  54
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  300734
                  LIB36-006-Q1-E1-G3
Seq. ID
                  BLASTX
Method
                  g2345154
NCBI GI
                  322
BLAST score
E value
                   4.0e-30
                  70
Match length
                  86
% identity
                  (AF015522) ribsomal protein S4 [Zea mays]
NCBI Description
                   300735
Seq. No.
                  LIB36-006-Q1-E1-H3
Seq. ID
Method
                  BLASTX
                  g115786
NCBI GI
                   174
BLAST score
E value
                   4.0e-13
                   46
Match length
                   85
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB) (LHCP) >gi 82680 pir A29119 chlorophyll a/b-binding
                   protein - maize >gi 22357 emb CAA68451_ (Y00379) LHCP [Zea
                   mays]
                   300736
Seq. No.
                   LIB36-007-Q1-E1-A1
Seq. ID
Method
                   BLASTX
                   g3063471
NCBI GI
                   303
BLAST score
                   1.0e-27
E value
Match length
                   95
                   58
% identity
```

(AC003981) F22013.33 [Arabidopsis thaliana] NCBI Description

300737 Seq. No.

LIB36-007-Q1-E1-C4 Seq. ID

Method BLASTX NCBI GI g2677824 BLAST score 196



5.0e-15 E value 96 Match length % identity (U93164) abscisic stress ripening protein homolog [Prunus NCBI Description armeniaca] 300738 Seq. No. LIB36-008-Q1-E1-A2 Seq. ID BLASTX Method g902525 NCBI GI 463 BLAST score 2.0e-46 E value 125 Match length 78 % identity (U29160) ubiquitin fusion protein [Zea mays] NCBI Description >gi 1589387 prf 2211240A ubiquitin fusion protein [Zea mays] Seq. No. 300739 LIB36-008-Q1-E1-C8 Seq. ID Method BLASTN g22356 NCBI GI BLAST score 118 5.0e-60 E value 196 Match length 91 % identity Maize mRNA for light-harvesting chlorophyll a/b binding NCBI Description protein LHCP 300740 Seq. No. LIB36-008-Q1-E1-E5 Seq. ID BLASTX Method g131225 NCBI GI 218 BLAST score 4.0e-18 E value 60 Match length 73 % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT NCBI Description V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K_protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare] 300741 Seq. No. LIB36-008-Q1-E1-F11 Seq. ID BLASTX Method NCBI GI g115771 277 BLAST score 6.0e-25 E value 59 Match length 90

% identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

300742 Seq. No.

Match length

% identity

89

61



```
LIB36-008-Q1-E1-F2
Seq. ID
Method
                  BLASTX
                  g115815
NCBI GI
                  329
BLAST score
                  8.0e-31
E value
                  84
Match length
                  75
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi_22355_emb_CAA39376_ (X55892) light-harvesting
                  chlorophyll a/b binding protein [Zea mays]
Seq. No.
                  300743
                  LIB36-009-Q1-E1-C3
Seq. ID
Method
                  BLASTX
                  g114551
NCBI GI
                  726
BLAST score
E value
                  3.0e-77
                  147
Match length
                  99
% identity
                  ATP SYNTHASE BETA CHAIN >gi_67833_pir__PWZMB
NCBI Description
                  H+-transporting ATP synthase (EC 3.6.1.34) beta chain -
                  maize chloroplast >gi_552732 (J01421) coupling factor
                  beta-subunit [Zea mays] >gi_902229_emb_CAA60293_ (X86563)
                  ATPase beta subunit [Zea mays]
                  300744
Seq. No.
                  LIB36-009-Q1-E1-D11
Seq. ID
Method
                  BLASTX
                  q2642154
NCBI GI
                  272
BLAST score
                   6.0e-24
E value
Match length
                   110
% identity
                   46
                   (AC003000) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3790595 (AF079186) RING-H2 finger protein RHC2a
                   [Arabidopsis thaliana]
Seq. No.
                   300745
                   LIB36-009-Q1-E1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4416302
BLAST score
                   281
E value
                   1.0e-25
                   67
Match length
% identity
NCBI Description
                   (AF105716) copia-type pol polyprotein [Zea mays]
Seq. No.
                   300746
                   LIB36-009-Q1-E1-F3
Seq. ID
Method
                   BLASTX
                   g4587597
NCBI GI
BLAST score
                   319
E value
                   2.0e-29
```



(AC006951) putative MAP kinase phosphatase [Arabidopsis NCBI Description thalianal 300747 Seq. No.

LIB36-010-Q1-E1-A12 Seq. ID

BLASTN Method g433459 NCBI GI 135 BLAST score 5.0e-70 E value 161 Match length 97 % identity

NCBI Description Z.mays mRNA for ferredoxin-thioredoxin reductase

300748 Seq. No.

LIB36-010-Q1-E1-B12 Seq. ID

BLASTN Method g1255218 NCBI GI 138 BLAST score 9.0e-72 E value 234 Match length 91 % identity

NCBI Description Zea mays blue-light photoreceptor-like mRNA

300749 Seq. No.

LIB36-010-Q1-E1-C3 Seq. ID

BLASTN Method g902200 NCBI GI 190 BLAST score 1.0e-102 E value 254 Match length 94 % identity

NCBI Description Z.mays complete chloroplast genome

300750 Seq. No.

LIB36-010-Q1-E1-D6 Seq. ID

BLASTX Method q2668742 NCBI GI 376 BLAST score 4.0e-36 E value 86 Match length % identity

(AF034945) glycine-rich RNA binding protein [Zea mays] NCBI Description

300751 Seq. No.

LIB36-010-Q1-E1-E1 Seq. ID

BLASTX Method q3885896 NCBI GI 192 BLAST score E value 9.0e-15 101 Match length % identity

(AF093636) plastocyanin precursor [Oryza sativa] NCBI Description

300752 Seq. No.

LIB36-010-Q1-E1-E6 Seq. ID

Method BLASTX NCBI GI g4544402



BLAST score 403 E value 3.0e-39 Match length 149 % identity 58

NCBI Description (AC007047) putative leucine rich repeat protein

[Arabidopsis thaliana]

Seq. No. 300753

Seq. ID LIB36-010-Q1-E1-F7

Method BLASTX
NCBI GI g3218550
BLAST score 163
E value 4.0e-11
Match length 75
% identity 40

NCBI Description (AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]

Seq. No. 300754

Seq. ID LIB36-011-Q1-E1-A11

Method BLASTX
NCBI GI 94581156
BLAST score 139
E value 5.0e-09
Match length 58
% identity 50

NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No. 300755

Seq. ID LIB36-011-Q2-E2-A10

Method BLASTX
NCBI GI g2244987
BLAST score 150
E value 1.0e-09
Match length 50
% identity 54

NCBI Description (Z97340) similarity to protein kinase - slime mold

(Dictyostelium) [Arabidopsis thaliana]

Seq. No. 300756

Seq. ID LIB36-011-Q2-E2-A11

Method BLASTX
NCBI GI g1174845
BLAST score 398
E value 1.0e-38
Match length 88
% identity 80

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE 2) (UBIQUITIN CARRIER PROTEIN)

>gi_101070_pir__S12529 ubiquitin-conjugating enzyme rhp6 -

fission yeast (Schizosaccharomyces pombe)

>gi_929893_emb_CAA90592_ (Z50728) ubiquitin-conjugating

enzyme e2-17 kd [Schizosaccharomyces pombe]

Seq. No. 300757

Seq. ID LIB36-011-Q2-E2-A12

Method BLASTX NCBI GI g3327033

% identity



```
BLAST score
                       440
                       1.0e-43
E value
Match length
                       148
                       61
% identity
NCBI Description (Z68198) 40S ribosomal protein [Schizosaccharomyces pombe]
                       300758
Seq. No.
                       LIB36-011-Q2-E2-A7
Seq. ID
                       BLASTX
Method
                       g1708366
NCBI GI
                       145
BLAST score
                       4.0e-09
E value
                       64
Match length
% identity
                       45
                       HEXOKINASE >gi_1041966_bbs_168854 (S78714)
NCBI Description
                       hexokinase=hexose-phosphorylating enzyme [Schwanniomyces
                       occidentalis, CBS819, ATCC2322, Peptide, 478 aa]
                       [Debaryomyces occidentalis]
                       300759
Seq. No.
                       LIB36-011-Q2-E2-A8
Seq. ID
Method
                       BLASTX
                       g4406372
NCBI GI
                       310
BLAST score
                       2.0e-28
E value
                       139
Match length
                       47
% identity
                       (AF109156) thiosulfate sulfurtransferase [Datisca
NCBI Description
                       glomerata]
                       300760
Seq. No.
                       LIB36-011-Q2-E2-B1
Seq. ID
                       BLASTX
Method
                       g4506635
NCBI GI
BLAST score
                       448
                       2.0e-44
E value
                       124
Match length
% identity
                       ribosomal protein L32 >gi_132886_sp_P02433_RL32_HUMAN 60S RIBOSOMAL PROTEIN L32 >gi_71335_pir__R5HU32_ribosomal
NCBI Description
                       protein L32 - human >gi_71336_pir__R5MS32 ribosomal protein L32 - mouse >gi_71337_pir__R5RT32 ribosomal protein L32 - rat >gi_36132_emb_CAA27048 (X03342) rpL32 (aa 1-135) [Homo sapiens] >gi_57117_emb_CAA29777 (X06483) ribosomal protein L32 [Rattus norvegicus] >gi_200781 (K02060) ribosomal
                       protein L32-3A [Mus musculus] >gi 226004 prf 1405339A
                        ribosomal protein L32 [Rattus norvegicus]
                        300761
 Seq. No.
                        LIB36-011-Q2-E2-B12
 Seq. ID
Method
                        BLASTX
                        g2443753
NCBI GI
                        352
BLAST score
                        3.0e-33
E value
                        128
Match length
```

42362

NCBI Description (AF020346) pyridoxal kinase [Rattus norvegicus]



```
300762
Seq. No.
                   LIB36-011-Q2-E2-B4
Seq. ID
Method
                   BLASTX
                   g4406378
NCBI GI
BLAST score
                   210
                   1.0e-16
E value
Match length
                   77
```

% identity (AF109913) plasma membrane H+-ATPase [Pichia angusta] NCBI Description

Seq. No. LIB36-011-Q2-E2-B7 Seq. ID Method BLASTX NCBI GI q1749582 469 BLAST score 5.0e-47 E value 150

Match length 57 % identity

(D89187) similar to Saccharomyces cerevisiae hypothetical NCBI Description

TRP-ASP repeats containing protein in MDS1-SWP1 intergenic

region, SWISS-PROT Accession Number P40217

[Schizosaccharomyces pombe]

Seq. No. 300764

LIB36-011-Q2-E2-B8 Seq. ID

Method BLASTX g119119 NCBI GI 340 BLAST score 7.0e-32 E value Match length 106 % identity 60

ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (SHORT CHAIN NCBI Description

ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1) >gi 92216 pir__S06477 enoyl-CoA hydratase (EC 4.2.1.17) precursor, mitochondrial - rat >gi_56072_emb_CAA34080_ (X15958) precursor polypeptide (AA -29 to 261) [Rattus norvegicus] >gi_227489_prf__1704377A enoyl-CoA hydratase

[Rattus norvegicus]

Seq. No. 300765

Seq. ID LIB36-011-Q2-E2-B9

Method BLASTX NCBI GI q3122971 BLAST score 224 3.0e-18 E value 68 Match length 54 % identity

NCBI Description PROBABLE TRNA

(5-METHYLAMINOMETHYL-2-THIOURIDYLATE) -METHYLTRANSFERASE >gi 2388924 emb CAB11659_ (Z98977) hypothetical protein

[Schizosaccharomyces pombe]

300766 Seq. No.

LIB36-011-Q2-E2-C10 Seq. ID

Method BLASTX NCBI GI q1168328



BLAST score 402 E value 4.0e-39 Match length 130 % identity 58

NCBI Description ACTIN-LIKE PROTEIN 3 >gi_629878_pir__S48844 actin-like

protein - slime mold (Dictyostelium discoideum)

>gi_2130164_pir__S69002 actin-like protein - slime mold (Dictyostelium discoideum) >gi_563346_emb_CAA86553_ (Z46418) actin-like protein [Dictyostelium discoideum]

Seq. No. 300767

Seq. ID LIB36-011-Q2-E2-C12

Method BLASTX
NCBI GI g133978
BLAST score 550
E value 2.0e-56
Match length 147
% identity 70

NCBI Description 40S RIBOSOMAL PROTEIN S6 (PHOSPHOPROTEIN NP33)

>gi_70932_pir__R3RTS6 ribosomal protein S6 - rat
>gi_70933_pir__R3MS6 ribosomal protein S6 - mouse
>gi_319910_pir__R3HU6 ribosomal protein S6 - human

>gi_36148_emb_CAA47719_ (X67309) ribosomal protein S6 [Homo sapiens] >gi_54010_emb_CAA68430_ (Y00348) ribosomal protein S6 [Mus musculus] >gi_206747 (M29358) ribosomal protein S6 [Rattus norvegicus] >gi_307393 (M77232) ribosomal protein S6 [Homo sapiens] >gi_1177549_emb_CAA90936_ (Z54209) rpS6

[Mus musculus]

Seq. No. 300768

Seq. ID LIB36-011-Q2-E2-C2

Method BLASTX
NCBI GI g2499017
BLAST score 455
E value 2.0e-45
Match length 118
% identity 69

NCBI Description ALPHA, ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 1

(TREHALOSE-6-PHOSPHATE SYNTHASE)

(UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)

>gi_551471 (U07184) trehalose-6-phosphate synthase subunit

1 [Aspergillus niger]

Seq. No. 300769

Seq. ID LIB36-011-Q2-E2-C4

Method BLASTX
NCBI GI g4557467
BLAST score 229
E value 7.0e-19
Match length 111
% identity 41

NCBI Description Cockayne syndrome 1 protein >gi_3121917_sp_Q13216_CSA_HUMAN

COCKAYNE SYNDROME WD-REPEAT PROTEIN CSA

>gi_1362773_pir__A57090 CSA protein - human >gi_975302

(U28413) CSA protein [Homo sapiens]

Seq. No. 300770



```
LIB36-011-Q2-E2-C6
Seq. ID
                  BLASTX
Method
                  g1513298
NCBI GI
                  238
BLAST score
                  6.0e-20
E value
                  129
Match length
                  35
% identity
NCBI Description (U66526) AbcA [Dictyostelium discoideum]
                  300771
Seq. No.
                  LIB36-011-Q2-E2-C8
Seq. ID
                  BLASTX
Method
                  g3204175
NCBI GI
BLAST score
                  164
                  3.0e-11
E value
                  101
Match length
% identity
                  39
NCBI Description (AJ006405) prostaglandin-D synthase [Gallus gallus]
                  300772
Seq. No.
                  LIB36-011-Q2-E2-C9
Seq. ID
                  BLASTX
Method
                   g3334494
NCBI GI
                   523
BLAST score
                   2.0e-53
E value
                   140
Match length
% identity
                   74
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi 2388954 emb CAB11687
                   (Z98979) 40s ribosomal protein s11 [Schizosaccharomyces
                   pombe]
                   300773
Seq. No.
                   LIB36-011-Q2-E2-D1
Seq. ID
Method
                   BLASTX
                   q478005
NCBI GI
BLAST score
                   293
E value
                   2.0e-26
                   121
Match length
% identity
NCBI Description profilin-IB - Acanthamoeba sp. (tentative sequence)
                   300774
Seq. No.
                   LIB36-011-Q2-E2-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g182403
BLAST score
                   352
E value
                   3.0e-33
Match length
                   125
 % identity
                   51
                   (M74090) TB2 [Homo sapiens]
NCBI Description
                   300775
 Seq. No.
                   LIB36-011-Q2-E2-D5
 Seq. ID
                   BLASTX
 Method
                   q3023751
 NCBI GI
```

320

2.0e-29

BLAST score

E value



```
133
Match length
                   30
% identity
                   70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
NCBI Description
                   ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__$55383
                   peptidylprolyl isomerase (EC 5.2.1.8) - wheat
                   >gi 854626 emb_CAA60505_ (X86903) peptidylprolyl isomerase
                   [Triticum aestivum]
Seq. No.
                   300776
                   LIB36-011-Q2-E2-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2414627
BLAST score
                   269
                    6.0e-24
E value
                   92
Match length
% identity
                    58
                   (Z99259) 40s ribosomal protein [Schizosaccharomyces pombe]
NCBI Description
                    300777
Seq. No.
                   LIB36-011-Q2-E2-D7
Seq. ID
Method
                    BLASTX
NCBI GI
                    q114517
BLAST score
                    422
                    2.0e-41
E value
                    120
Match length
                    71
% identity
                   ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                    >gi_67811_pir__PWHUA H+-transporting ATP synthase (EC
                    3.6.1.34) alpha chain precursor - human
                    >gi_28938_emb_CAA41789 (X59066) H(+)-transporting ATP
synthase [Homo sapiens] >gi_34468_emb_CAA46452 (X65460)
                    ATP synthase alpha subunit [Homo sapiens]
                    >qi 559317 dbj BAA05672 (D28126) ATP synthase alpha
                    subunit [Homo sapiens] >gi_559325_dbj_BAA03531_ (D14710)
                    inport precursor of human ATP synthase alpha subunit [Homo
                    sapiens] >gi_1090507_prf__2019238A ATP
                    synthase:SUB\overline{U}NIT=alp\overline{h}a [\overline{Ho}mo sapiens]
Seq. No.
                    300778
                    LIB36-011-Q2-E2-D8
Seq. ID
                    BLASTX
Method
NCBI GI
                    g3947746
                    211
BLAST score
                    1.0e-16
E value
                    132
Match length
                    33
% identity
                    (AJ009960) DNA photolyase [Trichoderma harzianum]
NCBI Description
                    300779
Seq. No.
                    LIB36-011-Q2-E2-E2
Seq. ID
Method
                    BLASTX
NCBI GI
                    a600159
BLAST score
                    361
                    2.0e-34
E value
                    93
Match length
```

(U17362) elongation factor 2 [Cricetulus griseus]

78

% identity

NCBI Description

```
Seq. No.
                  300780
                  LIB36-011-Q2-E2-E3
Seq. ID
Method
                  BLASTX
                  q3643267
NCBI GI
                  169
BLAST score
                  5.0e-24
E value
                  125
Match length
                  52
% identity
                  (AF090443) catalase [Dictyostelium discoideum]
NCBI Description
```

300781 Seq. No. LIB36-011-Q2-E2-E8 Seq. ID BLASTX Method

NCBI GI q2160185 BLAST score 199 2.0e-15 E value Match length 76 % identity 51

(AC000132) Similar to S. pombe ISP4 (gb D83992). NCBI Description

[Arabidopsis thaliana]

300782 Seq. No. LIB36-011-Q2-E2-F10 Seq. ID BLASTX Method NCBI GI g1749752 BLAST score 442

E value 7.0e-44 Match length 148 60 % identity

(D89272) similar to Saccharomyces cerevisiae T-complex NCBI Description

protein 1, theta subunit, SWISS-PROT Accession Number P47079

[Schizosaccharomyces pombe]

300783 Seq. No.

LIB36-011-Q2-E2-F11 Seq. ID

Method BLASTN g2618602 NCBI GI BLAST score 64 E value 2.0e-27 Match length 306 83

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MSJ1, complete sequence [Arabidopsis thaliana]

300784 Seq. No.

% identity

LIB36-011-Q2-E2-F8 Seq. ID

BLASTX Method NCBI GI g134509 BLAST score 165 E value 2.0e-11 68 Match length % identity 50

SIS1 PROTEIN >gi 101623 pir__A39660 heat shock protein SIS1 NCBI Description

- yeast (Saccharomyces cerevisiae) >gi_4474_emb_CAA41366_

(X58460) SIS1 protein [Saccharomyces cerevisiae] >gi 1301824 emb CAA95866 (Z71283) ORF YNL007c



[Saccharomyces cerevisiae]

```
300785
Seq. No.
                  LIB36-011-Q2-E2-F9
Seq. ID
                  BLASTX
Method
                  g4160343
NCBI GI
BLAST score
                  247
                  5.0e-21
E value
                  151
Match length
% identity
                  38
                  (AL035216) similar to rat synaptic glycoprotein sc2
NCBI Description
                   [Schizosaccharomyces pombe]
                  300786
Seq. No.
Seq. ID
                  LIB36-011-Q2-E2-G11
Method
                  BLASTX
                  g115390
NCBI GI
                  173
BLAST score
                  3.0e-12
E value
                  127
Match length
% identity
                   37
                  SQUIDULIN (OPTIC LOBE CALCIUM-BINDING PROTEIN) (SCABP)
NCBI Description
                  >gi_102715_pir__A33353 calcium-binding protein - squid
                   (Watasenia scintillans)
                   300787
Seq. No.
                  LIB36-011-Q2-E2-G3
Seq. ID
Method
                  BLASTX
                  q4029330
NCBI GI
                   279
BLAST score
                   7.0e-25
E value
                   89
Match length
                   57
% identity
                  (Y16743) ketol-acid reductoisomerase [Piromyces sp. E2]
NCBI Description
                   300788
Seq. No.
                   LIB36-011-Q2-E2-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g98110
                   382
BLAST score
                   8.0e-37
E value
                   129
Match length
                   56
% identity
                   alpha-amylase (EC 3.2.1.1) - Bacillus circulans
NCBI Description
                   >gi_39412_emb_CAA43194_ (X60779) amylase [Bacillus
                   circulans]
                   300789
Seq. No.
                   LIB36-011-Q2-E2-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q135399
BLAST score
                   440
E value
                   1.0e-43
                   109
Match length
                   73
% identity
                   TUBULIN ALPHA-1 CHAIN >gi 100716 pir__S20758 tubulin
NCBI Description
                   alpha-1 chain - rice >gi_20379_emb_CAA77988_ (Z11931) alpha
```

```
1 tubulin [Oryza sativa] >gi 1136124_emb CAA62918_ (X91808)
alfa-tubulin [Oryza sativa]
```

LIB36-011-Q2-E2-H5 Seq. ID

BLASTX Method g3152297 NCBI GI 606 BLAST score 4.0e-63 E value 150 Match length 75 % identity

(Y17297) 6-phosphogluconate dehydrogenase [Cunninghamella NCBI Description

elegans]

300791

Seq. No.

LIB36-011-Q2-E2-H8 Seq. ID

BLASTX Method g3860277 NCBI GI BLAST score 395 E value 2.0e-38 130 Match length 59 % identity

(AC005824) putative ribosomaļ protein L10 [Arabidopsis NCBI Description

thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

300792 Seq. No.

LIB36-012-Q1-E1-A10 Seq. ID

BLASTX Method g131388 NCBI GI 235 BLAST score 9.0e-20 E value 74 Match length 78 % identity

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir_S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi 21844 emb CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

300793 Seq. No.

Seq. ID LIB36-012-Q1-E1-B10

Method BLASTX q2129454 NCBI GI 155 BLAST score E value 3.0e-10 Match length 41 % identity 33

chlorophyll a/b-binding protein (clone GC18 and others) -NCBI Description

Euglena gracilis (var. bacillaris) (fragment)

>gi_510388_emb_CAA43633_ (X61361) light harvesting chlorophyll a /b binding protein of PSII [Euglena gracilis]

300794 Seq. No.

LIB36-012-Q1-E1-D6 Seq. ID



```
BLASTX
Method
                  g3024018
NCBI GI
                  344
BLAST score
                  1.0e-32
E value
                  79
Match length
                  84
% identity
                  INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
NCBI Description
                  >gi 1546919 emb_CAA69225_ (Y07920) translation initiation
                  factor 5A [Zea mays] >gi_2668738 (AF034943) translation
                  initiation factor 5A [Zea mays]
                  300795
Seq. No.
                  LIB36-012-Q1-E1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4580461
                  244
BLAST score
                  1.0e-20
E value
                  97
Match length
                  51
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                  300796
Seq. No.
                  LIB36-012-Q1-E1-F3
Seq. ID
                  BLASTX
Method
                   g133726
NCBI GI
BLAST score
                   181
                   7.0e-14
E value
Match length
                   34
% identity
                   100
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S11 >gi 70943_pir R3RZ11
NCBI Description
                   ribosomal protein S11 - rice chloroplast
                   >gi_12019_emb_CAA33980_ (X15901) ribosomal protein S11
                   [Oryza sativa] >gi_226640_prf__1603356BP ribosomal protein
                   S11 [Oryza sativa]
                   300797
Seq. No.
                   LIB36-013-Q1-E1-B2
Seq. ID
                   BLASTX
Method
                   q3800853
NCBI GI
                   226
BLAST score
                   3.0e-19
E value
Match length
                   53
                   87
% identity
                   (AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase
NCBI Description
                   activase precursor [Zea mays]
                   300798
Seq. No.
                   LIB36-013-Q1-E1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q112994
BLAST score
                   236
                   2.0e-20
E value
```

46 Match length 100 % identity

GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN NCBI Description

>gi_82685_pir__S04536 embryonic abundant protein, glycine-rich - maize >gi 22313_emb_CAA31077_ (X12564)



ABA-inducible gene protein [Zea mays] >gi_226091_prf__1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 300799

Seq. ID LIB36-013-Q1-E1-C4

Method BLASTN
NCBI GI g22312
BLAST score 128
E value 5.0e-66
Match length 167
% identity 94

NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA =

abscisic acid)

Seq. No. 300800

Seq. ID LIB36-013-Q1-E1-C9

Method BLASTX
NCBI GI g1076336
BLAST score 342
E value 3.0e-32
Match length 125
% identity 58

NCBI Description hypothetical protein H1.1flk - Arabidopsis thaliana

(fragment)

Seq. No. 300801

Seq. ID LIB36-013-Q1-E1-E10

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 5.0e-11
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300802

Seq. ID LIB36-013-Q1-E1-F1

Method BLASTN
NCBI GI g596079
BLAST score 120
E value 3.0e-61
Match length 120
% identity 100

NCBI Description Zea mays thiamine biosynthetic enzyme (thi1-2) mRNA,

complete cds

Seq. No. 300803

Seq. ID LIB36-013-Q1-E1-F6

Method BLASTN
NCBI GI g606814
BLAST score 64
E value 1.0e-27
Match length 170
% identity 97

NCBI Description Zea mays Golden Bantam carbonic anhydrase mRNA, complete

cds

NCBI Description

```
300804
Seq. No.
                  LIB36-013-Q1-E1-G10
Seq. ID
Method
                  BLASTX
                  g1708993
NCBI GI
BLAST score
                  425
                  5.0e-42
E value
                  99
Match length
                  82
% identity
                  CYSTATHIONINE BETA-LYASE PRECURSOR (CBL)
NCBI Description
                   (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
                  >gi 2129567_pir__S61429 cystathionine beta-lyase (EC
                  4.4.1.8) - Arabidopsis thaliana >gi_704397 (L40511)
                  cystathionine beta-lyase [Arabidopsis thaliana]
Seq. No.
                  300805
                  LIB36-014-Q1-E1-A8
Seq. ID
                  BLASTX
Method
                  q1122317
NCBI GI
                   208
BLAST score
                   2.0e-16
E value
                   69
Match length
% identity
                   64
                  (X94193) heat shock protein 17.9 [Pennisetum glaucum]
NCBI Description
Seq. No.
                   300806
                   LIB36-014-Q1-E1-B12
Seq. ID
Method
                   BLASTN
                   g2062691
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
                   36
Match length
                   100
% identity
                   Human sodium phosphate transporter (NPT4) mRNA, complete
NCBI Description
                   cds
                   300807
Seq. No.
                   LIB36-014-Q1-E1-D11
Seq. ID
Method
                   BLASTX
                   q2980793
NCBI GI
BLAST score
                   189
                   3.0e-14
E value
                   60
Match length
                   58
% identity
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   300808
Seq. No.
                   LIB36-014-Q1-E1-G10
Seq. ID
Method
                   BLASTX
                   g1708993
NCBI GI
BLAST score
                   208
                   1.0e-16
E value
Match length
                   76
                   54
% identity
                   CYSTATHIONINE BETA-LYASE PRECURSOR (CBL)
```

42372

>gi 2129567_pir__S61429 cystathionine beta-lyase (EC

(BETA-CYSTATHIONASE) (CYSTEINE LYASE)



4.4.1.8) - Arabidopsis thaliana >gi_704397 (L40511) cystathionine beta-lyase [Arabidopsis thaliana]

300809 Seq. No. LIB36-015-Q1-E1-A4 Seq. ID Method BLASTX g4585972 NCBI GI BLAST score 209 9.0e-17 E value 113 Match length 35 % identity NCBI Description (AC005287) Putative ATPase [Arabidopsis thaliana] Seq. No. 300810 LIB36-015-Q1-E1-B4 Seq. ID BLASTX Method g3885886 NCBI GI 545 BLAST score 6.0e-56 E value 105 Match length 92 % identity (AF093631) Rieske Fe-S precursor protein [Oryza sativa] NCBI Description 300811 Seq. No. LIB36-015-Q1-E1-C1 Seq. ID BLASTN Method NCBI GI g829147 120 BLAST score 3.0e-61 E value 183 Match length 92 % identity NCBI Description Z.mays gene for cyclophilin 300812 Seq. No. LIB36-015-Q1-E1-C2 Seq. ID Method BLASTX g548603 NCBI GI 152 BLAST score 2.0e-10 E value Match length 53 62 % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR NCBI Description (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi 478404 pir JQ2247 photosystem I chain D precursor barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare] 300813 Seq. No. LIB36-015-Q1-E1-C5 Seq. ID Method BLASTN NCBI GI g2062705 BLAST score 36 E value 6.0e-11 Match length 48 67 % identity

Seq. No.

300814

42373

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

```
LIB36-015-Q1-E1-F2
Seq. ID
                  BLASTX
Method
                  g1632831
NCBI GI
                  157
BLAST score
                  4.0e-13
E value
                  71
Match length
                  61
% identity
                  (Z49698) orf [Ricinus communis]
NCBI Description
                  300815
Seq. No.
                  LIB36-015-Q1-E1-G6
Seq. ID
                  BLASTX
Method
                  g294845
NCBI GI
                  175
BLAST score
E value
                  6.0e-13
Match length
                  58
% identity
                   57
                  (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                  H65-7052]
                  300816
Seq. No.
                  LIB36-015-Q1-E1-G8
Seq. ID
                  BLASTX
Method
                  g312179
NCBI GI
                   240
BLAST score
                   3.0e-20
E value
                   95
Match length
% identity
                   55
                   (X73151) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                   (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
                   glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                   >gi_1185554 (U45858) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays]
                   300817
Seq. No.
                   LIB36-016-Q1-E1-C12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g559531
BLAST score
                   57
                   9.0e-24
E value
Match length
                   105
                   89
% identity
NCBI Description Z.mays mRNA for cysteine proteinase
                   300818
Seq. No.
                   LIB36-016-Q2-E2-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2062169
BLAST score
                   290
                   5.0e-26
E value
```

Match length

NCBI Description

% identity

Seq. ID LIB36-016-Q2-E2-D12

123

thaliana]

(ACO01645) ABC transporter (PDR5-like) isolog [Arabidopsis

Seq. ID



```
BLASTX
Method
                  g2062169
NCBI GI
                  141
BLAST score
                  6.0e-09
E value
                  34
Match length
                  65
% identity
                  (ACO01645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                  thaliana]
                  300820
Seq. No.
                  LIB36-017-Q1-E1-B3
Seq. ID
                  BLASTX
Method
                  q1707928
NCBI GI
                  358
BLAST score
E value
                  5.0e-34
Match length
                  87
                  84
% identity
                  GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 2
NCBI Description
                  PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
                  PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE
                  ADENYL TRANSFERASE) >gi 1076806_pir__S49439
                  glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
                  maize >gi_558365_emb_CAA86227_ (Z38111) ADP-glucose
                  pyrophosphorylase [Zea mays]
Seq. No.
                  300821
                  LIB36-017-Q1-E1-B4
Seq. ID
Method
                  BLASTN
                  g2832242
NCBI GI
                  76
BLAST score
                  5.0e-35
E value
Match length
                  160
                  87
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                  300822
Seq. No.
                  LIB36-017-Q1-E1-C1
Seq. ID
Method
                  BLASTN
                  g3819189
NCBI GI
                  44
BLAST score
                  2.0e-15
E value
                  76
Match length
                  91
% identity
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0654
                  300823
Seq. No.
                  LIB36-017-Q1-E1-F10
Seq. ID
Method
                  BLASTX
                  g4468817
NCBI GI
BLAST score
                   207
E value
                   2.0e-16
Match length
                   44
                   84
% identity
                  (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   300824
```

LIB36-017-Q1-E1-F7



```
BLASŢX
    Method
                       g115786
    NCBI GI
    BLAST score
                       686
                       2.0e-72
    E value
    Match length
                       132
                       95
    % identity
    NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                       (CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding
                       protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
- 1/4<u>0</u>0
                       300825
    Seq. No.
                       LIB36-017-Q1-E1-F8
    Seq. ID
    Method
                       BLASTX
                       g2997591
    NCBI GI
    BLAST score
                       299
    E value
                       4.0e-27
    Match length
                       63
    % identity
                       90
                       (AF020814) glucose-6-phosphate/phosphate-translocator
    NCBI Description
                       precursor [Pisum sativum]
                       300826
    Seq. No.
                       LIB36-017-Q1-E1-H8
    Seq. ID
                       BLASTN
    Method
                       g311236
    NCBI GI
    BLAST score
                       71
                       1.0e-31
    E value
                       119
    Match length
    % identity
                       92
    NCBI Description Z.mays mRNA for ATPase (delta subunit)
                       300827
    Seq. No.
                       LIB36-018-Q1-E1-D3
    Seq. ID
    Method
                       BLASTX
                       g2980779
    NCBI GI
    BLAST score
                       252
                       7.0e-22
    E value
    Match length
                       84
                       60
     % identity
                       (AL022198) putative protein [Arabidopsis thaliana]
    NCBI Description
    Seq. No.
                       300828
                       LIB36-018-Q1-E1-D6
    Seq. ID
                       BLASTX
    Method
                       g1871187
    NCBI GI
                       159
    BLAST score
                       4.0e-11
    E value
                       42
    Match length
                       74
     % identity
                       (U90439) unknown protein [Arabidopsis thaliana]
     NCBI Description
     Seq. No.
                       300829
                       LIB36-018-Q1-E1-D7
     Seq. ID
                       BLASTN
     Method
```

g22378

174

NCBI GI BLAST score

2.0e-93 E value 182 Match length % identity NCBI Description Z.mays gene for nucleic acid binding protein 300830 Seq. No. LIB36-018-Q1-E1-F9 Seq. ID BLASTX Method g464981 NCBI GI BLAST score 248 3.0e-21 E value 47 Match length 98 % identity UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN NCBI Description LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum] 300831 Seq. No. LIB36-018-Q1-E1-G3 Seq. ID BLASTX Method g1209756 NCBI GI 171 BLAST score 4.0e-12 E value 40 Match length 75 % identity (U43629) integral membrane protein [Beta vulgaris] NCBI Description 300832 Seq. No. LIB36-018-Q1-E1-G6 Seq. ID

Method BLASTX
NCBI GI g3885896
BLAST score 169
E value 4.0e-12
Match length 72
% identity 51

NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 300833

Seq. ID LIB36-018-Q1-E1-H8

Method BLASTX
NCBI GI 94322323
BLAST score 180
E value 3.0e-13
Match length 116
% identity 34

NCBI Description (AF080543) amino acid transporter [Nepenthes alata]

Seq. No. 300834

Seq. ID LIB36-019-Q1-E1-A8

Method BLASTX
NCBI GI g482311
BLAST score 161
E value 8.0e-18
Match length 73
% identity 70

NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving



complex protein 1 [Oryza sativa]

 Seq. No.
 300835

 Seq. ID
 LIB36-019-Q1-E1-B9

 Method
 BLASTX

 NCBI GI
 g131388

NCBI GI g131388
BLAST score 329
E value 1.0e-30
Match length 94
% identity 81

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 300836

Seq. ID LIB36-019-Q1-E1-D5

Method BLASTX
NCBI GI g115786
BLAST score 358
E value 5.0e-34
Match length 106
% identity 71

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB) (LHCP) >gi_82680_pir_ A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea

mays]

Seq. No. 300837

Seq. ID LIB36-019-Q1-E1-G12

Method BLASTN
NCBI GI 9758352
BLAST score 252
E value 1.0e-139
Match length 287
% identity 97

NCBI Description Z.mays mRNA for cysteine synthase

Seq. No. 300838

Seq. ID LIB36-019-Q1-E1-H6

Method BLASTX
NCBI GI g3885886
BLAST score 378
E value 2.0e-36
Match length 99

% identity 81

NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 300839

Seq. ID LIB36-020-Q1-E1-A5

Method BLASTX
NCBI GI g2826844
BLAST score 212
E value 6.0e-17



```
Match length
                  60
% identity
                  62
                  (AJ002237) loxc homologue [Lycopersicon esculentum]
NCBI Description
                  300840
Seq. No.
                  LIB36-020-Q1-E1-A8
Seq. ID
                  BLASTX
Method
                  g3882356
NCBI GI
BLAST score
                  268
                  1.0e-23
E value
                  103
Match length
                  52
% identity
NCBI Description (U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis
                  thaliana]
                  300841
Seq. No.
                  LIB36-020-Q1-E1-E2
Seq. ID
                  BLASTX
Method
                  q1709846
NCBI GI
                  323
BLAST score
                  5.0e-30
E value
                  89
Match length
                  43
% identity
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336)
NCBI Description
                  22 kDa component of photosystem II [Lycopersicon
                  esculentum]
                  300842
Seq. No.
                  LIB36-020-Q1-E1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4585882
BLAST score
                  661
                  1.0e-69
E value
                  133
Match length
                  89
% identity
                  (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   300843
Seq. No.
                  LIB36-020-Q1-E1-G10
Seq. ID
                  BLASTX
Method
                   g1658313
NCBI GI
BLAST score
                   360
E value
                   2.0e-34
                   98
Match length
                   39
% identity
NCBI Description (Y08987) osr40g2 [Oryza sativa]
                   300844
Seq. No.
                   LIB36-020-Q1-E1-G12
Seq. ID
Method
                   BLASTN
                   q902200
NCBI GI
                   302
BLAST score
E value
                   1.0e-169
Match length
                   402
% identity
NCBI Description Z.mays complete chloroplast genome
```

E value

Match length

% identity



```
300845
Seq. No.
                  LIB36-020-Q1-E1-G5
Seq. ID
Method
                  BLASTX
                  g115771
NCBI GI
                  736
BLAST score
                  2.0e-78
E value
                  141
Match length
                  99
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi 22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding
                  preprotein (AA 1 - 262) [Zea mays]
Seq. No.
                  300846
                  LIB36-021-Q1-E1-D2
Seq. ID
                  BLASTX
Method
                  q1261917
NCBI GI
                  285
BLAST score
                  1.0e-25
E value
Match length
                  76
% identity
                  (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
NCBI Description
Seq. No.
                  300847
                  LIB36-021-Q1-E1-F4
Seq. ID
Method
                  BLASTX
                  g2911078
NCBI GI
BLAST score
                  145
                  3.0e-09
E value
Match length
                  46
                  61
% identity
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                  300848
Seq. No.
                  LIB36-021-Q1-E1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g122022
                  192
BLAST score
                   9.0e-15
E value
Match length
                   86
                   53
% identity
                  HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat
NCBI Description
                   >gi 21801 emb CAA42530 (X59873) histone H2B [Triticum
                   aestivum]
                   300849
Seq. No.
                   LIB36-021-Q1-E1-G5
Seq. ID
Method
                   BLASTN
                   g1617470
NCBI GI
                   186
BLAST score
```

NCBI Description Z.diploperennis DNA for Grandel-4 retrotransposon

1.0e-100

301



```
300850
Seq. No.
                    LIB36-021-Q1-E1-G6
 Seq. ID
 Method
                    BLASTN
                    g3821780
 NCBI GI
                    37
 BLAST score
                    2.0e-11
 E value
                    49
 Match length
                    67
 % identity
 NCBI Description Xenopus laevis cDNA clone 27A6-1
                    300851
 Seq. No.
                    LIB36-022-Q1-E1-E3
 Seq. ID
                    BLASTN
 Method
                    g1673455
 NCBI GI
 BLAST score
                    164
                    2.0e-87
 E value
                    181
 Match length
                    98
  % identity
 NCBI Description Z.mays rubisco small subunit gene
                    300852
  Seq. No.
                    LIB36-022-Q1-E1-F7
  Seq. ID
                    {\tt BLASTN}
 Method
                    g236729
  NCBI GI
  BLAST score
                    283
                    1.0e-158
  E value
                    348
  Match length
                    95
  % identity
  NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
                    300853
  Seq. No.
                    LIB36-022-Q1-E1-G5
  Seq. ID
                    BLASTN
  Method
  NCBI GI
                    g483411
  BLAST score
                    229
                    1.0e-126
  E value
                    354
  Match length
  % identity
                     96
                    Zea Mays calmodulin-binding protein mRNA, 3'end
  NCBI Description
                     300854
  Seq. No.
                    LIB36-022-Q1-E1-H3
  Seq. ID
                    BLASTX
  Method
                     q132147
  NCBI GI
  BLAST score
                     593
                     1.0e-61
  E value
  Match length
                     112
                     100
  % identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
  NCBI Description
                     (RUBISCO SMALL SUBUNIT) >gi 68089 pir_ RKZMS
                     ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                     precursor - maize >gi_22474_emb_CAA29784_ (X06535)
                     ribulose-1,5-bisphosphate carboxylase
                                                            (RuBPC) precursor
                     [Zea mays] >gi 217964 dbj_BAA00120_ (D00170) ribulose
                     1,5-bisphosphate carboxylase small subunit [Zea mays]
                     >gi_359512_prf__1312317A ribulosebisphosphate carboxylase
```

[Zea mays]

```
Seq. No.
                  300855
                  LIB83-001-Q1-E1-B11
Seq. ID
Method
                  BLASTX
                  g1931639
NCBI GI
BLAST score
                  498
                  2.0e-50
E value
                  141
Match length
                  66
% identity
                  (U95973) lysophospholipase isolog [Arabidopsis thaliana]
NCBI Description
                  300856
Seq. No.
                  LIB83-001-Q1-E1-B12
Seq. ID
                  BLASTN
Method
NCBI GI
                  g236729
                  138
BLAST score
E value
                   9.0e-72
                  180
Match length
                   95
% identity
NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
                   300857
Seq. No.
                  LIB83-001-Q1-E1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1172861
BLAST score
                   350
                   2.0e-33
E value
Match length
                   66
% identity
                   100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR
NCBI Description
                   (RUBISCO LARGE SUBUNIT) >gi_1363613_pir__S58560
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) large chain
                   - maize chloroplast >gi 18036 emb CAA78027_ (Z11973)
                   Ribulose bisphosphate carboxylase [Zea mays]
                   >gi 902230 emb_CAA60294_ (X86563) rubisco large subunit
                   [Zea mays]
                   300858
Seq. No.
                   LIB83-001-Q1-E1-G1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g311236
                   80
BLAST score
                   2.0e-37
E value
                   142
Match length
                   89
% identity
NCBI Description Z.mays mRNA for ATPase (delta subunit)
                   300859
Seq. No.
                   LIB83-001-Q1-E1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4415938
BLAST score
                   193
E value
                   9.0e-21
                   87
Match length
                   56
% identity
NCBI Description
                  (AC006418) unknown protein [Arabidopsis thaliana]
```



```
Seq. No.
                   300860
                   LIB83-002-Q1-E1-B9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
                   1.0e-10
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                    300861
Seq. No.
                   LIB83-002-Q1-E1-C11
Seq. ID
Method
                   BLASTX
                    g3885886
NCBI GI
BLAST score
                    353
                    2.0e-36
E value
                    94
Match length
% identity
                    81
                   (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
NCBI Description
                    300862
Seq. No.
                    LIB83-002-Q1-E1-D3
Seq. ID
                    BLASTN
Method
NCBI GI
                    g3821780
BLAST score
                    36
E value
                    1.0e-10
                    46
Match length
                    66
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                    300863
Seq. No.
                    LIB83-002-Q1-E1-E11
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4455323
BLAST score
                    250
E value
                    2.0e-21
Match length
                    124
% identity
                    43
                    (AL035525) aminopeptidase-like protein [Arabidopsis
NCBI Description
                    thaliana]
                    300864
Seq. No.
                    LIB83-002-Q1-E1-E8
Seq. ID
                    BLASTX
Method
NCBI GI
                    q115771
BLAST score
                    528
                    5.0e-54
E value
Match length
                    117
% identity
                    87
                    CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                    (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll a/b-binding protein precursor - maize
                    >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]
```

Seq. ID LIB83-002-Q1-E1-F4



```
Method
                  BLASTN
NCBI GI
                  q168527
BLAST score
                  115
                  4.0e-58
E value
                  124
Match length
                  98
% identity
NCBI Description Maize NADP-dependent malic enzyme (Mel) mRNA, complete cds
                  300866
Seq. No.
                  LIB83-002-Q1-E1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827002
BLAST score
                  557
                  2.0e-57
E value
                  125
Match length
% identity
                  84
NCBI Description (AF005993) HSP70 [Triticum aestivum]
                  300867
Seq. No.
                  LIB83-002-Q1-E1-G1
Seq. ID
Method
                  BLASTX
                  g3249064
NCBI GI
BLAST score
                  438
                  2.0e-43
E value
Match length
                  132
                  59
% identity
                  (AC004473) Strong similarity to trehalose-6-phosphate
NCBI Description
                  synthase homolog gb_2245136 from A. thaliana chromosome 4
                  contig gb Z97344. [Arabidopsis thaliana]
                  300868
Seq. No.
                  LIB83-003-Q1-E1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266578
BLAST score
                   241
E value
                   2.0e-20
Match length
                   56
                   77
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 1 >gi 100898 pir S17560
NCBI Description
                   metallothionein-like protein - maize > gi_236730 bbs 57629
                   (S57628) metallothionein homologue [Zea mays, Peptide, 76
                   aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186)
                   metallothionein- like protein [Zea mays]
                   >gi 228095 prf 1717215A metallothionein-like protein [Zea
                  mays]
                   300869
Seq. No.
                   LIB83-003-Q1-E1-A6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
E value
                   9.0e-11
Match length
                   36
                   100
```

NCBI Description Xenopus laevis cDNA clone 27A6-1

% identity



```
Seq. ID
                   LIB83-003-Q1-E1-C10
Method
                   BLASTX
                   q629669
NCBI GI
                   152
BLAST score
                   6.0e-10
E value
                   102
Match length
% identity
NCBI Description hypothetical protein - tomato
                   300871
Seq. No.
                   LIB83-003-Q1-E1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3004565
BLAST score
                   215
                   2.0e-17
E value
Match length
                   67
% identity
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]
                   300872
Seq. No.
                   LIB83-003-Q1-E1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4580461
BLAST score
                   612
                   8.0e-64
E value
Match length
                   142
                   81
% identity
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
                   300873
Seq. No.
                   LIB83-003-Q1-E1-F10
Seq. ID
                   BLASTX
Method
                   q4415937
NCBI GI
BLAST score
                   240
                   3.0e-20
E value
Match length
                   83
% identity
                   59
NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   300874
                   LIB83-003-Q1-E1-F11
Seq. ID
                   BLASTX
Method
                   g131176
NCBI GI
                    351
BLAST score
E value
                    3.0e-33
                    101
Match length
                    73
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
NCBI Description
                    (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                    >qi 72683 pir F1BH4 photosystem I chain IV precursor -
                   barley >gi 19087 emb CAA68782 (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi 226163 prf 1413233A
                    10.8kD photosystem I protein [Hordeum vulgare var.
```

Seq. ID LIB83-003-Q1-E1-F6

distichum]



```
BLASTX
 Method
                    g2499931
NCBI GI
                    296
 BLAST score
                    9.0e-27
 E value
                    77
 Match length
                    74
 % identity
                    ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)
 NCBI Description
                    >gi 2129534_pir__S71272 adenine phosphoribosyltransferase
                    (EC 2.4.2.7) - Arabidopsis thaliana
                    >gi_1321681_emb_CAA65609_ (X96866) adenine
                    phosphoribosyltransferase [Arabidopsis thaliana]
                    300876
  Seq. No.
                    LIB83-003-Q1-E1-H11
  Seq. ID
  Method
                    BLASTX
                    g112994
  NCBI GI
                    194
  BLAST score
                    8.0e-15
  E value
                    46
 Match length
                    91
  % identity
                    GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
  NCBI Description
                    >gi_82685_pir__S04536 embryonic abundant protein,
                    glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                    ABA-inducible gene protein [Zea mays]
                    >gi 226091_prf__1410284A abscisic acid inducible gene [Zea
                    mays]
                    300877
  Seq. No.
                    LIB83-004-Q1-E1-G10
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    g1657851
                    197
  BLAST score
                    4.0e-15
  E value
                    49
  Match length
                    35
  % identity
                    (U73214) cold acclimation protein WCOR518 [Triticum
  NCBI Description
                    aestivum]
                    300878
  Seq. No.
                    LIB83-004-Q1-E2-A11
  Seq. ID
  Method
                    BLASTX
                    g1171864
  NCBI GI
  BLAST score
                    293
  E value
                    2.0e-26
  Match length
                    81
                    70
  % identity
                    NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K
  NCBI Description
                    >gi_902226_emb_CAA60290_ (X86563) ndhK [Zea mays]
                     300879
  Seq. No.
  Seq. ID
                    LIB83-004-Q1-E2-A2
                    BLASTN
  Method
                     q1575129
  NCBI GI
  BLAST score
                     97
```

3.0e-47

197

87

E value Match length

% identity



65

Match length % identity

NCBI Description

```
NCBI Description Zea mays lumenal binding protein cBiPe3 mRNA, complete cds
                  300880
Seq. No.
                  LIB83-004-Q1-E2-C12
Seq. ID
                  BLASTX
Method
                  g132819
NCBI GI
BLAST score
                  277
                  1.0e-24
E value
Match length
                  67
                  72
% identity
                  50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24)
NCBI Description
                  >gi_71307_pir__R5PM24 ribosomal protein L24 precursor,
                  chloroplast - garden pea >gi 20873_emb_CAA32185_ (X14020)
                  CL24 ribosomal preprotein (AA -39 to 155) [Pisum sativum]
                  300881
Seq. No.
                  LIB83-004-Q1-E2-G11
Seq. ID
Method
                  BLASTX
                  g481190
NCBI GI
BLAST score
                  198
                  1.0e-15
E value
                  84
Match length
                   54
% identity
                  plastocyanin precursor - barley >gi_22705_emb_CAA68696_
NCBI Description
                   (Y00704) plastocyanin precursor [Hordeum vulgare]
                   >gi_431920_emb_CAA82201_ (Z28347) plastocyanin [Hordeum
                   vulgare]
                   300882
Seq. No.
                  LIB83-005-Q1-E1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   7.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   300883
Seq. No.
                   LIB83-005-Q1-E1-B5
Seq. ID
Method
                   BLASTX
                   g3297823
NCBI GI
BLAST score
                   354
E value
                   1.0e-33
                   125
Match length
% identity
                   50
                  (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
                   300884
Seq. No.
                   LIB83-005-Q1-E1-D11
Seq. ID
Method
                   BLASTX
                   q1399183
NCBI GI
BLAST score
                   279
                   8.0e-25
E value
```

42387

(U50739) Lycopene beta cyclase [Arabidopsis thaliana]

```
Seq. No.
                   300885
Seq. ID
                  LIB83-005-Q1-E1-D2
Method
                  BLASTX
NCBI GI
                   q4585576
BLAST score
                   257
E value
                   8.0e-36
Match length
                   108
% identity
NCBI Description
                   (AF134051) fructose-1,6-bisphosphatase precursor [Solanum
                   tuberosum]
Seq. No.
                   300886
Seq. ID
                   LIB83-005-Q1-E1-E5
Method
                  BLASTN
                   q405634
NCBI GI
BLAST score
                   191
                   1.0e-103
E value
                   207
Match length
                   99
% identity
NCBI Description Z.mays zmcpt mRNA triose phosphate/phosphate translocator
                   300887
Seq. No.
Seq. ID
                   LIB83-005-Q1-E1-E8
Method
                   BLASTX
NCBI GI
                   q3367519
BLAST score
                   537
                   5.0e-55
E value
Match length
                   134
                   78
% identity
                   (AC004392) Contains similarity to gb U51898
NCBI Description
                   Ca2+-independent phospholipase A2 from Rattus norvegicus.
                   [Arabidopsis thaliana]
Seq. No.
                   300888
                   LIB83-005-Q1-E1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2460251
BLAST score
                   190
                   2.0e-14
E value
Match length
                   41
% identity
                   93
                  (AF020791) ferrochelatase [Hordeum vulgare]
NCBI Description
                   300889
Seq. No.
                   LIB83-005-Q1-E1-G1
Seq. ID
Method
                   BLASTX
                   g3885896
NCBI GI
```

Method BLASTX
NCBI GI g388589
BLAST score 354
E value 1.0e-33
Match length 106
% identity 67

NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 300890

Seq. ID LIB83-005-Q1-E1-H10

Method BLASTX



```
q2500130
NCBI GI
BLAST score
                  518
E value
                  8.0e-53
Match length
                  136
% identity
                  73
                  THIOREDOXIN REDUCTASE 2 (NADPH-DEPENDENT THIOREDOXIN
NCBI Description
                  REDUCTASE 2) (NTR 2) >gi 1076358 pir S44026 thioredoxin
                  reductase (NADPH) (EC 1.6.4.5) A - Arabidopsis thaliana
                  (fragment) >gi 468524 emb CAA80655 (Z23108) NADPH
                  thioredoxin reductase [Arabidopsis thaliana]
Seq. No.
                  300891
Seq. ID
                  LIB83-005-Q1-E1-H11
Method
                  BLASTX
NCBI GI
                  q4038043
BLAST score
                  256
                  4.0e-22
E value
Match length
                  110
% identity
                  (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  300892
Seq. ID
                  LIB83-006-Q1-E1-A5
Method
                  BLASTX
NCBI GI
                  q2501190
BLAST score
                  307
E value
                  6.0e-31
Match length
                  106
% identity
                  72
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                  >gi 2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
                  - maize >gi 596080 (U17351) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  300893
                  LIB83-006-Q1-E1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3252866
BLAST score
                  209
                  1.0e-16
E value
Match length
                  116
                  37
% identity
NCBI Description (AF033535) putative zinc transporter [Arabidopsis thaliana]
```

Seq. ID LIB83-006-Q1-E1-F7

Method BLASTX
NCBI GI g2696227
BLAST score 438
E value 2.0e-43
Match length 98
% identity 84

NCBI Description (D55711) chitinase [Oryza sativa]

Seq. No. 300895

Seq. ID LIB83-006-Q1-E1-G9

% identity

48



```
BLASTX
Method
                  g2369690
NCBI GI
BLAST score
                  219
                  8.0e-18
E value
                  89
Match length
                  55
% identity
NCBI Description (Y11988) FPF1 protein [Arabidopsis thaliana]
                  300896
Seq. No.
                  LIB83-006-Q1-E1-H11
Seq. ID
                  BLASTX
Method
                   g1648931
NCBI GI
                   607
BLAST score
                   3.0e-63
E value
Match length
                   137
% identity
                   87
                  (X92428) HOX1B protein [Zea mays]
NCBI Description
                   300897
Seq. No.
                   LIB83-007-Q1-E1-A10
Seq. ID
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   35
                   3.0e-10
E value
                   35
Match length
% identity
                   100
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   300898
Seq. No.
                   LIB83-007-Q1-E1-A11
Seq. ID
                   BLASTX
Method
                   g3004555
NCBI GI
                   143
BLAST score
                   7.0e-09
E value
Match length
                   135
                   27
% identity
                   (AC003673) similar to salt inducible protein [Arabidopsis
NCBI Description
                   thaliana]
                   300899
Seq. No.
                   LIB83-007-Q1-E1-B7
Seq. ID
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   300900
Seq. No.
Seq. ID
                   LIB83-007-Q1-E1-C2
Method
                   BLASTN
NCBI GI
                   q4416300
BLAST score
                   132
                   2.0e-68
E value
Match length
                   178
```



NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No. 300901

Seq. ID LIB83-007-Q1-E1-D7

Method BLASTN
NCBI GI g3821780
BLAST score 35
E value 3.0e-10
Match length 35
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300902

Seq. ID LIB83-007-Q1-E1-E3

Method BLASTX
NCBI GI g2149640
BLAST score 156
E value 1.0e-10
Match length 63
% identity 56

NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No. 300903

Seq. ID LIB83-007-Q1-E1-E7

Method BLASTX
NCBI GI g3885896
BLAST score 174
E value 1.0e-12
Match length 83
% identity 51

NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 300904

Seq. ID LIB83-007-Q1-E1-E8

Method BLASTX
NCBI GI g4539009
BLAST score 313
E value 8.0e-29
Match length 102
% identity 56

NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 300905

Seq. ID LIB83-007-Q1-E1-H4

Method BLASTX
NCBI GI g3242328
BLAST score 326
E value 7.0e-31
Match length 60
% identity 100

NCBI Description (X98083) cinnamoyl-CoA reductase [Zea mays]

Seq. No. 300906

Seq. ID LIB83-008-Q1-E1-B10

Method BLASTN NCBI GI g3041776

```
BLAST score
                   1.0e-18
E value
                   93
Match length
                   88
% identity
                  Oryza sativa mRNA for fructose-1,6-bisphosphatase
NCBI Description
                   (plastidic isoform), complete cds
                   300907
Seq. No.
                  LIB83-008-Q1-E1-B4
Seq. ID
                  BLASTX
Method
                   g4504079
NCBI GI
                   185
BLAST score
                   8.0e-14
E value
                   112
Match length
% identity
                   39
                  UNKNOWN >gi 2706632_dbj_BAA24035_ (AB006969) hGAA1 [Homo
NCBI Description
                   sapiens]
                   300908
Seq. No.
                   LIB83-008-Q1-E1-E1
Seq. ID
Method
                   BLASTN
                   g1816587
NCBI GI
BLAST score
                   61
                   3.0e-26
E value
                   61
Match length
                   100
% identity
                  Zea mays LON2 protease (LON2) mRNA, complete cds
NCBI Description
                   300909
Seq. No.
                   LIB83-008-Q1-E1-E12
Seq. ID
Method
                   BLASTX
                   g1001111
NCBI GI
BLAST score
                   152
                   6.0e-10
E value
Match length
                   115
% identity
                   30
                  (D64001) hypothetical protein [Synechocystis sp.]
NCBI Description
                   300910
Seq. No.
                   LIB83-008-Q1-E1-G6
Seq. ID
Method
                   BLASTN
                   g3282393
NCBI GI
BLAST score
                   38
E value
                   6.0e-12
                                       - 15
Match length
                   122
% identity
                   83
NCBI Description Oryza sativa aie2 mRNA, partial cds
                   300911
Seq. No.
                   LIB83-008-Q1-E1-H10
Seq. ID
Method
                   BLASTN
                   g3821780
NCBI GI
                   35
BLAST score
                   4.0e-10
E value
Match length
                   35
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

NCBI GI



```
300912
Seq. No.
                  LIB83-008-Q1-E1-H12
Seq. ID
Method
                  BLASTX
                  g3643610
NCBI GI
                   353
BLAST score
                   1.0e-33
E value
                   75
Match length
% identity
                   88
                   (AC005395) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   300913
Seq. No.
                   LIB83-008-Q1-E1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2217970
BLAST score
                   189
                   3.0e-14
E value
                   134
Match length
% identity
                   13
NCBI Description (Z97074) p40 [Homo sapiens]
Seq. No.
                   300914
                   LIB83-009-Q1-E1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2062167
BLAST score
                   284
E value
                   2.0e-25
Match length
                   104
% identity
                   54
                   (ACO01645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                   thaliana]
                   300915
Seq. No.
                   LIB83-009-Q1-E1-E10
Seq. ID
Method
                   BLASTX
                   g4544415
NCBI GI
                   196
BLAST score
                   4.0e-15
E value
Match length
                   109
% identity
                   39
                   (AC006955) putative polyprotein [Arabidopsis thaliana]
NCBI Description
                   300916
Seq. No.
                   LIB83-009-Q1-E1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4415919
                   200
BLAST score
                   8.0e-16
E value
Match length
                   56
                   70
% identity
                   (AC006282) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   300917
Seq. No.
                   LIB83-009-Q1-E1-E3
Seq. ID
Method
                   BLASTN
```

42393

g2668741



```
BLAST score
E value
                  2.0e-63
                  244
Match length
                  88
% identity
                  Zea mays glycine-rich RNA binding protein (GRP) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  300918
                  LIB83-009-Q1-E1-G8
Seq. ID
Method
                  BLASTN
                  g4336609
NCBI GI
BLAST score
                  311
E value
                  1.0e-175
Match length
                  376
% identity
                  96
                  Zea mays sigma factor (sig3) mRNA, nuclear gene encoding
NCBI Description
                  chloroplast protein, complete cds
                  300919
Seq. No.
                  LIB83-009-Q1-E1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2326946
BLAST score
                  55
                  4.0e-22
E value
Match length
                  126
% identity
                  93
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29
Seq. No.
                  300920
                  LIB83-010-Q1-E1-A11
Seq. ID
Method
                  BLASTX
                  g1707364
NCBI GI
BLAST score
                  144
                   4.0e-11
E value
Match length
                  50
                  76
% identity
                  (X94626) AATP2 [Arabidopsis thaliana]
NCBI Description
                   300921
Seq. No.
Seq. ID
                  LIB83-010-Q1-E1-A5
Method
                  BLASTX
NCBI GI
                   q3643599
BLAST score
                   540
E value
                   2.0e-55
Match length
                  137
% identity
                   74
                   (AC005395) putative trytophanyl-tRNA synthetase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   300922
```

Seq. ID LIB83-010-Q1-E1-F4

Method BLASTX
NCBI GI g3252866
BLAST score 189
E value 3.0e-15
Match length 74
% identity 61

% identity

100

NCBI Description Xenopus laevis cDNA clone 27A6-1



```
NCBI Description
                  (AF033535) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
                  300923
Seq. ID
                  LIB83-010-Q1-E1-G7
Method
                  BLASTX
                  g2244996
NCBI GI
BLAST score
                  191
                  2.0e-14
E value
Match length
                  44
% identity
                  77
                  (Z97341) similarity to a membrane-associated salt-inducible
NCBI Description
                  protein [Arabidopsis thaliana]
                  300924
Seq. No.
Seq. ID
                  LIB83-011-Q1-E1-A11
Method
                  BLASTX
NCBI GI
                  q2088651
BLAST score
                  232
E value
                  2.0e-19
Match length
                  118
% identity
                  47
                  (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  300925
Seq. ID
                  LIB83-011-Q1-E1-A4
Method
                  BLASTX
NCBI GI
                  g1170660
BLAST score
                  255
E value
                  5.0e-22
Match length
                  79
% identity
                  65
                  MEVALONATE KINASE (MK) >gi 541880 pir S42088 mevalonate
NCBI Description
                  kinase (EC 2.7.1.36) - Arabidopsis thaliana
                  >gi 456614 emb CAA54820 (X77793) mevalonate kinase
                   [Arabidopsis thaliana]
                  300926
Seq. No.
Seq. ID
                  LIB83-011-Q1-E1-B1
Method
                  BLASTX
NCBI GI
                  g549986
BLAST score
                  185
                  2.0e-22
E value
Match length
                  78
% identity
                  72
NCBI Description
                  (U13149) possible apospory-associated protein [Pennisetum
                  ciliare]
                  300927
Seq. No.
Seq. ID
                  LIB83-011-Q1-E1-D9
Method
                  BLASTN
NCBI GI
                  g3821780
                  36
BLAST score
E value
                  8.0e-11
Match length
                  36
```

Method

BLASTX



Seq. No.

300928

```
Seq. ID
                  LIB83-011-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  g3608137
BLAST score
                  182
                  2.0e-13
E value
Match length
                  73
% identity
                   48
                  (AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
                   300929
Seq. No.
Seq. ID
                  LIB83-011-Q1-E1-F6
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
E value
                   9.0e-11
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   300930
                   LIB83-011-Q1-E1-F8
Seq. ID
                   BLASTX
Method
                   g1653230
NCBI GI
                   158
BLAST score
E value
                   1.0e-10
                   55
Match length
% identity
                   (D90912) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   300931
                   LIB83-011-Q1-E1-G11
Seq. ID
Method
                   BLASTX
                   g3426035
NCBI GI
                   153
BLAST score
E value
                   4.0e-10
Match length
                   45
% identity
                   62
                   (AC005168) putative ripening-associated protein
NCBI Description
                   [Arabidopsis thaliana]
                   300932
Seq. No.
                   LIB83-012-Q1-E1-A7
Seq. ID
                   BLASTX
Method
                   g1655536
NCBI GI
BLAST score
                   160
                   5.0e-11
E value
                   69
Match length
                   48
% identity
                   (Y09095) chloride channel [Arabidopsis thaliana]
NCBI Description
                   >gi 1742957 emb CAA96059 (Z71447) CLC-c chloride channel
                   protein [Arabidopsis thaliana]
                   300933
Seq. No.
                   LIB83-012-Q1-E1-B4
Seq. ID
```

BLAST score

E value

146

3.0e-09



```
g4557657
NCBI GI
BLAST score
                  165
                  2.0e-11
E value
Match length
                  101
% identity
                  35
                  immature colon carcinoma transcript 1
NCBI Description
                  >gi 2136011 pir S63540 protein DS 1, 24K - human
                  >qi 1045059 emb CAA57387 (X81788) ICT1 protein [Homo
                  sapiens]
                  300934
Seq. No.
                  LIB83-012-Q1-E1-C5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  36
                  1.0e-10
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  300935
                  LIB83-012-Q1-E1-C9
Seq. ID
Method
                  BLASTX
                  g2224810
NCBI GI
BLAST score
                  394
E value
                  2.0e-38
Match length
                  105
% identity
                  70
                  (Z97022) cysteine proteinase [Hordeum vulgare]
NCBI Description
Seq. No.
                  300936
                  LIB83-012-Q1-E1-D6
Seq. ID
                  BLASTX
Method
                  g1323748
NCBI GI
BLAST score
                  240
                  3.0e-20
E value
                  122
Match length
                   47
% identity
                  (U32430) thiol protease [Triticum aestivum]
NCBI Description
Seq. No.
                  300937
                  LIB83-012-Q1-E1-F7
Seq. ID
Method
                  BLASTX
                  g2760836
NCBI GI
BLAST score
                  191
                   2.0e-14
E value
                  75
Match length
                   51
% identity
                   (AC003105) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   300938
Seq. No.
                  LIB83-012-Q1-E1-G1
Seq. ID
Method
                  BLASTX
                   g3451473
NCBI GI
```



```
Match length
                  44
                  57
% identity
                  (ALO31349) 4-nitrophenylphosphatase [Schizosaccharomyces
NCBI Description
                  pombe]
                  300939
Seq. No.
                  LIB83-012-Q1-E1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4467128
BLAST score
                  221
                  4.0e-18
E value
                  112
Match length
% identity
                  46
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  300940
                  LIB83-013-Q1-E1-A3
Seq. ID
Method
                  BLASTX
                  g2213611
NCBI GI
BLAST score
                  155
E value
                  3.0e-10
                  115
Match length
                  30
% identity
                  (AC000103) F21J9.5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  300941
                  LIB83-013-Q1-E1-B8
Seq. ID
Method
                  BLASTX
                  g3608412
NCBI GI
BLAST score
                  369
                  2.0e-35
E value
Match length
                  118
                  59
% identity
                  (AF079355) protein phosphatase-2c [Mesembryanthemum
NCBI Description
                  crystallinum]
                   300942
Seq. No.
                  LIB83-013-Q1-E1-B9
Seq. ID
Method
                  BLASTN
                   g3821780
NCBI GI
BLAST score
                   36
E value
                   4.0e-11
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   300943
                   LIB83-013-Q1-E1-D5
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g1170949
BLAST score 158
E value 1.0e-10
Match length 105
% identity 34

NCBI Description SERINE/THREONINE-PROTEIN KINASE MHK >gi_481207_pir_ S38327 protein kinase - Arabidopsis thaliana >gi_166811 (L07249)

protein kinase [Arabidopsis thaliana]

E value

5.0e-10



```
300944
Seq. No.
                  LIB83-013-Q1-E1-E10
Seq. ID
Method
                  BLASTX
                  g3201680
NCBI GI
BLAST score
                  246
                  4.0e-21
E value
Match length
                  90
                  57
% identity
NCBI Description (AF060941) extra-large G-protein [Arabidopsis thaliana]
                  300945
Seq. No.
                  LIB83-013-Q1-E1-E11
Seq. ID
Method
                  BLASTX
                  g2809246
NCBI GI
BLAST score
                  363
                  1.0e-34
E value
                  119
Match length
                  56
% identity
NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]
                  300946
Seq. No.
                  LIB83-013-Q1-E1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168527
BLAST score
                  130
                  4.0e-67
E value
Match length
                  144
% identity
                  98
NCBI Description Maize NADP-dependent malic enzyme (Mel) mRNA, complete cds
                  300947
Seq. No.
                  LIB83-013-Q1-E1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1497987
BLAST score
                  548
                  2.0e-56
E value
Match length
                  133
% identity
                  79
NCBI Description (U62798) SCARECROW [Arabidopsis thaliana]
                  300948
Seq. No.
                  LIB83-013-Q1-E1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961383
BLAST score
                  216
E value
                  1.0e-17
                  46
Match length
                  85
% identity
NCBI Description (AL022141) putative protein [Arabidopsis thaliana]
                  300949
Seq. No.
                  LIB83-014-Q1-E1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3212866
BLAST score
                  153
```

% identity

54



```
Match length
                    64
  % identity
                    53
                    (AC004005) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    300950
 Seq. No.
                    LIB83-014-Q1-E1-C5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4262146
 BLAST score
                    154
                    4.0e-10
 E value
 Match length
                    111
  % identity
                    32
                    (AC005275) predicted protein of unknown function
 NCBI Description
                    [Arabidopsis thaliana]
                    300951
 Seq. No.
                    LIB83-014-Q1-E1-C8
  Seq. ID
 Method
                    BLASTX
                    g132918
 NCBI GI
 BLAST score
                    202
                    8.0e-16
 E value
 Match length
                    56
                    79
  % identity
  NCBI Description
                    50S RIBOSOMAL PROTEIN L35, CHLOROPLAST PRECURSOR (CL35)
                    >gi_81486_pir__A36107 ribosomal protein L35 precursor,
                    chloroplast - spinach >gi 170139 (M60449) ribosomal protein
                    L35 [Spinacia oleracea]
                    300952
  Seq. No.
  Seq. ID
                    LIB83-014-Q1-E1-D6
 Method
                    BLASTN
                    g1159878
  NCBI GI
  BLAST score
                    48
  E value
                    7.0e-18
  Match length
                    80
  % identity
                    90
  NCBI Description A.fatua mRNA for DNA-binding protein (clone ABF2)
                    300953
  Seq. No.
  Seq. ID
                    LIB83-014-Q1-E1-D8
  Method
                    BLASTX
  NCBI GI
                    q4115388
  BLAST score
                    488
  E value
                    3.0e-49
  Match length
                    133
  % identity
                    68
                    (AC005967) putative prolylcarboxypeptidase [Arabidopsis
  NCBI Description
                    thaliana]
  Seq. No.
                    300954
  Seq. ID
                    LIB83-014-Q1-E1-E11
  Method
                    BLASTX
  NCBI GI
                    q4099921
  BLAST score
                    209
  E value
                    9.0e-17
                    72
  Match length
```





```
(U91982) EREBP-3 homolog [Stylosanthes hamata]
NCBI Description
                  300955
Seq. No.
                  LIB83-014-Q1-E1-E2
Seq. ID
Method
                  BLASTX
                  g4376637
NCBI GI
                  195
BLAST score
                  5.0e-15
E value
                  134
Match length
% identity
                  34
NCBI Description (AE001620) tyrosyl tRNA Synthetase [Chlamydia pneumoniae]
                  300956
Seq. No.
                  LIB83-015-Q1-E1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2642158
BLAST score
                  292
                  2.0e-26
E value
                  79
Match length
% identity
                  68
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  300957
Seq. No.
                  LIB83-015-Q1-E1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g825756
BLAST score
                  157
E value
                  2.0e-10
Match length
                  71
% identity
                  51
                  (U12391) beta-galactosidase alpha peptide [Cloning vector
NCBI Description
                  pSport2]
                  300958
Seq. No.
                  LIB83-015-Q1-E1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334150
BLAST score
                  146
E value
                   3.0e-09
Match length
                   43
                   67
% identity
                  MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR
NCBI Description
                   (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2129847_pir__JC4312
                   chlorophyll magnesium chelatase (EC \overline{4.99.-.-}) - soybean
                   chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase
                   subunit (46 kD) [Glycine max]
                   300959
Seq. No.
                  LIB83-015-Q1-E1-D11
Seq. ID
```

Method BLASTN
NCBI GI g296593
BLAST score 52
E value 3.0e-20
Match length 72
% identity 93

NCBI Description H. vulgare pZE40 gene

E value

Match length

2.0e-25

112



```
300960
Seq. No.
                  LIB83-015-Q1-E1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g602292
BLAST score
                  217
                  1.0e-17
E value
                  93
Match length
                  54
% identity
                  (U17987) RCH2 protein [Brassica napus]
NCBI Description
                  300961
Seq. No.
                  LIB83-015-Q1-E1-G6
Seq. ID
                  BLASTX
Method
                  q2406563
NCBI GI
BLAST score
                   356
E value
                  8.0e-34
                  139
Match length
                  18
% identity
                  (U62897) carboxypeptidase D precursor [Rattus norvegicus]
NCBI Description
Seq. No.
                   300962
                   LIB83-015-Q1-E1-H1
Seq. ID
Method
                   BLASTX
                   g3355474
NCBI GI
BLAST score
                   284
E value
                   2.0e-25
                   92
Match length
% identity
                   59
                  (AC004218) unknown protein [Arabidopsis thaliana]
NCBI Description
                   300963
Seq. No.
                   LIB83-016-Q1-E1-C1
Seq. ID
                   BLASTX
Method
                   g2213632
NCBI GI
BLAST score
                   498
                   2.0e-50
E value
                   127
Match length
                   67
% identity
                  (AC000103) F21J9.24 [Arabidopsis thaliana]
NCBI Description
                   300964
Seq. No.
                   LIB83-016-Q1-E1-C2
Seq. ID
                   BLASTX
Method
                   g483410
NCBI GI
BLAST score
                   195
E value
                   6.0e-15
                   74
Match length
                   57
% identity
                  (L01496) calmodulin-binding protein [Zea mays]
NCBI Description
Seq. No.
                   300965
                   LIB83-016-Q1-E1-H6
Seq. ID
Method
                   BLASTX
                   q1838961
NCBI GI
BLAST score
                   284
```



% identity (Y10994) acyl carrier protein [Casuarina glauca] NCBI Description 300966 Seq. No. LIB84-001-Q1-E1-A4 Seq. ID Method BLASTX g4056456 NCBI GI 258 BLAST score 2.0e-22 E value Match length 74 70 % identity NCBI Description (AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and qb AA395179 come from this gene. [Arabidopsis thaliana] 300967 Seq. No. Seq. ID LIB84-001-Q1-E1-E9 Method BLASTX NCBI GI g3024440 BLAST score 217 4.0e-20 E value 76 Match length 72 % identity PROTEASOME DELTA CHAIN PRECURSOR (MULTICATALYTIC NCBI Description ENDOPEPTIDASE COMPLEX DELTA CHAIN) >gi 1743356_emb CAA70699_ (Y09505) proteasome delta subunit [Nicotiana tabacum] Seq. No. 300968 LIB84-001-Q1-E1-G11 Seq. ID Method BLASTX NCBI GI q2673913 BLAST score 200 2.0e-15 E value Match length 128 % identity 37 (AC002561) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 300969 Seq. ID LIB84-003-Q1-E1-B11 Method BLASTX NCBI GI q4139264 BLAST score 157 E value 2.0e-13 Match length 69 % identity 61 NCBI Description (AF111812) actin [Brassica napus] Seq. No. 300970

Seq. ID LIB84-003-Q1-E1-B7 Method BLASTX

NCBI GI g1652591
BLAST score 201
E value 1.0e-15
Match length 66
% identity 56



NCBI Description (D90906) chloroplast import-associated channel IAP75 [Synechocystis sp.]

Seq. No. 300971
Seq. ID LIB84-003-Q1-E1-C10

Method BLASTX
NCBI GI g115771
BLAST score 412
E value 1.0e-40
Match length 80
% identity 93

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll

a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 300972

Seq. ID LIB84-003-Q1-E1-D12

Method BLASTX
NCBI GI g3335355
BLAST score 162
E value 1.0e-11
Match length 45
% identity 24

NCBI Description (AC004512) Match to polyubiquitin DNA gb_L05401 from A.

thaliana. Contains insertion of mitochondrial NADH

dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene with an expressed insert. EST gb_AA586248 comes from this

region. [Arabi

Seq. No. 300973

Seq. ID LIB84-003-Q1-E1-D2

Method BLASTX
NCBI GI g4220592
BLAST score 364
E value 9.0e-35
Match length 141
% identity 53

NCBI Description (AB010086) nicotianamine synthase 1 [Hordeum vulgare]

Seq. No. 300974

Seq. ID LIB84-003-Q1-E1-E6

Method BLASTX
NCBI GI g4455287
BLAST score 184
E value 7.0e-14
Match length 61
% identity 61

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 300975

Seq. ID LIB84-003-Q1-E1-F10

Method BLASTN
NCBI GI g12474
BLAST score 114
E value 3.0e-57



Match length 86 % identity

NCBI Description Zea mays chloroplast tV-UAC gene for transfer RNA-Val (UAC)

Seq. No.

300976

Seq. ID

LIB84-003-Q1-E1-G11

Method NCBI GI BLASTX g3377950

BLAST score E value

326

Match length % identity

2.0e-30 113 55

NCBI Description

(AJ009830) cysteine proteinase precursor, AN11 [Ananas

comosus]

Seq. No.

300977

Seq. ID

LIB84-003-Q1-E1-G7

Method NCBI GI BLAST score BLASTX g1877221 267 2.0e-23

E value Match length % identity

109 51

NCBI Description

(Z83834) Mlo [Hordeum vulgare] >gi 2894377 emb CAA74909.1

(Y14573) Mlo protein [Hordeum vulgare]

Seq. No.

300978

Seq. ID

LIB84-003-Q1-E1-H10

Method BLASTN g902200 NCBI GI BLAST score 156 E value 2.0e-82 354

Match length 99 % identity

NCBI Description Z.mays complete chloroplast genome

Seq. No.

300979

Seq. ID

LIB84-004-Q1-E1-A2

Method NCBI GI BLAST score BLASTX g132147 326

E value Match length % identity

2.0e-30 90 72

NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_68089_pir__RKZMS

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - maize >gi_22474_emb_CAA29784_ (X06535)

ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi 359512 prf 1312317A ribulosebisphosphate carboxylase

[Zea mays]

Seq. No.

300980

Seq. ID

LIB84-004-Q1-E1-A5

Method BLASTX



```
g3024762
NCBI GI
                  166
BLAST score
                  4.0e-16
E value
Match length
                  130
% identity
                  41
                  TRNA PSEUDOURIDINE SYNTHASE B (TRNA PSEUDOURIDINE 55
NCBI Description
                  SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE)
                  (URACIL HYDROLYASE) >gi 2624315 emb CAA15588 (AL008967)
                  truB. [Mycobacterium tuberculosis]
                  300981
Seq. No.
                  LIB84-004-Q1-E1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  432
E value
                  1.0e-42
Match length
                  86
% identity
                  98
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
Seq. No.
                  300982
                  LIB84-004-Q1-E1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g¥352200
BLAST score
                  185
E value
                  2.0e-14
Match length
                  69
% identity
                  75
                  CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
NCBI Description
                  >gi 480909 pir S37497 triose
                  phosphate/3-phosphoglycerate/phosphate translocator - maize
                  >gi 405635 emb CAA81349 (Z26595) triose
                  phosphate/phosphate translocator [Zea mays]
                  300983
Seq. No.
                  LIB84-004-Q1-E1-D9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g19090
BLAST score
                   46
                  1.0e-16
E value
Match length
                  98
                  87
% identity
NCBI Description H.vulgare PsaG mRNA
                   300984
Seq. No.
Seq. ID
                  LIB84-004-Q1-E1-F3
Method
                  BLASTN
NCBI GI
                  g596077
BLAST score
                   114
E value
                   2.0e-57
Match length
                   298
% identity
                   85
```

NCBI Description

Zea mays thiamine biosynthetic enzyme (thil-1) mRNA,

complete cds

Seq. No.

300985

Seq. ID

LIB84-004-Q1-E1-F7

Match length

% identity

81

78

```
BLASTX
Method
                  g3152613
NCBI GI
BLAST score
                   271
E value
                   7.0e-24
Match length
                   127
% identity
                  (AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   300986
Seq. No.
Seq. ID
                   LIB84-004-Q1-E1-G12
Method
                   BLASTX
NCBI GI
                   g3925363
BLAST score
                   379
                   1.0e-43
E value
Match length
                   127
% identity
                   76
                   (AF067961) homeodomain protein [Malus domestica]
NCBI Description
                   300987
Seq. No.
                   LIB84-005-Q1-E1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4508077
BLAST score
                   177
E value
                   2.0e-13
Match length
                   49
% identity
                   (AC005882) 62114 [Arabidopsis thaliana]
NCBI Description
                   300988
Seq. No.
                   LIB84-005-Q1-E1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455309
BLAST score
                   223
E value
                   3.0e-18
Match length
                   70
% identity
                   61
                   (AL035528) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   300989
Seq. No.
                   LIB84-005-Q1-E1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4115536
BLAST score
                   345
                   1.0e-32 -
E value
Match length
                   121
                   57
% identity
                   (AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna
NCBI Description
                   mungo]
                   300990
Seq. No.
                   LIB84-006-Q1-E1-A3
Seq. ID
Method
                   BLASTX
                   q1800219
NCBI GI
BLAST score
                   327
                   7.0e-31
E value
```



```
NCBI Description (U56731) phytochrome C [Sorghum bicolor]
Seq. No.
                  300991
Seq. ID
                  LIB84-006-Q1-E1-B3
Method
                  BLASTX
NCBI GI
                  g4454472
BLAST score
                  169
E value
                  2.0e-12
Match length
                  54
% identity
                  57
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  300992
                  LIB84-006-Q1-E1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174745
BLAST score
                  262
E value
                  4.0e-23
Match length
                  73
                  73
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                   >gi 1363523 pir S53761 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - rye
                   >gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase
                   [Secale cereale] >gi_1095494_prf__2109226B triosephosphate
                   isomerase [Secale cereale]
                   300993
Seq. No.
                  LIB84-006-Q1-E1-E6
Seq. ID
Method
                   BLASTX
                   q4006872
NCBI GI
BLAST score
                   266
                   2.0e-23
E value
                  95
Match length
                   52
% identity
                  (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   300994
Seq. No.
                   LIB84-008-Q1-E1-A3
Seq. ID
Method
                   BLASTX
                   q3290006
NCBI GI
BLAST score
                   315
                   4.0e-29
E value
                   73
Match length
                   77
% identity
                   (U82201) pathogenesis related protein-5 [Zea mays]
NCBI Description
                   300995
Seq. No.
                   LIB84-008-Q1-E1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2505870
BLAST score
                   333
                   4.0e-31
E value
Match length
                   76
                   82
% identity
                  (Y12227) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

NCBI GI

g998429



```
300996
   Seq. No.
                     LIB84-008-Q1-E1-A9
   Seq. ID
Method
                     BLASTX
                     g2244876
  NCBI GI
   BLAST score
                     222
                     9.0e-19
   E value
                     112
  Match length
                     50
   % identity
                     (Z97338) hypothetical protein [Arabidopsis thaliana]
   NCBI Description
                     300997
   Seq. No.
                     LIB84-008-Q1-E1-B12
   Seq. ID
                     BLASTN
   Method
   NCBI GI
                     g902200
   BLAST score
                     78
                     8.0e-36
   E value
   Match length
                     141
                     90
   % identity
   NCBI Description Z.mays complete chloroplast genome
                     300998
   Seq. No.
                     LIB84-008-Q1-E1-G11
   Seq. ID
                     BLASTX
   Method
                      g4185141
   NCBI GI
   BLAST score
                      410
                      4.0e-40
   E value
   Match length
                      122
   % identity
                      67
                      (AC005724) putative calmodulin-binding protein [Arabidopsis
   NCBI Description
                      thaliana]
                      300999
   Seq. No.
                      LIB84-008-Q1-E1-G4
   Seq. ID
                      BLASTX
   Method
   NCBI GI
                      g4191779
                      259
   BLAST score
                      2.0e-22
   E value
   Match length
                      132
                      44
   % identity
                     (AC005917) putative recA protein [Arabidopsis thaliana]
   NCBI Description
                      301000
   Seq. No.
                      LIB84-010-Q1-E1-C4
   Seq. ID
   Method
                      BLASTN
   NCBI GI
                      g5091496
   BLAST score
                      44
                      2.0e-15
   E value
                      48
   Match length
                      98
   % identity
                      Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
   NCBI Description
                      complete sequence
                      301001
   Seq. No.
   Seq. ID
                      LIB84-010-Q1-E1-D7
   Method
                      BLASTN
```

Match length



```
BLAST score
                   36
                   9.0e-11
E value
Match length
                   64
% identity
                   89
                  GRF1=general regulatory factor [Zea mays, XL80, Genomic,
NCBI Description
                  5348 nt]
                  301002
Seq. No.
                  LIB84-011-Q1-E1-C8
Seq. ID
Method
                  BLASTX
                  g2246378
NCBI GI
BLAST score
                  220
                   7.0e-18
E value
                   87
Match length
% identity
                   51
                  (Z86094) plastid protein [Arabidopsis thaliana]
NCBI Description
                   301003
Seq. No.
                   LIB84-011-Q1-E1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512684
BLAST score
                   160
                   6.0e-11
E value
Match length
                   76
% identity
                   47
NCBI Description
                   (AC006931) unknown protein [Arabidopsis thaliana]
                   >gi 4559324 gb AAD22986.1 AC007087 5 (AC007087) unknown
                   protein [Arabidopsis thaliana]
                   301004
Seq. No.
                   LIB84-012-Q1-E1-C9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q236729
BLAST score
                   69
                   8.0e-31
E value
Match length
                   126
% identity
                   89
                  metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
NCBI Description
Seq. No.
                   301005
                   LIB84-012-Q1-E12-D5
Seq. ID
                   BLASTN
Method
                   g2668739
NCBI GI
BLAST score
                   78
                   8.0e-36
E value
Match length
                   192
% identity
                   93
                   Zea mays translation initiation factor GOS2 (TIF) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   301006
Seq. ID
                   LIB84-012-Q1-E12-E4
Method
                   BLASTX
                   g417103
NCBI GI
BLAST score
                   184
E value
                   5.0e-16
```



% identity
NCBI Description

HISTONE H3.2, MINOR >gi 282871 pir __S24346 histone
H3.3-like protein - Arabidopsis thaliana
>gi 16324 emb CAA42957 (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi 404825 emb CAA42958 (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi 488563
(U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460)
histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone
H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2
[Medicago sativa] >gi 488577 (U09465) histone H3.2
[Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone
H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422)
histone H3 variant H3.3 [Lycopersicon esculentum]
>gi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AF093633) histone H3 [Oryza sativa]
>gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 301007

Seq. ID LIB84-013-Q1-E1-D10

Method BLASTX
NCBI GI g4262183
BLAST score 283
E value 2.0e-25
Match length 71
% identity 77

NCBI Description (AC005508) 51434 [Arabidopsis thaliana]

Seq. No. 301008

Seq. ID LIB84-013-Q1-E1-F2

Method BLASTX
NCBI GI g3281861
BLAST score 182
E value 2.0e-13
Match length 116
% identity 32

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 301009

Seq. ID LIB84-013-Q1-E1-G11

Method BLASTX
NCBI GI g3643605
BLAST score 176
E value 9.0e-13
Match length 67
% identity 52

NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301010

Seq. ID LIB84-013-Q1-E1-G4

Method BLASTX
NCBI GI g3650028
BLAST score 375
E value 4.0e-36



```
104
Match length
% identity
                  62
                   (AC005396) putative 22 kDa peroxisomal membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                  301011
Seq. No.
                  LIB84-013-Q1-E1-H10
Seq. ID
                  BLASTX
Method
                  g2832643
NCBI GI
BLAST score
                  300
                  2.0e-27
E value
Match length
                  93
% identity
                  (AL021710) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  301012
                  LIB84-013-Q1-E1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1653665
BLAST score
                  219
                   8.0e-18
E value
Match length
                   130
                   37
% identity
                  (D90915) peptide chain release factor [Synechocystis sp.]
NCBI Description
                   301013
Seq. No.
                   LIB84-013-Q1-E1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4099914
BLAST score
                   216
                   2.0e-17
E value
Match length
                   83
% identity
                   54
                   (U91857) ethylene-responsive element binding protein
NCBI Description
                   homolog [Stylosanthes hamata]
Seq. No.
                   301014
                   LIB84-013-Q1-E1-H6
Seq. ID
                   BLASTX
Method
                   g115786
NCBI GI
BLAST score
                   333
                   3.0e-31
E value
Match length
                   82
                   79
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding
                   protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
                   mays]
                   301015
Seq. No.
                   LIB84-014-Q1-E1-A1
Seq. ID
                   BLASTN
Method
```

Method BLASTN
NCBI GI g2062691
BLAST score 37
E value 2.0e-11
Match length 37
% identity 100

BLAST score

E value

390

8.0e-38



```
NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete
                   cds
Seq. No.
                   301016
                   LIB84-014-Q1-E1-C6
Seq. ID
Method
                   BLASTX
                   q2494893
NCBI GI
                   392
BLAST score
                   5.0e-38
E value
Match length
                   100
% identity
                   64
                   CHROMATIN ASSEMBLY FACTOR 1 P48 SUBUNIT (CAF-1 P48 SUBUNIT)
NCBI Description
                   (RETINOBLASTOMA BINDING PROTEIN P48)
                   (RETINOBLASTOMA-BINDING PROTEIN 4) >gi_2137734_pir__I49366 retinoblastoma-binding protein mRbAp48 - mouse >gi_1016275
                   (U35141) retinoblastoma-binding protein mRbAp48 [Mus
                   musculus] >qi 1585656 prf 2201425A retinoblastoma-binding
                   protein [Mus musculus]
                   301017
Seq. No.
                   LIB84-014-Q1-E1-D9
Seq. ID
Method
                   BLASTN
                   g4176423
NCBI GI
BLAST score
                   53
                   5.0e-21
E value
Match length
                   73
% identity
                   93
                   Oryza sativa rpl12-2 gene for chloroplast ribosomal protein
NCBI Description
                   L12, complete cds
                   301018
Seq. No.
                   LIB84-014-Q1-E1-G7
Seq. ID
                   BLASTN
Method
                   g2446997
NCBI GI
BLAST score
                   111
                   1.0e-55
E value
                   292
Match length
                   91
% identity
NCBI Description Zea mays FAD7 gene for fatty acid desaturase, complete cds
                   301019
Seq. No.
                   LIB84-015-Q1-E1-B6
Seq. ID
                   BLASTX
Method
                   g4582468
NCBI GI
                   209
BLAST score
                   1.0e-32
E value
                   101
Match length
                   76
% identity
                   (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                   C-terminal domain [Arabidopsis thaliana]
Seq. No.
                    301020
                    LIB84-015-01-E1-C4
Seq. ID
                   BLASTX
Method
                    g3377762
NCBI GI
```





Match length 129
% identity 63
NCBI Description (AF079850) nodule-enhanced malate dehydrogenase [Pisum sativum]

 Seq. No.
 301021

 Seq. ID
 LIB84-015-Q1-E1-C6

 Method
 BLASTX

NCBI GI g3738329
BLAST score 381
E value 9.0e-37
Match length 95
% identity 81

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 301022

Seq. ID LIB84-015-Q1-E1-F6

Method BLASTX
NCBI GI g2664210
BLAST score 380
E value 1.0e-36
Match length 79
% identity 90

NCBI Description (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis

thaliana]

Seq. No. 301023

Seq. ID LIB84-015-Q1-E1-H5

Method BLASTX
NCBI GI g1076800
BLAST score 340
E value 5.0e-32
Match length 118
% identity 59

NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -

maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate

peroxidase [Zea mays]

Seq. No. 301024

Seq. ID LIB84-016-Q1-E1-E8

Method BLASTX
NCBI GI g2459446
BLAST score 264
E value 5.0e-23
Match length 135
% identity 43

NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis

thaliana]

Seq. No. 301025

Seq. ID LIB84-016-Q1-E1-F2

Method BLASTX
NCBI GI g115815
BLAST score 518
E value 6.0e-53
Match length 105

% identity

74



```
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi 22355 emb CAA39376_ (X55892) light-harvesting
                  chlorophyll a/b binding protein [Zea mays]
                  301026
Seq. No.
                  LIB84-016-Q1-E1-G9
Seq. ID
                  BLASTN
Method
                  g607147
NCBI GI
                  54
BLAST score
                  4.0e-22
E value
Match length
                  66
% identity
                  95
                  P.abies (L.) Karst. Lhcb1*1 mRNA for light-harvesting
NCBI Description
                  chlorophyll a/b-binding protein
                  301027
Seq. No.
                  LIB84-017-Q1-E1-A6
Seq. ID
Method
                  BLASTX
                  g2425066
NCBI GI
                  153
BLAST score
                  1.0e-10
E value
Match length
                  61
% identity
                  49
NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]
Seq. No.
                  301028
                  LIB84-017-Q1-E1-B6
Seq. ID
Method
                  BLASTX
                  q2407279
NCBI GI
BLAST score
                  213
                  4.0e-17
E value
Match length
                  101
% identity
                  50
NCBI Description (AF017362) aldolase [Oryza sativa]
                  301029
Seq. No.
                  LIB84-017-Q1-E1-C11
Seq. ID
Method
                  BLASTN
                  g22324
NCBI GI
                  42
BLAST score
                                                                   .2-
E value
                  9.0e-15
                  110
Match length
% identity
                  85
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)
                  301030
Seq. No.
                  LIB84-017-Q1-E1-F2
Seq. ID
Method
                  BLASTX
                  q4455248
NCBI GI
                  271
BLAST score
                  7.0e-24
E value
                  77
Match length
```

42415

NCBI Description (AL035523) acyl carrier-like protein [Arabidopsis thaliana]

E value

Match length

% identity

8.0e-39

95

83

```
Seq. No.
                  301031
                  LIB84-021-Q1-E1-A8
Seq. ID
Method
                  BLASTN
                  g4140643
NCBI GI
BLAST score
                  52
                  2.0e-20
E value
                  108
Match length
                   87
% identity
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   301032
Seq. No.
                  LIB84-021-Q1-E1-B1
Seq. ID
Method
                   BLASTX
                   q2828292
NCBI GI
BLAST score
                   411
                   2.0e-40
E value
                   121
Match length
% identity
                   68
                   (AL021687) neoxanthin cleavage enzyme-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   301033
Seq. No.
                   LIB84-021-Q1-E1-B5
Seq. ID
Method
                   BLASTX
                   g4505337
NCBI GI
BLAST score
                   146
                   8.0e-10
E value
Match length
                   69
                   52
% identity
NCBI Description
                   nucleotide binding protein 1 (E.coli MinD like)
                   >gi 1709232 sp P53384_NBP_HUMAN NUCLEOTIDE-BINDING PROTEIN
                   (NBP) >gi_1082661_pir__JC4010 nucleotide-binding protein -
                   human >gi 515644 (U01833) putative nucleotide-binding
                   protein [Homo sapiens]
                   301034
Seq. No.
                   LIB84-021-Q1-E1-F12
Seq. ID
Method
                   BLASTX
                   g531467
NCBI GI
BLAST score
                   304
E value
                   7.0e-28
Match length
                   119
                   52
% identity
NCBI Description
                   (U12977) similar to glycerol-3-phosphate-dehydrogenase,
                   GenBank Accession Number U00039, and Swiss-Prot Accession
                   Number P13706 [Pseudomonas lemoignei]
Seq. No.
                   301035
Seq. ID
                   LIB84-022-Q1-E1-G12
                   BLASTX
Method
NCBI GI
                   g2632254
BLAST score
                   396
```

NCBI GI

BLAST score



```
NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]
                  301036
Seq. No.
                  LIB84-023-Q1-E1-B3
Seq. ID
                  BLASTX
Method
                  g2239260
NCBI GI
                  533
BLAST score
                  1.0e-54
E value
                  109
Match length
                  95
% identity
NCBI Description (Y13734) cinnamoyl CoA reductase [Zea mays]
                  301037
Seq. No.
                  LIB84-023-Q1-E1-B4
Seq. ID
Method
                  BLASTX
                  g3738333
NCBI GI
                  141
BLAST score
                  3.0e-11
E value
Match length
                  63
                  53
% identity
                  (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
                  301038
Seq. No.
                  LIB84-023-Q1-E1-B6
Seq. ID
                  BLASTN
Method
                  g2062705
NCBI GI
                   33
BLAST score
                   3.0e-09
E value
Match length
                   41
                   95
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                   301039
Seq. No.
                   LIB84-023-Q1-E1-D5
Seq. ID
                   BLASTX
Method
                   g4587589
NCBI GI
BLAST score
                   242
                   1.0e-20
E value
                   107
Match length
% identity
                   45
                  (AC007232) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301040
Seq. No.
                   LIB84-023-Q1-E1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539437
BLAST score
                   304
                   7.0e-28
E value
Match length
                   111
% identity
                   56
                  (AL049523) putative protein [Arabidopsis thaliana]
NCBI Description
                   301041
Seq. No.
                   LIB84-023-Q1-E1-E6
Seq. ID
Method
                   BLASTX
```

42417

g1658313

```
E value 9.0e-39
Match length 91
% identity 45
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 301042
Seq. ID LIB84-023-Q1-E1-F11
Method BLASTY
```

Method BLASTX
NCBI GI g3873752
BLAST score 185
E value 7.0e-14
Match length 85
% identity 46

NCBI Description (Z66519) similar to oxalyl-CoA decarboxylase; cDNA EST EMBL:D71591 comes from this gene; cDNA EST EMBL:D66565 comes from this gene; cDNA EST EMBL:D73312 comes from this gene; cDNA EST EMBL:D70388 comes from this gene; cDNA EST

 Seq. No.
 301043

 Seq. ID
 LIB84-024-Q1-E1-D1

 Method
 BLASTN

 NCBI GI
 g433459

 BLAST score
 104

 E value
 1.0e-51

E value 1.0e-51
Match length 192
% identity 90

NCBI Description Z.mays mRNA for ferredoxin-thioredoxin reductase

 Seq. No.
 301044

 Seq. ID
 LIB84-024-Q1-E1-E4

 Method
 BLASTX

NCBI GI g1431629 BLAST score 151 E value 7.0e-10 Match length 56 % identity 46

NCBI Description (X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No. 301045

Seq. ID LIB84-024-Q1-E1-E5

Method BLASTX
NCBI GI g115771
BLAST score 567
E value 1.0e-58
Match length 109
% identity 96

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll

a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 301046

Seq. ID LIB84-024-Q1-E1-G10

Method BLASTX
NCBI GI g3522943
BLAST score 336

Method

NCBI GI

BLASTX

g3293555



```
1.0e-31
E value
Match length
                  83
% identity
                  (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  301047
                  LIB84-024-Q1-E1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1708899
BLAST score
                  139
E value
                  6.0e-09
                  56
Match length
% identity
                  MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1
NCBI Description
                  (MAN(9)-ALPHA-MANNOSIDASE) >gi_2133635_pir S60709 alpha
                  1,2 mannosidase precursor - fruit fly (Drosophila
                  melanogaster) >gi 840754 emb CAA57962 (X82640) alpha 1,2
                  mannosidase [Drosophila melanogaster]
                  301048
Seq. No.
                  LIB84-025-Q1-E1-B12
Seq. ID
Method
                  BLASTX
                  q3335060
NCBI GI
BLAST score
                  342
                  1.0e-36
E value
                  100
Match length
% identity
                   (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
NCBI Description
                   thaliana] >gi 4468989 emb CAB38303 (AL035605) plasma
                  membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
Seq. No.
                   301049
                  LIB84-025-Q1-E1-B9
Seq. ID
                  BLASTX
Method
                   g3643605
NCBI GI
                   158
BLAST score
                   8.0e-11
E value
                   55
Match length
                   53
% identity
                   (ACO05395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301050
Seq. No.
                   LIB84-026-Q1-E1-A11
Seq. ID
                   BLASTN
Method
                   g218171
NCBI GI
                   46
BLAST score
                   8.0e-17
E value
                   98
Match length
                   87
% identity
                   Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                   a/b binding protein of photosystem II (LHCPII), complete
                   301051
Seq. No.
                   LIB84-026-Q1-E1-B5
Seq. ID
```



```
BLAST score
                  8.0e-35
E value
Match length
                  71
                  97
% identity
                  (AF072931) chlorophyll a/b binding protein [Medicago
NCBI Description
                  sativa]
                  301052
Seq. No.
                  LIB84-026-Q1-E1-B7
Seq. ID
Method
                  BLASTX
                  g115800
NCBI GI
                  430
BLAST score
                  1.0e-42
E value
                  101
Match length
% identity
                  81
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-3) (LHCP) >gi 81771 pir S01962 chlorophyll
                  a/b-binding protein 3 precursor - soybean
                  >qi 18552 emb CAA31419 (X12981) chlorophyll a/b binding
                  preprotein (AA - 32 to 231) [Glycine max]
                  301053
Seq. No.
                  LIB84-026-Q1-E1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g12429
                  143
BLAST score
                  1.0e-74
E value
                  247
Match length
                  90
% identity
NCBI Description
                  Maize chloroplast ORF170 and psaA gene
                   301054
Seq. No.
                  LIB84-026-Q1-E1-D6
Seq. ID
                  BLASTX
Method
                   g1170029
NCBI GI
                   149
BLAST score
                   4.0e-27
E value
Match length
                   99
                   77
% identity
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA)
NCBI Description
                   (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)
                   >gi_100581_pir__A35789 glutamate-1-semialdehyde
                   2,1-aminomutase (EC 5.4.3.8) - barley >gi 506383 (M31545)
                   glutamate 1-semialdehyde aminotransferase [Hordeum vulgare]
Seq. No.
                   301055
                   LIB84-026-Q1-E1-F3
Seq. ID
Method
                   BLASTX
                   g2979559
NCBI GI
BLAST score
                   214
```

E value 3.0e-17 Match length 45 % identity

(AC003680) putative DNA binding protein [Arabidopsis NCBI Description

thaliana]

301056 Seq. No.



```
LIB84-026-Q1-E1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g405634
BLAST score
                  166
                  1.0e-88
E value
                  238
Match length
% identity
                  93
                  Z.mays zmcpt mRNA triose phosphate/phosphate translocator
NCBI Description
                  301057
Seq. No.
                  LIB84-027-Q1-E1-B7
Seq. ID
Method
                  BLASTX
                  g4056433
NCBI GI
BLAST score
                  164
E value
                  2.0e-11
Match length
                  119
% identity
                  32
                  (ACO05990) Similar to anter-specific proline-rich protein
NCBI Description
                  (CEX) gb X60376 from Brassica napus. [Arabidopsis thaliana]
                  301058
Seq. No.
                  LIB84-027-Q1-E1-D7
Seq. ID
Method
                  BLASTN
                  q4165327
NCBI GI
BLAST score
                  52
                  2.0e-20
E value
                  80
Match length
% identity
                  91
                  Oryza sativa 3-hydroxy-3-methylglutaryl-CoA reductase gene,
NCBI Description
                  promoter region and complete cds
                  301059
Seq. No.
                  LIB84-027-Q1-E1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512663
BLAST score
                  249
                  2.0e-21
E value
Match length
                  100
% identity
                  23
                  (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4544470_gb_AAD22377.1_AC006580 9 (AC006580)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  301060
Seq. ID
                  LIB84-027-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                  q4584524
                  183
BLAST score
E value
                  1.0e-13
                  95
Match length
% identity
                  41
                  (AL049607) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 301061

Seq. ID LIB84-027-Q1-E1-H10

Method BLASTX NCBI GI g2244926

NCBI Description



```
BLAST score
                   178
                   5.0e-13
E value
Match length
                   95
% identity
                   42
                  (297339) glutaredoxin [Arabidopsis thaliana]
NCBI Description
                   301062
Seq. No.
                   LIB84-027-Q1-E1-H11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   9.0e-11
E value
Match length
                   36
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   301063
Seq. No.
                   LIB84-028-Q1-E1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4262236
BLAST score
                   242
E value
                   1.0e-20
Match length
                   70
                   67
% identity
                   (AC006200) putative ribose 5-phosphate isomerase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   301064
Seq. ID
                   LIB84-028-Q1-E1-C1
Method
                   BLASTX
                   g100878
NCBI GI
BLAST score
                   420
                   1.0e-41
E value
Match length
                   87
% identity
                   91
                   glutamate--ammonia ligase (EC 6.3.1.2) - maize
NCBI Description
                   301065
Seq. No.
                   LIB84-028-Q1-E1-C10
Seq. ID
                   BLASTX
Method
                   g4585882
NCBI GI
BLAST score
                   271
                   6.0e-24
E value
                   54
Match length
                   96
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   301066
Seq. No.
                   LIB84-028-Q1-E1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3004555
BLAST score
                   372
                   6.0e-36
E value
                   98
Match length
                   66
% identity
```

42422

(AC003673) similar to salt inducible protein [Arabidopsis



thaliana]

301072

BLASTX

g1352200

LIB84-028-Q1-E1-H7

Seq. No.

Seq. ID

Method

NCBI GI

```
301067
Seq. No.
Seq. ID
                  LIB84-028-Q1-E1-C9
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  36
                  9.0e-11
E value
                  36
Match length
                  100
% identity
                  Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
                  301068
Seq. No.
                  LIB84-028-Q1-E1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3063710
BLAST score
                  262
E value
                   7.0e-23
                  123
Match length
                   48
% identity
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                   301069
Seq. No.
                  LIB84-028-Q1-E1-E5
Seq. ID
                   BLASTX
Method
                   g1835731
NCBI GI
BLAST score
                   295
                   8.0e-27
E value
                   81
Match length
% identity
                   72
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                   301070
                   LIB84-028-Q1-E1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4582488
BLAST score
                   504
E value
                   3.0e-51
                   110
Match length
% identity
                   88
                   (AL021768) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   301071
                   LIB84-028-Q1-E1-F5
Seq. ID
Method
                   BLASTX
                   g3413699
NCBI GI
                   184
BLAST score
E value
                   9.0e-14
                   122
Match length
                   43
% identity
                   (AC004747) putative heat shock protein [Arabidopsis
NCBI Description
                   thaliana]
```



```
BLAST score
                  460
                  4.0e-46
E value
                  92
Match length
                  100
% identity
                  CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
NCBI Description
                  >gi 480909 pir S37497 triose
                  phosphate/3-phosphoglycerate/phosphate translocator - maize
                  >gi 405635 emb CAA81349 (Z26595) triose
                  phosphate/phosphate translocator [Zea mays]
                  301073
Seq. No.
                  LIB84-029-Q1-E1-A12
Seq. ID
                  BLASTX
Method
                  g2501296
NCBI GI
BLAST score
                  174
                  1.0e-12
E value
                  61
Match length
                  54
% identity
NCBI Description DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720_ (D90908) DNA
                  gyrase B subunit [Synechocystis sp.]
                  301074
Seq. No.
                  LIB84-029-Q1-E1-B8
Seq. ID
                  BLASTN
Method
                  q2832242
NCBI GI
BLAST score
                  203
                  1.0e-110
E value
Match length
                  329
% identity
                  91
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                  301075
Seq. No.
                  LIB84-029-Q1-E1-D6
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                   36
                   4.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   301076
Seq. No.
                   LIB84-029-Q1-E1-D7
Seq. ID
                   BLASTX
Method
                   g531829
NCBI GI
BLAST score
                   153
                   4.0e-10
E value
                   45
Match length
                   67
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
```

Seq. No. 301077

Seq. ID LIB84-029-Q1-E1-E3

Method BLASTX
NCBI GI g2624328
BLAST score 279



```
E value
                  7.0e-25
                                   14
Match length
                  81
% identity
                  67
NCBI Description
                  (AJ002894) OsGRP2 [Oryza sativa]
                  301078
Seq. No.
                  LIB84-029-Q1-E1-F2
Seq. ID
Method
                  BLASTX
                  q2494034
NCBI GI
BLAST score
                  375
                  4.0e-36
E value
Match length
                  97
% identity
                  69
                  DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG
NCBI Description
                  KINASE 1) >gi 2129573 pir__S71467 diacylglycerol kinase -
                  Arabidopsis thaliana >qi 1374772 dbj BAA09856 (D63787)
                  diacylglycerol kinase [Arabidopsis thaliana]
Seq. No.
                  301079
Seq. ID
                  LIB84-030-Q1-E1-A6
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  37
E value
                  2.0e-11
Match length
                  37
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  301080
                  LIB84-030-Q1-E1-B6
Seq. ID
Method
                  BLASTX
                  g4510347
NCBI GI
BLAST score
                  170
                  5.0e-12
E value
Match length
                  44
                  70
% identity
                  (AC006921) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  301081
Seq. No.
                  LIB84-030-Q1-E1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  244
                  7.0e-21
E value
Match length
                  61
                  72
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  301082
Seq. No.
                  LIB84-030-Q1-E1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22356
BLAST score
                  60
E value
                  2.0e-25
Match length
                  166
                  84
% identity
```

NCBI Description Maize mRNA for light-harvesting chlorophyll a/b binding



protein LHCP

```
Seq. No.
                  301083
                  LIB84-030-Q1-E1-F7
Seq. ID
Method
                  BLASTX
                  g4006848
NCBI GI
BLAST score
                  175
                  3.0e-13
E value
                  48
Match length
                  62
% identity
                  (AJ131433) selenocysteine methyltransferase [Astragalus
NCBI Description
                  bisulcatus]
Seq. No.
                  301084
                  LIB84-030-Q1-E1-F9
Seq. ID
Method
                  BLASTX
                  g4586259
NCBI GI
BLAST score
                  462
                  3.0e-46
E value
Match length
                  134
% identity
                  62
                  (AL049640) hydrolase-like protein [Arabidopsis thaliana]
NCBI Description
                  301085
Seq. No.
                  LIB84-030-Q1-E1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2501189
BLAST score
                  141
                  3.0e-09
E value
                  57
Match length
% identity
                  51
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                  301086
Seq. ID
                  LIB84-030-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                   q283038
                   269
BLAST score
                  1.0e-23
E value
                  119
Match length
% identity
NCBI Description
                  chlorophyll a/b-binding protein (cab-m7) precursor - maize
                   >gi_22230_emb_CAA37474_ (X53398) light harvesting
                   chlorophyll a /b binding protein [Zea mays]
Seq. No.
                   301087
                  LIB84-030-Q1-E1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3269296
BLAST score
                   419
E value
                   3.0e-41
```

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

126

58

Match length % identity



```
301088
Seq. No.
                  LIB84-030-Q1-E1-H6
Seq. ID
Method
                  BLASTX
                  q476418
NCBI GI
BLAST score
                  550
                  1.0e-56
E value
                  106
Match length
                  94
% identity
NCBI Description cytochrome c - maize
                  301089
Seq. No.
                  LIB84-030-Q1-E1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4490722
                  178
BLAST score
                  5.0e-13
E value
                  54
Match length
                  54
% identity
                  (AL035709) 1-aminocyclopropane-1-carboxylate synthase
NCBI Description
                   [Arabidopsis thaliana]
                  301090
Seq. No.
                  afb700380804.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q488500
BLAST score
                  200
                  1.0e-109
E value
Match length
                  287
                  93
% identity
NCBI Description Human mRNA for KIAA0049 gene, complete cds
                  301091
Seq. No.
                  afb700380809.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3004572
BLAST score
                  167
E value
                   5.0e-89
                  294
Match length
                   94
% identity
NCBI Description Homo sapiens BAC clone RG119C02 from 7p15, complete
                  sequence [Homo sapiens]
                   301092
Seq. No.
Seq. ID
                   afb700380822.h1
Method
                  BLASTX
                   g3098603
NCBI GI
                   376
BLAST score
E value
                   2.0e-36
Match length
                   93
% identity
                   75
                   (AF052191) katanin p60 subunit [Strongylocentrotus
NCBI Description
                  purpuratus]
```

Seq. ID afb700380846.h1

Method BLASTX

Match length

% identity

30 97

```
----
```

```
NCBI GI
                   g4240321
BLAST score
                   372
                   5.0e-36
E value
                   96
Match length
                   77
% identity
                  (AB020723) KIAA0916 protein [Homo sapiens]
NCBI Description
                   301094
Seq. No.
                   afb700380857.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4559304
BLAST score
                   548
E value
                   1.0e-56
Match length
                   102
                   100
% identity
                  (AF127021) T7-like RNA polymerase [Zea mays]
NCBI Description
                   301095
Seq. No.
                   afb700380901.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829208
BLAST score
                   144
E value
                   3.0e-09
Match length
                   28
% identity
                   93
NCBI Description
                  (AF044076) candidate tumor suppressor p33ING1 [Homo
                   sapiens]
                   301096
Seq. No.
Seq. ID
                   afb700380906.h1
Method
                   BLASTN
NCBI GI
                   g887356
BLAST score
                   105
E value
                   2.0e-52
                   138
Match length
% identity
                   94
NCBI Description Homo sapiens (clone s153) mRNA fragment
                   301097
Seq. No.
Seq. ID
                   afb700380989.h1
Method
                   BLASTX
NCBI GI
                   q4262224
BLAST score
                   278
E value
                   6.0e-25
Match length
                   79
                   63
% identity
NCBI Description
                   (AC006200) putative amino acid or GABA permease
                   [Arabidopsis thaliana]
Seq. No.
                   301098
                   afb700380994.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q133820
                   150
BLAST score
E value
                   3.0e-10
```



NCBI Description 40S RIBOSOMAL PROTEIN S17 >gi_304526 (M13933) ribosomal protein S17 [Cricetulus griseus] >gi_1526555_dbj_BAA04943_ (D25213) ribosomal protein S17 [Mus musculus]

Seq. No. 301099

Seq. ID afb700381015.h1

Method BLASTN
NCBI GI 94505760
BLAST score 229
E value 1.0e-126
Match length 301
% identity 95

NCBI Description Homo sapiens placental growth factor, vascular endothelial

growth factor-related protein (PGF) mRNA

>gi_35521_emb_X54936_HSPLGF H.sapiens mRNA for placenta
growth factor (PlGF) >gi_512448_emb_A18411.1_A18411 PIGF

gene seq ID No:1

Seq. No. 301100

Seq. ID afb700381017.h1 Method BLASTN

NCBI GI g4416300 BLAST score 36 E value 5.0e-11 Match length 44 % identity 48

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 301101

Seq. ID afb700381056.hl

Method BLASTN
NCBI GI g4416300
BLAST score 79
E value 2.0e-36
Match length 159
% identity 87

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 301102

Seq. ID afb700381068.hl

Method BLASTX
NCBI GI g3176726
BLAST score 224
E value 6.0e-19
Match length 56
% identity 71

NCBI Description (AC002392) putative serine proteinase [Arabidopsis

thaliana]

Seq. No. 301103

Seq. ID afb700381113.h1

Method BLASTX
NCBI GI g1710756
BLAST score 188
E value 2.0e-14



Match length 80 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)

Seq. No.

301104

Seq. ID

afb700381116.h1

Method NCBI GI BLASTN g4507580

BLAST score

194

E value Match length 1.0e-105

% identity

238 96

NCBI Description Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA >gi_29850_emb_X60592_HSCDW40 Human

CDw40 mRNA for nerve growth factor receptor-related B-lymphocyte activation molecule >gi 590074_gb_I07284_

Sequence 31 from Patent EP

Seq. No.

301105

Seq. ID

afb700381138.h1

Method NCBI GI BLASTN g4102714

BLAST score

117

E value

3.0e-59

Match length % identity

276 86

NCBI Description Homo sapiens serine protease mRNA, complete cds

Seq. No.

301106

Seq. ID

afb700381156.hl

Method NCBI GI BLASTX g3661529

BLAST score

E value

262

Match length

5.0e-23

% identity

52 96

NCBI Description

(AF089814) growth suppressor related [Homo sapiens]

Seq. No.

301107

Seq. ID

afb700381157.hl

Method NCBI GI BLASTN

BLAST score

g1617516 171

E value

1.0e-91

Match length

227 94

% identity NCBI Description

Human orphan G protein-coupled receptor (RDC1) mRNA,

partial cds

Seq. No.

301108

Seq. ID

afb700381181.hl BLASTN

Method NCBI GI

q1698488

BLAST score

37

E value Match length 1.0e-11

% identity



```
NCBI Description Peltoboykinia tellimoides 18S ribosomal RNA, complete
                  sequence
Seq. No.
                  301109
                  afb700381189.hl
Seq. ID
                  BLASTN
Method
                  q2281061
NCBI GI
BLAST score
                  79
                  1.0e-36
E value
Match length
                  171
% identity
                  87
                  Human Chromosome 11 Cosmid cSRL16b6, complete sequence
NCBI Description
                   [Homo sapiens]
Seq. No.
                  301110
Seq. ID
                  afb700381218.h1
Method
                  BLASTX
NCBI GI
                  q2501624
BLAST score
                   381
E value
                   5.0e-37
Match length
                   97
% identity
                  79
                  UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)
NCBI Description
                  >gi 1652159 dbj BAA17083_ (D90903) urease alpha subunit
                   [Synechocystis sp.]
Seq. No.
                   301111
Seq. ID
                   afb700381224.h1
Method
                  BLASTX
NCBI GI
                   g899254
BLAST score
                   153
E value
                   3.0e-10
Match length
                   40
% identity
                   65
                  (Z50038) predicted trithorax protein [Drosophila virilis]
NCBI Description
Seq. No.
                   301112
                   afb700381226.h1
Seq. ID
Method
                   BLASTX
                   g2984709
NCBI GI
BLAST score
                   227
E value
                   5.0e-23
Match length
                   68
                   85
% identity
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
Seq. No.
                   301113
                   afb700381301.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4056615
                                                     eξ$1° ≤
```

BLAST score 154 E value 2.0e-10 Match length 39 74 % identity

(AF067401) Scl1 protein [Oryza sativa] NCBI Description

Seq. No. 301114



```
afb700381303.hl
Seq. ID
Method
                  BLASTX
                  g3025299
NCBI GI
BLAST score
                  395
                  1.0e-38
E value
                  100
Match length
                  72
% identity
                  HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi 2088660
NCBI Description
                  (AF002109) ABC1 isolog [Arabidopsis thaliana]
                  301115
Seq. No.
                  afb700381326.h1
Seq. ID
Method
                  BLASTN
                  g3549156
NCBI GI
BLAST score
                  172
E value
                  4.0e-92
                  264
Match length
                  92
% identity
                  Homo sapiens chromosome 19, cosmid R30017, complete
NCBI Description
                  sequence [Homo sapiens]
Seq. No.
                  301116
                  afb700381330.hl
Seq. ID
Method
                  BLASTX
                  g1717793
NCBI GI
BLAST score
                  151
                  4.0e-10
E value
Match length
                  91
% identity
                  38
                  PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR)
NCBI Description
                  >gi 1083553 pir A55117 tsg24 protein - mouse
                  >gi 642252 emb CAA56450 (X80169) tsg24 [Mus musculus]
                  301117
Seq. No.
                  afb700381357.h1
Seq. ID
Method
                  BLASTX
                  g3080424
NCBI GI
BLAST score
                  214
                  2.0e-17
E value
                  100
Match length
% identity
                  53
                  (AL022604) NAD+ dependent isocitrate dehydrogenase subunit
NCBI Description
                  1 [Arabidopsis thaliana]
                  301118
Seq. No.
Seq. ID
                  afb700381361.h1
Method
                  BLASTX
NCBI GI
                  g2911056
BLAST score
                  170
E value
                  3.0e-12
Match length
                  76
% identity
                  45
NCBI Description (AL021961) hypothetical protein [Arabidopsis thaliana]
```

Seq. ID afb700381372.h1

Method BLASTX



```
g2978255
NCBI GI
                  153
BLAST score
                  1.0e-10
E value
Match length
                  35
                  83
% identity
                  (AB007407) myeloid zinc finger protein-2 [Mus musculus]
NCBI Description
                  301120
Seq. No.
                  afb700381414.h1
Seq. ID
                  BLASTX
Method
                  g2498329
NCBI GI
                  384
BLAST score
                  2.0e-37
E value
                  100
Match length
% identity
                  74
                  PATTERN FORMATION PROTEIN EMB30 >gi 2129665_pir__S65571
NCBI Description
                  pattern-formation protein GNOM - Arabidopsis thaliana
                  >gi 1209633 (U36433) GNOM gene product [Arabidopsis
                  thaliana] >gi 1335997 (U56140) similar to the Saccharomyces
                  cerevisiae Sec7 protein, GenBank Accession Number J03918
                  [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the
                  Saccharomyces cerevisiae Sec7 protein, GenBank Accession
                  Number J03918 [Arabidopsis thaliana]
                  301121
Seq. No.
Seq. ID
                  afb700381428.h1
Method
                  BLASTN
NCBI GI
                  g3789930
BLAST score
                  156
E value
                  2.0e-82
Match length
                  288
                  89
% identity
NCBI Description Homo sapiens H19 gene, complete sequence
                  301122
Seq. No.
                  afb700381439.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3043415
BLAST score
                  324
                  2.0e-30
E value
Match length
                  62
% identity
                  98
NCBI Description (Y17053) At-hsc70-3 [Arabidopsis thaliana]
                  301123
Seq. No.
Seq. ID
                  afb700381471.h1
Method
                  BLASTX
                  q4538911
NCBI GI
BLAST score
                  182
```

7.0e-14 E value Match length 42 % identity 83

NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

301124 Seq. No.

Seq. ID afb700381501.hl

Method BLASTN



```
g3417305
NCBI GI
BLAST score
                  244
                  1.0e-135
E value
Match length
                   304
                   95
% identity
                  Homo sapiens chromosome 17, clone hRPC1107_A_17, complete
NCBI Description
                   sequence [Homo sapiens]
                   301125
Seq. No.
                   afb700381513.h1
Seq. ID
Method
                  BLASTN
                   g4335966
NCBI GI
BLAST score
                   226
E value
                   1.0e-124
Match length
                   290
% identity
                   95
                  Homo sapiens cell adhesion molecule (BL1A) mRNA, complete
NCBI Description
                   301126
Seq. No.
Seq. ID
                   afb700381522.hl
Method
                   BLASTN
NCBI GI
                   g558364
BLAST score
                   96
                   1.0e-46
E value
Match length
                   96
                   100
% identity
                  Z.mays mRNA for ADP-glucose pyrophosphorylase
NCBI Description
                   301127
Seq. No.
                   afb700381529.h1
Seq. ID
Method
                   BLASTX
                   q4586036
NCBI GI
                   203
BLAST score
                   4.0e-16
E value
Match length
                   96
% identity
                   41
                   (AC007109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   301128
                   afb700381530.h1
Seq. ID
Method
                   BLASTN
                   g181962
NCBI GI
BLAST score
                   133
                   7.0e-69
E value
Match length
                   181
% identity
                   93
                   Human elongation factor EF-1-alpha gene, complete cds.
NCBI Description
                   >gi 2170857_dbj_E02629_E02629 DNA of human polypeptide
                   chain elongation factor-1 alpha
```

Seq. ID afb700381590.h1

Method BLASTN
NCBI GI g577824
BLAST score 46
E value 5.0e-17

```
Match length
                   58
                  95
% identity
                  Z.mays gene for H2B histone (gH2B3)
NCBI Description
                  301130
Seq. No.
Seq. ID
                  afb700381593.hl
                  BLASTN
Method
NCBI GI
                  g22487
                  34
BLAST score
                   4.0e-10
E value
Match length
                  38
                   97
% identity
                  Maize gene for sucrose synthase
NCBI Description
                   301131
Seq. No.
Seq. ID
                  afb700381620.h1
Method
                  BLASTX
NCBI GI
                   q88969
                   252
BLAST score
                   1.0e-41
E value
                   103
Match length
                   85
% identity
                  ubiquitin--protein ligase (EC 6.3.2.19) E1 - human
NCBI Description
                   >gi 340072 (M58028) ubiquitin-activating enzyme E1 [Homo
                   sapīens]
Seq. No.
                   301132
Seq. ID
                   afb700381624.h1
                   BLASTX
Method
NCBI GI
                   g4309738
                   175
BLAST score
                   8.0e-13
E value
Match length
                   52
% identity
                   54
                  (AC006439) putative tubby protein [Arabidopsis thaliana]
NCBI Description
                   301133
Seq. No.
Seq. ID
                   afb700381625.hl
Method
                   BLASTN
NCBI GI
                   g2576343
BLAST score
                   48
E value
                   5.0e-18
Match length
                   92
```

% identity 88

Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete NCBI Description

sequence [Homo sapiens]

Seq. No. 301134

afb700381648.hl Seq. ID

Method BLASTX NCBI GI g183613 BLAST score 212 E value 2.0e-17 Match length 45 % identity 84

(M75161) granulin [Homo sapiens] NCBI Description



301135 Seq. No. Seq. ID afb700381654.h1 Method BLASTN g2098573 NCBI GI BLAST score 36 7.0e-11 E value Match length 48 % identity 94 Human DNA from overlapping chromosome 19 cosmids R31396, NCBI Description F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence [Homo sapiens] Seq. No. 301136 Seq. ID afb700381687.hl Method BLASTX NCBI GI g2833293 BLAST score 166 7.0e-12 E value Match length 84 40 % identity PROBABLE ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC) NCBI Description >gi 2146865 pir S72578 gene C35D10.1 protein -Caenorhabditis elegans >gi 687,880 (U21324) similar to S. cerevisiae hypothetical protein YKL166 [Caenorhabditis elegans] Seq. No. 301137 afb700381693.h1 Seq. ID Method BLASTX NCBI GI q4502193 BLAST score 350 E value 1.0e-40 Match length 94 94 % identity NCBI Description v-raf murine sarcoma 3611 viral oncogene homolog 1 >gi_1730068_sp_P10398_KRAA_HUMAN A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (ONCOGENE PKS2) >gi_625217_pir__TVHUAF protein kinase A-raf-1 (EC 2.7.1.-) - human >gi_780127 (L24038) ARAF1 [Homo sapiens] >gi 1405977 (U01337) Ser/Thr protein kinase [Homo sapiens] Seq. No. 301138 Seq. ID afb700381694.h1 Method BLASTN NCBI GI g1596166 BLAST score 205 1.0e-112 E value 277 Match length

% identity

NCBI Description Human mRNA for RTP, complete cds

Seq. No. 301139

Seq. ID afb700381736.h1

Method BLASTN NCBI GI g307374 BLAST score 209 E value 1.0e-114



```
Match length 255
% identity 96
NCBI Description Homo sapiens RHOA proto-oncogene multi-drug-resistance protein mRNA, 3' end
```

 Seq. No.
 301140

 Seq. ID
 afb700381831.h1

 Method
 BLASTX

Method BLASTX
NCBI GI g3360291
BLAST score 168
E value 3.0e-12
Match length 52
% identity 63

NCBI Description (AF023165) leucine-rich repeat transmembrane protein kinase

2 [Zea mays]

Seq. No. 301141

Seq. ID afb700381832.h1

Method BLASTN
NCBI GI g6249668
BLAST score 57
E value 1.0e-23
Match length 148
% identity 85

NCBI Description Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map

10p11.2-10p12.1, complete sequence [Homo sapiens]

Seq. No. 301142

Seq. ID afb700381837.h1

Method BLASTX
NCBI GI g2984709
BLAST score 143
E value 3.0e-09
Match length 39
% identity 74

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 301143

Seq. ID afb700381851.h1

Method BLASTX
NCBI GI g312179
BLAST score 457
E value 7.0e-46
Match length 90
% identity 97

NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi_1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Seq. No. 301144

Seq. ID afb700381860.h1

Method BLASTX
NCBI GI g4007113
BLAST score 487
E value 2.0e-49



Match length 102 % identity 92

NCBI Description (AL022237) bK1191B2.3.1 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1) [Homo sapiens]

Seq. No. 301145

Seq. ID afb700381862.h1

Method BLASTX
NCBI GI g3785977
BLAST score 441
E value 5.0e-44
Match length 103
% identity 81

NCBI Description (AC005560) putative growth regulator protein [Arabidopsis

thaliana]

Seq. No. 301146

Seq. ID afb700381882.h1

Method BLASTX
NCBI GI 94506285
BLAST score 340
E value 2.0e-37
Match length 86
% identity 92

NCBI Description Protein tyrosine phosphatase IVA2 >gi_894159 (U14603)

protein-tyrosine phosphatase [Homo sapiens] >gi_1777757 (U48297) protein tyrosine phosphatase PTPCAAX2 [Homo sapiens] >gi_1817730 (L48723) protein tyrosine phosphatase

[Homo sapiens] >gi 2992630 (AF035644) mPRL-2 [Mus musculus]

Seq. No. 301147

Seq. ID afb700381915.h1

Method BLASTN
NCBI GI 94504864
BLAST score 86
E value 1.0e-40
Match length 196
% identity 92

NCBI Description Homo sapiens KH-type splicing regulatory protein (KHSRP)

mRNA, and translated products

>gi 2055426 gb U94832 HSU94832 Human KH type splicing

regulatory protein KSRP mRNA, complete cds

Seq. No. 301148

Seq. ID afb700381949.h1

Method BLASTN
NCBI GI g507770
BLAST score 65
E value 3.0e-28
Match length 137
% identity 88

NCBI Description Zea mays D3L H(+)-transporting ATPase (Mhal) gene, complete

cds

Seq. No. 301149

Seq. ID afb700381966.h1

Method BLASTX



NCBI GI g3914019
BLAST score 293
E value 7.0e-27
Match length 76
% identity 80
NCBI Description S-ADENOSYLO

S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_2305014

(AF004317) S-adenosyl-L-methionine synthetase homolog [Musa

acuminata]

Seq. No. 301150

Seq. ID afb700381967.h1

Method BLASTX
NCBI GI g3289993
BLAST score 376
E value 2.0e-36
Match length 81
% identity 91

NCBI Description (AC005258) R30783 1 [Homo sapiens]

Seq. No. 301151

Seq. ID afb700381976.h1

Method BLASTX
NCBI GI g399144
BLAST score 182
E value 6.0e-14
Match length 53
% identity 66

NCBI Description COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR

>gi_2144887_pir__C1HUQC complement subcomponent C1q chain C

precursor - human

Seq. No. 301152

Seq. ID arm700460708.h1

Method BLASTX
NCBI GI g3929647
BLAST score 150
E value 2.0e-22
Match length 75
% identity 63

NCBI Description (AJ004881) Immutans protein [Arabidopsis thaliana]

Seq. No. 301153

Seq. ID arm700460849.h1

Method BLASTN
NCBI GI g532624
BLAST score 65
E value 1.0e-28
Match length 117
% identity 90

NCBI Description Zea mays malate synthase (MS) mRNA, complete cds

Seq. No. 301154

Seq. ID arm700460850.h1

Method BLASTN
NCBI GI g168584
BLAST score 58

i.



```
2.0e-24
E value
Match length
                  118
% identity
                  88
                  Corn pyruvate, orthophosphate dikinase gene, exons 2-19
NCBI Description
Seq. No.
                  301155
                  arm700460852.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2282583
BLAST score
                  55
E value
                  1.0e-22
Match length
                  103
                  88
% identity
                  Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete
NCBI Description
Seq. No.
                  301156
Seq. ID
                  arm700460870.hl
Method
                  BLASTN
NCBI GI
                  q1632767
BLAST score
                  81
E value
                   3.0e-38
Match length
                  89
                   98
% identity
                  Maize mRNA for calcium dependent protein kinase, complete
NCBI Description
Seq. No.
                   301157
Seq. ID
                  bdu700382077.h1
Method
                  BLASTN
                   g433043
NCBI GI
BLAST score
                   35
                   3.0e-10
E value
Match length
                   51
% identity
                   92
                  Zea mays W-22 clone PREM-1E retroelement PREM-1, partial
NCBI Description
                   sequence
                   301158
Seq. No.
                   bdu700382215.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2911052
BLAST score
                   245
                   2.0e-21
E value
Match length
                   65
                   69
% identity
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   301159
Seq. No.
                   bdu700382237.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076758
BLAST score
                   176
                   6.0e-13
E value
                   43
Match length
                   72
% identity
```

NCBI Description heat-shock protein precursor - rye >gi_2130093_pir__\$65776

heat-shock protein, 82K, precursor - rye >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein [Secale cereale]

Seq. No. 301160 Seq. ID bdu700382269.h1

Method BLASTX
NCBI GI g218179
BLAST score 448
E value 7.0e-45
Match length 98
% identity 90

NCBI Description (D10207) H-ATPase [Oryza sativa] >gi_444339_prf__1906387A H

ATPase [Oryza sativa]

Seq. No. 301161

Seq. ID bdu700382287.h1

Method BLASTN
NCBI GI g3283878
BLAST score 63
E value 4.0e-27
Match length 163
% identity 87

NCBI Description Homo sapiens clone 24732 unknown mRNA, partial cds

Seq. No. 301162

Seq. ID bdu700382306.h1

Method BLASTX
NCBI GI g4539662
BLAST score 339
E value 4.0e-32
Match length 98
% identity 60

NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 301163

Seq. ID bdu700382321.h1

Method BLASTN
NCBI GI g4309811
BLAST score 255
E value 1.0e-141
Match length 287
% identity 97

NCBI Description Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1,

complete sequence [Homo sapiens]

Seq. No. 301164

Seq. ID bdu700382376.h1

Method BLASTX
NCBI GI g1064931
BLAST score 165
E value 1.0e-11
Match length 45
% identity 71

NCBI Description (X92965) cyclin A-like protein [Nicotiana tabacum]

Seq. No. 301165

```
bdu700382380.h1
Seq. ID
                  BLASTX
Method
                  g2213594
NCBI GI
BLAST score
                  355
                  6.0e-34
E value
Match length
                  86
                  76
% identity
                  (AC000348) T7N9.14 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  301166
                  bdu700382422.h1
Seq. ID
                  BLASTX
Method
                  g117478
NCBI GI
BLAST score
                  195
E value
                  1.0e-15
Match length
                  67
% identity
                  57
                  CROOKED NECK PROTEIN
NCBI Description
                                                                             2.
                  301167
Seq. No.
                  bdu700382427.h1
Seq. ID
                  BLASTX
Method
                  g126047
NCBI GI
BLAST score
                  198
                  7.0e-16
E value
Match length
                   40
                   97
% identity
                  L-LACTATE DEHYDROGENASE M CHAIN (LDH-A)
NCBI Description
                   >gi_65922_pir__DEHULM L-lactate dehydrogenase (EC 1.1.1.27)
                   chain M - human >gi_34313_emb_CAA26088_ (X02152) lactate
                   dehydrogenase-A [Homo sapiens] >gi_780261_emb_CAA26879_
                   (X03077) lactate dehydrogenase-A [Homo sapiens]
                   301168
Seq. No.
                   bdu700382431.h1
Seq. ID
                   BLASTN
Method
                   g4506860
NCBI GI
                   126
BLAST score
                   5.0e-65
E value
                   126
Match length
% identity
                   100
                   Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
NCBI Description
                   >gi 28679 emb_X67016_HSAMPH H.sapiens mRNA for amphiglycan
                   301169
Seq. No.
                   bdu700382462.h1
Seq. ID
                   BLASTX
Method
                   g2462732
NCBI GI
                   170
BLAST score
E value
                   2.0e-26
Match length
                   90
% identity
                   63
```

NCBI Description

Seq. ID bdu700382474.h1

Method BLASTN

42442

(AC002292) Hypothetical Protein [Arabidopsis thaliana]



```
g4416300
NCBI GI
                  55
BLAST score
                  3.0e-22
E value
Match length
                  87
% identity
                  45
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                  region, complete sequence
                  301171
Seq. No.
                  bdu700382478.h1
Seq. ID
                  BLASTN
Method
                  g6683125
NCBI GI
                  107
BLAST score
                  1.0e-53
E value
Match length
                  115
% identity
                   98
NCBI Description Human mRNA for KIAA0339 gene, complete cds
                   301172
Seq. No.
                   bdu700382489.h1
Seq. ID
Method
                   BLASTX
                   g3170741
NCBI GI
BLAST score
                   407
                   4.0e-42
E value
                   94
Match length
% identity
                   90
                   (AF062139) immunoglobulin heavy chain variable region [Homo
NCBI Description
                   sapiens] >gi 3170743 (AF062140) immunoglobulin heavy chain
                   variable region [Homo sapiens]
                   301173
Seq. No.
                   bdu700382560.h1
Seq. ID
                   BLASTX
Method
                   g1184776
NCBI GI
BLAST score
                   158
                   2.0e-12
E value
                   49
Match length
                   84
% identity
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC4 [Zea mays]
                   301174
Seq. No.
                   bdu700382617.h1
Seq. ID
                   BLASTN
Method
                   g22458
NCBI GI
BLAST score
                   294
                   1.0e-165
E value
                   309
Match length
                   99
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                   301175
Seq. No.
```

Seq. ID bdu700382660.h1

Method BLASTN
NCBI GI g4506044
BLAST score 92
E value 9.0e-45



Match length 96 % identity

Homo sapiens proteoglycan 1, secretory granule (PRG1) mRNA NCBI Description >qi 32432 emb X17042 HSHPCP Human mRNA for hematopoetic

proteoglycan core protein

301176 Seq. No.

bdu700382741.h1 Seq. ID

BLASTX Method NCBI GI g123648 235 BLAST score 1.0e-24 E value Match length 72 % identity 82

HEAT SHOCK COGNATE 71 KD PROTEIN >gi_87625_pir__A27077 heat NCBI Description shock cognate protein 70 - human >gi 32467 emb CAA68445

(Y00371) 71 Kd heat shock cognate protein [Homo sapiens]

Seq. No. 301177

bdu700382770.h1 Seq. ID

Method BLASTX NCBI GI g2245020 BLAST score 236 2.0e-20 E value Match length 58 % identity 71

(Z97341) growth regulator homolog [Arabidopsis thaliana] NCBI Description

301178 Seq. No.

bdu700382785.h1 Seq. ID

Method BLASTX g2462753 NCBI GI BLAST score 151 2.0e-10 E value Match length 41 % identity 59

(AC002292) putative polygalacturonase [Arabidopsis NCBI Description

thaliana]

301179 Seq. No.

Seq. ID bdu700382801.h1

Method BLASTN g455025 NCBI GI BLAST score 55 E value 1.0e-22 Match length 79 46 % identity

NCBI Description Human beta globin region on chromosome 11

301180 Seq. No.

Seq. ID bdu700382804.h1

Method BLASTX NCBI GI a548493 BLAST score 229 1.0e-19 E value Match length 68 % identity

Match length

% identity

83 57



```
NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_629854_pir__S30067 polygalacturonase - maize
                  >gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                  mays]
                  301181
Seq. No.
                  bdu700382862.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3643593
BLAST score
                  158
                  6.0e-11
E value
Match length
                  57
% identity
                  61
                  (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  301182
Seq. No.
                  bdu700382886.hl
Seq. ID
Method
                  BLASTX
                  g283050
NCBI GI
BLAST score
                  214
                  7.0e-33
E value
                  88
Match length
                  81
% identity
NCBI Description
                  polygalacturonase (EC 3.2.1.15) precursor (clone W2265) -
                  maize (fragment) >gi_22428_emb_CAA44247_ (X62383)
                  polygalacturonase [Zea mays]
Seq. No.
                  301183
Seq. ID
                  bdu700382895.h1
Method
                  BLASTX
                  g1839188
NCBI GI
BLAST score
                  268
                  4.0e-24
E value
Match length
                  70
                   66
% identity
NCBI Description
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
Seq. No.
                  301184
Seq. ID
                  bdu700382901.h1
Method
                  BLASTN
NCBI GI
                  g2984708
BLAST score
                  112
E value
                   2.0e-56
Match length
                   131
                   97
% identity
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
NCBI Description
Seq. No.
                   301185
Seq. ID
                  bdu700382914.h1
Method
                  BLASTX
                  q3176674
NCBI GI
                  226
BLAST score
E value
                   6.0e-19
```



```
(AC003671) Contains similarity to Ste20-like kinase homolog
NCBI Description
                   from A. thaliana chromosome 4 contig gb_Z97336.
                   [Arabidopsis thaliana]
Seq. No.
                  301186
                  bdu700382917.h1
Seq. ID
Method
                  BLASTX
                  g280401
NCBI GI
BLAST score
                   146
                   2.0e-15
E value
Match length
                   57
% identity
                   68
                   H+-transporting ATPase (EC 3.6.1.35) - curled-leaved
NCBI Description
                   tobacco >gi 170206 (M27888) H+-translocating ATPase
                   [Nicotiana plumbaginifolia]
Seq. No.
                   301187
                   bdu700382927.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2316016
BLAST score
                   194
E value
                   2.0e-15
                   60
Match length
                   65
% identity
                   (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   301188
                   bdu700382930.h1
Seq. ID
Method
                   BLASTX
                   g3236353
NCBI GI
BLAST score
                   333
                   1.0e-31
E value
                   86
Match length
                   73
% identity
                   (AF033664) cbp146 [Mus musculus]
NCBI Description
                   301189
Seq. No.
                   bdu700382966.h1
Seq. ID
                   BLASTX
Method
                   g2832632
NCBI GI
                   280
BLAST score
                   2.0e-27
E value
                   72
Match length
                   81
% identity
                   (AL021711) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301190
Seq. No.
                   bdu700382977.h1
Seq. ID
                   BLASTN
Method
                   g22458
NCBI GI
BLAST score
                   72
E value
                   2.0e-32
                   181
Match length
```

NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)

301191

% identity

Seq. No.



```
bdu700382992.h1
Seq. ID
                  BLASTN
Method
                  q643596
NCBI GI
BLAST score
                  147
                  2.0e-77
E value
                  179
Match length
                  96
% identity
                  Corn mRNA for cysteine proteinase, clone CCP, complete cds
NCBI Description
Seq. No.
                  301192
                  bdu700383027.h1
Seq. ID
                  BLASTN
Method
                  g995938
NCBI GI
BLAST score
                  70
E value
                  3.0e-31
Match length
                  118
% identity
                  89
                  Human 13kD differentiation-associated protein mRNA, partial
NCBI Description
Seq. No.
                  301193
                  bdu700383036.h1
Seq. ID
Method
                  BLASTX
                  g3935168
NCBI GI
BLAST score
                  350
E value
                  2.0e-33
Match length
                  85
% identity
                  76
                  (AC004557) F17L21.11 [Arabidopsis thaliana]
NCBI Description
                  301194
Seq. No.
                  bdu700383041.h1
Seq. ID
                  BLASTX
Method
                   g2120736
NCBI GI
                   149
BLAST score
                   8.0e-10
E value
                   89
Match length
                   36
% identity
                  X-Pro dipeptidyl-peptidase (EC 3.4.14.11) - Xanthomonas
NCBI Description
                  maltophilia >gi 1753197 dbj BAA11872_ (D83263) dipeptidyl
                  peptidase IV [Stenotrophomonas maltophilia]
                   301195
Seq. No.
                   bdu700383058.h1
Seq. ID
                   BLASTX
Method
                   g4218991
NCBI GI
BLAST score
                   347
                   5.0e-33
E value
                   95
Match length
                   65
% identity
                   (AF098632) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
```

Seq. ID bdu700383070.h1

Method BLASTX
NCBI GI g4262162
BLAST score 161



```
3.0e-11
E value
                   94
Match length
                   37
% identity
                   (AC005275) putative glycosylation enzyme [Arabidopsis
NCBI Description
                   thaliana]
                   301197
Seq. No.
                   bdu700383111.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3646451
BLAST score
                   163
                   1.0e-11
E value
Match length
                   87
% identity
                    40
                    (AL031603) mRNA cap methyltransferase [Schizosaccharomyces
NCBI Description
                    301198
Seq. No.
                   bdu700383114.h1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g283049
BLAST score
                    486
                    2.0e-49
E value
                    93
Match length
                    100
% identity
                   polygalacturonase (EC 3.2.1.15) precursor (clone W2247) -
NCBI Description
                    maize (fragment) >gi_481079_pir__S37718 polygalacturonase -
                    maize >gi_22426_emb_CAA4424\overline{8}_ (\overline{X6}2384) polygalacturonase
                    [Zea mays] >gi_{\overline{2}878\overline{3}0} emb_CA\overline{A}47234 (X66692)
                    polygalacturonase [Zea mays]
                    301199
Seq. No.
                    bdu700383135.hl
Seq. ID
                    BLASTX
Method
                    g4038030
NCBI GI
                    309
BLAST score
                    1.0e-28
E value
                    94
Match length
% identity
                    (AC005936) putative protein kinase, 5' partial [Arabidopsis
NCBI Description
                    thaliana]
                    301200
Seq. No.
                    bdu700383193.h1
Seq. ID
                    BLASTX
Method
                    g416731
NCBI GI
                    203
BLAST score
                    3.0e-16
E value
                    40
Match length
```

100 % identity

POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir JQ1107 NCBI Description

18.3K protein precursor, pollen - maize

>gi_255569_bbs_113677 (S44171) pollen specific protein [Zea

mays=corn, Peptide, 170 aa] [Zea mays] >gi 1588669 prf 2209273A Zm13 [Zea mays]

Seq. No. 301201

NCBI GI

BLAST score



```
cat700016008.rl
Seq. ID
                  BLASTX
Method
                  q1362108
NCBI GI
BLAST score
                  169
                  2.0e-12
E value
                  54
Match length
% identity
                  69
NCBI Description histone H3 homolog - common tobacco
Seq. No.
                  301202
                  cat700016084.rl
Seq. ID
                  BLASTN
Method
                  g18266
NCBI GI
BLAST score
                  44
E value
                  8.0e-16
Match length
                  56
                  95
% identity
NCBI Description C.stellata mRNA for ribosomal protein L27
                  301203
Seq. No.
                  cat700016209.rl
Seq. ID
Method
                  BLASTX
                  g3687249
NCBI GI
BLAST score
                  160
                   3.0e-11
E value
Match length
                   44
% identity
                   66
                  (AC005169) putative copia-like transposable element
NCBI Description
                   [Arabidopsis thaliana]
                   301204
Seq. No.
                   cat700016243.rl
Seq. ID
                   BLASTX
Method
                   g4262228
NCBI GI
                   341
BLAST score
                   2.0e-32
E value
                   85
Match length
                   71
% identity
                   (AC006200) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   301205
Seq. No.
                   cat700016271.rl
Seq. ID
                   BLASTN
Method
                   g1314406
NCBI GI
BLAST score
                   145
                   5.0e-76
E value
                   145
Match length
                   100
% identity
                   Zea mays ssp. parviglumis Doebley M106 ITS1, 5.8S ribosomal
NCBI Description
                   RNA, ITS2
                   301206
Seq. No.
                   cat700016327.rl
Seq. ID
                   BLASTX
Method
```

42449

g3004950

NCBI Description



```
6.0e-19
E value
Match length
                   44
                   100
% identity
                   (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
NCBI Description
                   301207
Seq. No.
                   cat700016372.rl
Seq. ID
                   BLASTX
Method
                   g4539660
NCBI GI
BLAST score
                   238
                   1.0e-20
E value
Match length
                   57
                   72
% identity
                   (AF061282) polyprotein [Sorghum bicolor]
NCBI Description
Seq. No.
                   301208
                   cat700016375.rl
Seq. ID
Method
                   BLASTN
                   g2723470
NCBI GI
BLAST score
                   56
E value
                   6.0e-23
Match length
                   120
% identity
                   87
NCBI Description Oryza sativa mRNA for sucrose transporter, complete cds
Seq. No.
                   301209
                   cat700016453.rl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245123
BLAST score
                   275
                   7.0e-25
E value
Match length
                   69
                   71
% identity
                   (Z97343) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   301210
Seq. No.
                   cat700016454.rl
Seq. ID
                   BLASTN
Method
                   g1657760
NCBI GI
BLAST score
                   57
                   1.0e-23
E value
Match length
                   176
                   84
% identity
                   Zea mays retrotransposon Cinful 5' LTR and and primer
NCBI Description
                   binding site DNA sequence
                   301211
Seq. No.
                   cat700016510.rl
Seq. ID
Method
                   BLASTX
                   g4585979
NCBI GI
BLAST score
                   207
E value
                   5.0e-17
Match length
                   72
                   60
% identity
```

[Arabidopsis thaliana]

(AC005287) Similar to ABC-transporter atp-binding protein



```
Seq. No.
                  301212
Seq. ID
                  cat700016585.rl
Method
                  BLASTX
                  g2130141
NCBI GI
BLAST score
                  163
                  8.0e-12
E value
                  68
Match length
% identity
                  46
                  mudrA protein - maize transposon MuDR >gi 540581 (M76978)
NCBI Description
                  mudrA [Zea mays] >gi 595816 (U14597) mudrA gene product
                  [Zea mays]
                  301213
Seq. No.
Seq. ID
                  cat700016592.rl
Method
                  BLASTX
NCBI GI
                  g586021
BLAST score
                  174
                  4.0e-13
E value
Match length
                  69
                  49
% identity
                  PROBABLE PEPTIDYL-TRNA HYDROLASE (PTH) (STAGE V SPORULATION
NCBI Description
                  PROTEIN C) >gi 2127242 pir S66083 stage V sporulation
                  protein - Bacillus subtilis >gi_467442_dbj_BAA05288_
                  (D26185) stage V sporulation [Bacillus subtilis]
                  >gi 2632320 emb CAB11829 (Z99104) thermosensitive mutant
                  blocks spore coat formation (stage V sporulation) [Bacillus
                  subtilis]
Seq. No.
                  301214
Seq. ID
                  cat700016744.r1
Method
                  BLASTX
NCBI GI
                  g2088647
                  261
BLAST score
                  3.0e-23
E value
Match length
                  71
% identity
                  72
                  (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3158394 (AF036340) LRR-containing F-box protein
                  [Arabidopsis thaliana]
Seq. No.
                  301215
Seq. ID
                  cat700016764.rl
Method
                  BLASTX
                  g3860263
NCBI GI
BLAST score
                  224
                  6.0e-19
E value
Match length
                  71
                  61
% identity
NCBI Description
                   (AC005824) putative cytochrome p450 protein [Arabidopsis
                  thaliana]
```

Seq. ID cat700016831.r2

Method BLASTX NCBI GI g462234 BLAST score 186 E value 3.0e-14

Match length

NCBI Description

% identity

47

62



```
Match length
                   40
                  90
% identity
                  HISTONE H2A >gi 419741 pir S30155 histone H2A - Norway
NCBI Description
                  spruce >gi 297871 emb CAA48030 (X67819) histone H2A [Picea
                  abies]
                  301217
Seq. No.
                  cat700016835.r2
Seq. ID
Method
                  BLASTX
                  g3786009
NCBI GI
BLAST score
                  203
                  2.0e-16
E value
Match length
                  64
% identity
                  61
NCBI Description
                  (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                  301218
Seq. ID
                  cat700016883.rl
Method
                  BLASTN
NCBI GI
                  g1185553
BLAST score
                  86
                  7.0e-41
E value
Match length
                  99
                  53
% identity
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
NCBI Description
                  gene, complete cds
Seq. No.
                  301219
Seq. ID
                   cat700017172.rl
Method
                  BLASTX
                  g2462763
NCBI GI
BLAST score
                  282
                   9.0e-26
E value
Match length
                  65
% identity
                  78
NCBI Description
                  (AC002292) Highly similar to auxin-induced protein
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  301220
Seq. No.
                   cat700017201.rl
Seq. ID
Method
                  BLASTX
                   g3702341
NCBI GI
BLAST score
                   197
E value
                   1.0e-15
Match length
                  70
% identity
                   50
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301221
Seq. No.
Seq. ID
                   cat700017234.rl
Method
                  BLASTX
NCBI GI
                   g4530595
BLAST score
                   155
E value
                   7.0e-11
```

42452

(AF132477) heme oxygenase 2 [Arabidopsis thaliana]

NCBI Description

```
301222
Seq. No.
Seq. ID
                   cat700017238.rl
Method
                   BLASTX
NCBI GI
                   q4056502
BLAST score
                   199
                   5.0e-16
E value
                   64
Match length
% identity
                   (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
                   301223
Seq. No.
                   cat700017249.r1
Seq. ID
                   BLASTX
Method
                   g585963
NCBI GI
BLAST score
                   172
E value
                   8.0e-13
Match length
                   48
% identity
                   75
                   PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT
NCBI Description
                   301224
Seq. No.
                   cat700017326.rl
Seq. ID
                   BLASTX
Method
                   q3928519
NCBI GI
                   379
BLAST score
E value
                   5.0e-37
                   78
Match length
% identity
                   (AB011670) wpk4 protein kinase [Triticum aestivum]
NCBI Description
                   301225
Seq. No.
                   cat700017338.rl
Seq. ID
Method
                   BLASTX
                   g416922
NCBI GI
BLAST score
                   268
E value
                   4.0e-24
                   70
Match length
% identity
                   73
                   DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE)
NCBI Description
                   (DUTP PYROPHOSPHATASE) (P18) >gi_282947_pir__JQ1599 dUTP
                   pyrophosphatase (EC 3.6.1.23) - Tomato
                   >qi 251897 bbs 109276 (S40549) deoxyuridine triphosphatase,
                   dUTPase, P18 \{\overline{E}C\ 3.6.1.23\} [tomatoes, Tint Tim cultivar
                   LA154, Peptide, 169 aa] [Lycopersicon esculentum]
                   301226
Seq. No.
                   cat700017371.rl
Seq. ID
                   BLASTX
Method
                   g1705463
NCBI GI
BLAST score
                   363
                   4.0e-35
E value
Match length
                   77
                   92
% identity
```

42453

BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi 2129547_pir_

biotin sythase - Arabidopsis thaliana $>gi_10453\overline{16}$ ($\overline{U2}4147$) biotin sythase [Arabidopsis thaliana] $>gi_1403662$ (U31806)



BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413) biotin synthase [Arabidopsis thaliana] >gi_2288983 (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >gi_1589016_prf__2209438A biotin synthase [Arabidopsis thaliana]

301227 Seq. No. Seq. ID cat700017381.r1 Method BLASTX NCBI GI g4559334 BLAST score 219 2.0e-18 E value 56 Match length % identity (AC007087) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 301228 Seq. ID cat700017562.rl BLASTN Method q3747043 NCBI GI BLAST score 73 E value 4.0e-33 77 Match length 99 % identity Zea mays blue copper protein mRNA, partial cds NCBI Description Seq. No. 301229 cat700017669.rl Seq. ID Method BLASTN NCBI GI g22292 BLAST score 70 3.0e-31 E value Match length 70 100 % identity Z.mays mRNA for glycine-rich protein NCBI Description Seq. No. 301230 cat700017758.rl Seq. ID Method BLASTX q3513727 NCBI GI BLAST score 260 3.0e-23 E value Match length 72 67 % identity (AF080118) contains similarity to TPR domains (Pfam: NCBI Description TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana] 301231 Seq. No. cat700017884.rl

Seq. ID cat700017884.1
Method BLASTX
NCBI GI g3393018
BLAST score 161
E value 1.0e-11
Match length 67

```
% identity
                    (AL031174) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                    301232
  Seq. No.
                    cat700017912.rl
  Seq. ID
  Method
                    BLASTX
                    q1172977
  NCBI GI
                    271
  BLAST score
                    2.0e-24
  E value
                    63
  Match length
  % identity
                    60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
  NCBI Description
                    ribosomal protein L18 [Arabidopsis thaliana]
                     301233
  Seq. No.
  Seq. ID
                    cat700018032.rl
                    BLASTX
  Method
  NCBI GI
                     q4467125
                     284
  BLAST score
                     7.0e-26
  E value
                     64
  Match length
                     78
  % identity
                    (AL035538) putative protein [Arabimopsis thaliana]
  NCBI Description
                     301234
  Seq. No.
                     cat700018050.rl
  Seq. ID
  Method
                     BLASTX
                     q322752
  NCBI GI
                     262
  BLAST score
  E value
                     2.0e-23
                     73
  Match length
  % identity
                     60
                     auxin-independent growth promoter - Nicotiana tabacum
  NCBI Description
                     >gi 559921_emb_CAA56570_ (X80301) axi 1 [Nicotiana tabacum]
                     301235
  Seq. No.
                     cat700018068.r1
  Seq. ID
  Method
                     BLASTX
                     g4093155
  NCBI GI
  BLAST score
                     197
                     8.0e-16
  E value
  Match length
                     71
  % identity
                     (AF088281) phytochrome-associated protein 1 [Arabidopsis
  NCBI Description
                     thaliana]
                     301236
  Seq. No.
                     cat700018158.rl
   Seq. ID
                     BLASTX
  Method
                     q112994
  NCBI GI
                     239
  BLAST score
                     1.0e-20
  E value
  Match length
                     54
                     91
   % identity
                    GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
  NCBI Description
                     >gi_82685_pir__S04536 embryonic abundant protein,
                     glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
```



ABA-inducible gene protein [Zea mays] >gi_226091_prf__1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 301237 Seq. ID cat700018189.r1

Method BLASTX
NCBI GI g3269285
BLAST score 144
E value 1.0e-09
Match length 60
% identity 53

NCBI Description (AL030978) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301238

Seq. ID cat700018373.r1

Method BLASTX
NCBI GI g1706956
BLAST score 166
E value 4.0e-12
Match length 70
% identity 41

NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]

Seq. No. 301239

Seq. ID cat700018510.r1

Method BLASTX
NCBI GI 970774
BLAST score 385
E value 1.0e-37
Match length 78
% identity 100

NCBI Description histone H4 (TH091) - wheat >gi_170747 (M12277) histone H4

[Triticum aestivum]

Seq. No. 301240

Seq. ID cat700018543.r1

Method BLASTX
NCBI GI g4539452
BLAST score 346
E value 3.0e-33
Match length 70
% identity 84

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seg. No. 301241

Seq. ID cat700018555.r1

Method BLASTX
NCBI GI g3152566
BLAST score 159
E value 3.0e-11
Match length 77
% identity 45

NCBI Description (AC002986) Similar to hypothetical protein YLR002c, gb Z7314 from S. cerevisiae. [Arabidopsis thaliana]

Seq. ID

Method

```
301242
Seq. No.
Seq. ID
                  cat700018762.rl
                  BLASTX
Method
                  g2281090
NCBI GI
BLAST score
                  203
                  2.0e-16
E value
                  72
Match length
% identity
                  (AC002333) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301243
Seq. No.
Seq. ID
                   cat700018814.rl
                   BLASTX
Method
NCBI GI
                   q584825
                   310
BLAST score
                   5.0e-29
E value
                   67
Match length
                   85
% identity
                  B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot
NCBI Description
                   >gi 297889 emb CAA51078 (X72385) B2 protein [Daucus
                   carota]
                   301244
Seq. No.
                   cat700018855.rl
Seq. ID
                   BLASTX
Method
                   g2290400
NCBI GI
                   244
BLAST score
                   3.0e-21
E value
                   70
Match length
                   69
% identity
                  (U91339) stearoyl-ACP desaturase [Helianthus annuus]
NCBI Description
                   301245
Seq. No.
                   cat700018911.rl
Seq. ID
                   BLASTX
Method
                   q2499477
NCBI GI
                   161
BLAST score
E value
                   2.0e-11
                   29
Match length
                   97
% identity
                   2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
NCBI Description
                   ANTIOXIDANT PROTEIN) >gi_861010_emb_CAA84396_ (Z34917) bas1
                   protein [Hordeum vulgare]
                   301246
Seq. No.
                   cat700019030.rl
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22322
BLAST score
                   82
                   2.0e-38
E value
Match length
                   165
% identity
                   88
                  Z.mays mRNA for H2B histone (clone cH2B214)
NCBI Description
                   301247
```

42457

cat700019045.rl

BLASTX

Seq. ID

Method



```
g134946
 NCBI GI
                   277
 BLAST score
                   5.0e-25
 E value
 Match length
                   79
 % identity
                   65
                   ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
 NCBI Description
                   (STEAROYL-ACP DESATURASE) >gi_66361_pir__OHSPAD
                   acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6)
                   precursor - spinach >gi_21230_emb_CAA44687_ (X62898)
                   stearoyl-acyl-[acyl-carrier-protein] desaturase [Spinacia
                   oleracea]
                   301248
 Seq. No.
                   cat700019120.rl
 Seq. ID
 Method
                   BLASTX
                   g4262240
 NCBI GI
                   209
 BLAST score
                   4.0e-17
 E value
                   49
 Match length
                   73
 % identity
 NCBI Description (AC006200) putative stress protein [Arabidopsis thaliana]
                   301249
 Seq. No.
                   cat700019139.rl
Seq. ID
                   BLASTX
 Method
                   g595295
 NCBI GI
                   199
 BLAST score
                   7.0e-16
 E value
 Match length
                   80
                   50
 % identity
 NCBI Description (U09269) delta6-palmitoyl-acyl carrier protein desaturase
                   precursor [Thunbergia alata]
                   301250
 Seq. No.
                   cat700019151.rl
 Seq. ID
                   BLASTX
 Method
                   g3786011
 NCBI GI
                   309
 BLAST score
                   8.0e-29
 E value
                   72
 Match length
 % identity
                   (AC005499) putative elongation factor [Arabidopsis
 NCBI Description
                   thaliana]
                   301251
 Seq. No.
                   cat700019203.r1
 Seq. ID
                   BLASTN
 Method
                   g22292
 NCBI GI
                   87
 BLAST score
 E value
                   2.0e-41
 Match length
                   175
 % identity
                   87
 NCBI Description Z.mays mRNA for glycine-rich protein
                    301252
 Seq. No.
```

42458

cat700019228.rl

BLASTX



```
NCBI GI
                   q542157
BLAST score
                   177
E value
                   2.0e-13
Match length
                   66
% identity
                   58
NCBI Description ribosomal 5S RNA-binding protein - Rice
Seq. No.
                  301253
                  cat700019237.rl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3219858
BLAST score
                  194
E value
                  2.0e-15
                   43
Match length
% identity
                   86
                  DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE
NCBI Description
                   >gi_2129724_pir__S71204 RNA polymerase II 13.6 kDa chain -
                   Arabidopsis thaliana >gi 881501 (U28048) RNA polymerase II
                  13.6 kDa subunit [Arabidopsis thaliana]
Seq. No.
                   301254
Seq. ID
                   cat700019241.r1
Method
                  BLASTX
NCBI GI
                  g2706450
BLAST score
                  181
E value
                  1.0e-13
Match length
                   69
% identity
                   58
NCBI Description
                  (AJ225172) magnesium dependent soluble inorganic
                  pyrophosphatase [Solanum tuberosum]
                   301255
Seq. No.
                   cat700019270.rl
Seq. ID
Method
                  BLASTX
                   g2832661
NCBI GI
BLAST score
                   232
                  1.0e-19
E value
Match length
                   80
% identity
                   60
NCBI Description
                  (AL021710) pherophorin - like protein [Arabidopsis
                   thalianal
                   301256
Seq. No.
Seq. ID
                   cat700019281.rl
Method
                   BLASTX
NCBI GI
                   g2347207
BLAST score
                  140
E value
                   6.0e-09
                  57
Match length
```

40 % identity

(AC002338) APG protein isolog [Arabidopsis thaliana] NCBI Description

>gi 3150400 (AC004165) putative APG-like protein

[Arabidopsis thaliana]

Seq. No.

301257

Seq. ID cat700019338.rl

Method BLASTX

BLAST score

E value

257 8.0e-23

```
q2505874
NCBI GI
BLAST score
                  176
                  2.0e-13
E value
                  69
Match length
% identity
NCBI Description (Y12776) putative kinase [Arabidopsis thaliana]
                  301258
Seq. No.
                  cat700019396.r1
Seq. ID
                  BLASTX
Method
                  q1524383
NCBI GI
                  152
BLAST score
                  2.0e-10
E value
Match length
                   47
% identity
                   68
                  (X63374) 3-phosphoshikimate 1-carboxyvinyltransferase [Zea
NCBI Description
                  mays]
                   301259
Seq. No.
                   cat700019404.rl
Seq. ID
                   BLASTX
Method
                   g1206013
NCBI GI
                   262
BLAST score
                   3.0e-23
E value
                   61
Match length
                   77
% identity
                  (U44087) beta-D-glucosidase precursor [Zea mays]
NCBI Description
                   301260
Seq. No.
                   cat700019425.rl
Seq. ID
                   BLASTX
Method
                   g3128195
NCBI GI
                   320
BLAST score
                   4.0e-30
E value
                   77
Match length
                   79
% identity
                   (AC004521) putative phosphoribosyl pyrophosphate synthetase
NCBI Description
                   [Arabidopsis thaliana] >gi_3341673 (AC003672) putative
                   phosphoribosyl pyrophosphate synthetase [Arabidopsis
                   thaliana]
                   301261
Seq. No.
                   cat700019446.rl
Seq. ID
                   BLASTX
Method
                   g3935181
NCBI GI
                   187
BLAST score
                   2.0e-14
E value
                   46
Match length
                   70
 % identity
                   (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
                   301262
 Seq. No.
                   cat700019462.rl
 Seq. ID
                   BLASTX
 Method
                   g4165488
 NCBI GI
```

```
60
Match length
% identity
                   (AJ132399) alpha-tubulin 3 [Hordeum vulgare]
NCBI Description
                   301263
Seq. No.
                   cat700019515.rl
Seq. ID
                   BLASTX
Method
                   q404688
NCBI GI
                   220
BLAST score
                   2.0e-18
E value
Match length
                   75
                    55
% identity
                   (L19074) cytochrome P450 [Catharanthus roseus]
NCBI Description
                    301264
Seq. No.
Seq. ID
                    cat700019575.rl
Method
                    BLASTX
NCBI GI
                    g2130003
                    196
BLAST score
                    3.0e-21
E value
                    64
Match length
                    81
% identity
                    squamosa-promoter binding protein 1 - garden snapdragon
NCBI Description
                    >gi 1183866_emb CAA63113 (X92369) squamosa-promoter
                    binding protein 1 [Antirrhinum majus]
                    301265
Seq. No.
                    cat700019675.rl
Seq. ID
                    BLASTX
Method
NCBI GI
                    g1174745
BLAST score
                    149
                    5.0e-10
E value
Match length
                    49
                    76
% identity
                    TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                    >gi_1363523_pir__S53761 triose-phosphate isomerase (EC
                    5.3.1.1) precursor, chloroplast - rye
                    >gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase
[Secale cereale] >gi_1095494_prf__2109226B triosephosphate
                    isomerase [Secale cereale]
                    301266
 Seq. No.
                    cat700019710.rl
 Seq. ID
                    BLASTN
 Method
                    g168500
 NCBI GI
                    49
 BLAST score
                     9.0e-19
 E value
                    164
 Match length
                     83
 % identity
                    Maize (Zea mays) histone H4 gene (H4C14), complete cds
 NCBI Description
```

Seq. ID cat700019715.r1

Method BLASTX
NCBI GI g2511531
BLAST score 409
E value 2.0e-40



```
78
 Match length
                   100
 % identity
                    (AF008120) alpha tubulin 1 [Eleusine indica]
 NCBI Description
                   >gi 3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
                   [Eleusine indica]
                   301268
 Seq. No.
                   cat700019756.rl
 Seq. ID
                   BLASTX
Method
                   g2344901
 NCBI GI
                   144
 BLAST score
                   2.0e-09
 E value
                   31
 Match length
 % identity
                   84
                    (AC002388) serine/threonine protein kinase isolog
 NCBI Description
                    [Arabidopsis thaliana]
                    301269
 Seq. No.
                    cat700019764.rl
 Seq. ID
                    BLASTX
 Method
                    g4586246
 NCBI GI
 BLAST score
                    143
                    2.0e-09
 E value
 Match length
                    39
 % identity
                    67
                    (AL049640) putative protein [Arabidopsis thaliana]
 NCBI Description
                    301270
 Seq. No.
                    cat700019795.rl
 Seq. ID
                    BLASTX
 Method
                    q2058313
 NCBI GI
 BLAST score
                    137
                    9.0e-09
 E value
                    45
 Match length
                    51
  % identity
                    (X97433) cinnamoyl-CoA reductase [Eucalyptus gunnii]
 NCBI Description
                    301271
  Seq. No.
                    cat700019839.rl
  Seq. ID
                    BLASTX
  Method
                    g1619297
  NCBI GI
                    389
  BLAST score
                    3.0e-38
  E value
                    73
 Match length
                    100
  % identity
                    (Y08490) alpha-tubulin 2 [Hordeum vulgare]
  NCBI Description
                    301272
  Seq. No.
                    cat700020112.r1
  Seq. ID
                    BLASTX
  Method
                    g4587607
  NCBI GI
  BLAST score
                    221
                    2.0e-18
  E value
                    75
  Match length
                    53
  % identity
                    (AC006951) putative antisense basic fibroblast growth
  NCBI Description
                    factor [Arabidopsis thaliana]
```

```
301273
Seq. No.
                  cat700020186.rl
Seq. ID
Method
                  BLASTX
                  q4567209
NCBI GI
                  168
BLAST score
                  3.0e-12
E value
                  79
Match length
                  47
% identity
                  (AC007168) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  301274
Seq. No.
                  cat700020314.rl
Seq. ID
                  BLASTN
Method
NCBI GI
                  q22378
BLAST score
                  35
                  2.0e-10
E value
                  43
Match length
                  95
% identity
NCBI Description Z.mays gene for nucleic acid binding protein
                  301275
Seq. No.
                   cat700020344.rl
Seq. ID
                  BLASTX
Method
                   g1172633
NCBI GI
BLAST score
                   186
                   2.0e-14
E value
Match length
                   42
                   86
% identity
                  PROLIFERA PROTEIN >gi_675491 (L39954) contains MCM2/3/5
NCBI Description
                   family signature; PROSITE; PS00847; disruption leads to
                   early lethal phenotype; similar to MCM2/3/5 family, most
                   similar to YBR1441 [Arabidopsis thaliana]
                   301276
Seq. No.
                   cat700020388.rl
Seq. ID
                   BLASTX
Method
                   g1405353
NCBI GI
                   170
BLAST score
                   2.0e-12
E value
                   62
Match length
                   56
% identity
                   (D86086) canalicular multispecific organic anion
NCBI Description
                   transporter [Rattus norvegicus]
                   301277
Seq. No.
                   cat700020406.rl
Seq. ID
                   BLASTX
Method
                   q166384
NCBI GI
                   163
BLAST score
                   9.0e-12
E value
Match length
                   33
                   94
 % identity
```

NCBI Description (M35867) histone H3 (H3-1.1) [Medicago sativa]

Seq. No. 301278

Seq. ID cat700020418.rl



```
BLASTN
Method
                  g575730
NCBI GI
                  187
BLAST score
                  1.0e-101
E value
                  187
Match length
% identity
                  100
NCBI Description Z.mays mRNA for transmembrane protein
                   301279
Seq. No.
Seq. ID
                  cat700020521.rl
                  BLASTX
Method
                   q4584545
NCBI GI
                   190
BLAST score
                   8.0e-15
E value
                   65
Match length
% identity
NCBI Description (AL049608) putative protein [Arabidopsis thaliana]
                   301280
Seq. No.
                   cat700020544.r1
Seq. ID
                   BLASTN
Method
                   q22292
NCBI GI
                   88
BLAST score
                   4.0e-42
E value
                   116
Match length
                   94
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
                   301281
Seq. No.
                   cat700020547.r1
Seq. ID
                   BLASTX
Method
                   q2832644
NCBI GI
BLAST score
                   150
                   3.0e-10
E value
                   44
Match length
 % identity
                   70
                   (AL021710) teosinte branched1 - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   301282
 Seq. No.
                   cat700020591.r1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g3687243
                   205
 BLAST score
                   1.0e-16
 E value
 Match length
                   44
                   89
 % identity
                    (AC005169) putative ribosomal protein [Arabidopsis
 NCBI Description
                   thaliana]
                    301283
 Seq. No.
                    cat700020621.rl
 Seq. ID
 Method
                   BLASTX
                    g4585875
 NCBI GI
                    220
 BLAST score
```

2.0e-18

58

E value

Match length



```
% identity
NCBI Description
                 (AC005850) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  301284
Seq. ID
                  cat700020642.rl
Method
                  BLASTX
NCBI GI
                  g2662341
BLAST score
                  383
E value
                  1.0e-37
Match length
                  73
                  97
% identity
NCBI Description
                  (D63580) EF-1 alpha [Oryza sativa]
                  >qi 2662345 dbj BAA23659 (D63582) EF-1 alpha [Oryza
                  satīva] >gi 2662347 dbj BAA23660 (D63583) EF-1 alpha
                  [Oryza sativa]
Seq. No.
                  301285
Seq. ID
                  cat700020659.r1
Method
                  BLASTX
NCBI GI
                  g3236252
BLAST score
                  145
E value
                  1.0e-09
Match length
                  56
% identity
                  55
NCBI Description (AC004684) CER1-like protein [Arabidopsis thaliana]
Seq. No.
                  301286
                  cat700020669.rl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729671
BLAST score
                  151
                  2.0e-10
E value
Match length
                  32
                  94
% identity
NCBI Description HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]
                  301287
Seq. No.
                  cat700020717.rl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1362086
BLAST score
                  405
                  6.0e-40
E value
Match length
                  83
% identity
                  94
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir $65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
```

>gi 886471_emb_CAA58474_ (X83499) methionine synthase

[Catharanthus roseus]

Seq. No.

301288

Seq. ID

cat700020833.r1

Method NCBI GI BLASTX q135398 415

BLAST score

Method

NCBI GI

E value

BLAST score

BLASTX

232

g886740

7.0e-20



```
3.0e-41
E value
Match length
                  77
% identity
                  100
NCBI Description
                  TUBULIN ALPHA-1 CHAIN >gi 82731 pir S15773 tubulin alpha-1
                  chain - maize >qi 22147 emb CAA33734 (X15704)
                  alphal-tubulin [Zea mays]
                  301289
Seq. No.
                  cat700020905.rl
Seq. ID
Method
                  BLASTX
                  g82733
NCBI GI
                  291
BLAST score
                  1.0e-26
E value
Match length
                  83
% identity
                  72
                  ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937)
NCBI Description
                  ubiquitin fusion protein [Zea mays] >gi_902527 (U29161)
                  ubiquitin fusion protein [Zea mays]
                  >gi 1589388 prf 2211240B ubiquitin fusion protein [Zea
                  mays]
                  301290
Seq. No.
Seq. ID
                  cat700020907.rl
Method
                  BLASTX
NCBI GI
                  g4115386
BLAST score
                  144
E value
                  1.0e-09
Match length
                  72
% identity
                  47
NCBI Description
                 (AC005967) unknown protein [Arabidopsis thaliana]
                  301291
Seq. No.
Seq. ID
                  cat700020950.rl
Method
                  BLASTX
NCBI GI
                  g2624328
                  195
BLAST score
E value
                  2.0e-15
Match length
                  60
                  60
% identity
                 (AJ002894) OsGRP2 [Oryza sativa]
NCBI Description
                  301292
Seq. No.
Seq. ID
                  cat700021164.rl
Method
                  BLASTX
NCBI GI
                  q121982
BLAST score
                  168
E value
                  3.0e-12
Match length
                  36
% identity
                  92
NCBI Description HISTONE H2A.2.2
Seq. No.
                  301293
Seq. ID
                  cat700021167.rl
```

```
Match length
% identity
                  (X84376) histone 4 [Zea mays]
NCBI Description
                  301294
Seq. No.
Seq. ID
                  cat700021185.rl
                  BLASTX
Method
NCBI GI
                  q3142295
                  179
BLAST score
                  1.0e-13
E value
                   70
Match length
% identity
                   (AC002411) Strong similarity to phosphoribosylanthranilate
NCBI Description
                   transferase gb_D86180 from Pisum sativum. [Arabidopsis
                   thaliana]
                   301295
Seq. No.
Seq. ID
                   cat700021266.rl
                   BLASTX
Method
                   g2191187
NCBI GI
                   161
BLAST score
                   1.0e-11
E value
                   52
Match length
                   62
% identity
                   (AF007271) contains similarity to a DNAJ-like domain
NCBI Description
                   [Arabidopsis thaliana]
                   301296
Seq. No.
                   cat700021355.rl
Seq. ID
                   BLASTX
Method
```

q2274859 NCBI GI 168 BLAST score

3.0e-12 E value 32 Match length % identity 97

(AJ000016) Cks1 protein [Arabidopsis thaliana] NCBI Description >gi 4510420_gb_AAD21506.1_ (AC006929) putative

cyclin-dependent kinase regulatory subunit [Arabidopsis

thaliana]

301297 Seq. No.

Seq. ID cat700021473.rl

Method BLASTX g4539671 NCBI GI 169 BLAST score 2.0e-12 E value Match length 53 68 % identity

(AF061282) serine carboxypeptidase [Sorghum bicolor] NCBI Description

301298 Seq. No.

cat700021486.rl Seq. ID

Method BLASTN g22320 NCBI GI 34 BLAST score 8.0e-10 E value 64 Match length

```
% identity
NCBI Description Maize H1 mRNA for H1 histone
                  301299
Seq. No.
                  cat700021541.rl
Seq. ID
                  BLASTX
Method
                  q4038471
NCBI GI
                  228
BLAST score
                  3.0e-19
E value
                  52
Match length
% identity
                  83
NCBI Description (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
                  301300
Seq. No.
                  cat700021543.rl
Seq. ID
Method
                  BLASTN
                  q662931
NCBI GI
BLAST score
                  41
                   6.0e-14
E value
                   61
Match length
                   92
% identity
NCBI Description G.max mRNA for heat shock transcription factor
                   301301
Seq. No.
                   cat700021548.rl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1304409
                   162
BLAST score
                   1.0e-11
E value
Match length
                   61
% identity
                   52
NCBI Description (U40344) myristyl-ACP desaturase [Pelargonium hortorum]
                   301302
Seq. No.
                   cat700021636.rl
Seq. ID
                   BLASTN
Method
                   g2645165
NCBI GI
BLAST score
                   69
                   1.0e-30
E value
                   85
Match length
 % identity
                   95
NCBI Description Oryza sativa mRNA, similar to ribosomal protein
                   301303
 Seq. No.
                   cat700021704.rl
 Seq. ID
                   BLASTX
 Method
                   g3152596
 NCBI GI
                   156
 BLAST score
                   6.0e-11
 E value
                   75
 Match length
                   56
 % identity
 NCBI Description (AC002986) YUP8H12R.36 [Arabidopsis thaliana]
                   301304
 Seq. No.
                   cat700021768.rl
 Seq. ID
```

BLASTX

g4006878

Method

NCBI GI



```
BLAST score
                  5.0e-14
E value
Match length
                  60
                  53
% identity
NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
Seq. No.
                  301305
                  cat700021776.rl
Seq. ID
                  BLASTN
Method
                  q1906603
NCBI GI
                  48
BLAST score
                  2.0e-18
E value
                   64
Match length
                   94
% identity
                  Zea mays ACCase gene, intron containing colonist1 and
NCBI Description
                   colonist2 retrotransposons and reverse transcriptase
                  pseudogene, complete sequence
                   301306
Seq. No.
                   cat700021789.rl
Seq. ID
                   BLASTX
Method
                   q498931
NCBI GI
                   205
BLAST score
                   1.0e-16
E value
                   70
Match length
                   63
% identity
                   (Z12825) ORF167; homologous to reverse transcriptases from
NCBI Description
                   retroviral-like transposons TNT 1-94 from tobacco and COPIA
                   from Drosophila [Beta vulgaris]
                   301307
Seq. No.
Seq. ID
                   cat700021845.r1
                   BLASTN
Method
                   q312178
NCBI GI
BLAST score
                   71
                   4.0e-32
E value
                   75
Match length
                   49
% identity
                  Z.mays GapC2 gene
NCBI Description
                   301308
Seq. No.
Seq. ID
                   cat700021935.rl
                   BLASTX
Method
NCBI GI
                   q3335363
                   155
BLAST score
                   9.0e-11
E value
                   72
Match length
 % identity
                   40
                   (AC003028) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301309
 Seq. No.
                   cat700022019.rl
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g2583135
```

319

67

5.0e-30

BLAST score

Match length

E value



```
% identity
                  (AC002387) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3822216 (AF074948) FIL [Arabidopsis thaliana]
                  >gi_4322477_gb_AAD16053_ (AF087015) abnormal floral organs
                  protein [Arabidopsis thaliana]
                  301310
Seq. No.
                  ceu700421522.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  g462195
                  436
BLAST score
                  2.0e-43
E value
                  93
Match length
% identity
                  89
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                  >gi 100682 pir S21636 GOS2 protein - rice
                  >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                  >gi_3789950 (AF094774) translation initiation factor [Oryza
                  sativa]
                  301311
Seq. No.
                  ceu700421529.h1
Seq. ID
                  BLASTX
Method
                  g2244989
NCBI GI
BLAST score
                  223
                  1.0e-18
E value
Match length
                  71
% identity
                  62
                  (Z97340) strong similarity to naringenin 3-dioxygenase
NCBI Description
                  [Arabidopsis thaliana]
                  301312
Seq. No.
                  ceu700421531.h1
Seq. ID
                  BLASTX
Method
                  g3292817
NCBI GI
                  244
BLAST score
                  6.0e-21
E value
Match length
                  95
                  55
% identity
                  (AL031018) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  301313
Seq. No.
                  ceu700421571.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3721836
BLAST score
                  202
                  4.0e-16
E value
                  59
Match length
                  75
% identity
                  (AB013384) HIP3 [Homo sapiens]
NCBI Description
Seq. No.
                  301314
                  ceu700421578.hl
Seq. ID
                  BLASTX
Method
```

NCBI GI q3269291

BLAST score 190 E value 1.0e-14



```
Match length 76
% identity 57
NCBI Description (AL030978) putative receptor protein kinase [Arabidopsis thaliana]
```

Seq. No. 301315

Seq. ID ceu700421596.hl

Method BLASTX
NCBI GI 94210948
BLAST score 257
E value 1.0e-22
Match length 50
% identity 96

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 301316

Seq. ID ceu700421675.hl

Method BLASTN
NCBI GI 94503730
BLAST score 78
E value 3.0e-36
Match length 98
% identity 95

NCBI Description Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA,

and translated products >gi_3319236_gb_AF038847_AF038847 Homo sapiens 36 kDa FK506 binding protein (FKBP36) mRNA,

complete cds

Seq. No. 301317

Seq. ID ceu700421714.h1

Method BLASTN
NCBI GI g1657753
BLAST score 187
E value 1.0e-101
Match length 199
% identity 98

NCBI Description Human elastin (ELN) gene, partial cds, and LIM-kinase

(LIMK1) gene, complete cds

Seq. No. 301318

Seq. ID ceu700421719.h1

Method BLASTN
NCBI GI g22430
BLAST score 233
E value 1.0e-128
Match length 275
% identity 97

NCBI Description Maize pseudo-Gpa2 pseudogene for glyceraldehyde-3-phosphate

dehydrogenase subunit A

Seq. No. 301319

Seq. ID ceu700421726.h1

Method BLASTN
NCBI GI g3413919
BLAST score 146
E value 8.0e-77
Match length 158



```
% identity
NCBI Description Homo sapiens mRNA for KIAA0479 protein, partial cds
                  301320
Seq. No.
                  ceu700421728.hl
Seq. ID
                  BLASTX
Method
                  q3292816
NCBI GI
BLAST score
                  169
                  3.0e-12
E value
                  60
Match length
% identity
                  60
                  (AL031018) putative fizzy-related protein [Arabidopsis
NCBI Description
                  thaliana]
                  301321
Seq. No.
Seq. ID
                   ceu700421730.hl
Method
                  BLASTX
NCBI GI
                   q4585897
                   189
BLAST score
                   1.0e-14
E value
                   55
Match length
% identity
                   64
                  (AC007133) hypothetical protein, 5' partial [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   301322
                   ceu700421753.hl
Seq. ID
                   BLASTN
Method
                   g22221
NCBI GI
BLAST score
                   44
                   1.0e-15
E value
Match length
                   60
% identity
                   93
NCBI Description Z.mays ZSF4C3 gene for zein
                   301323
Seq. No.
                   ceu700421774.hl
Seq. ID
                   BLASTN
Method
                   q4454705
NCBI GI
                   146
BLAST score
                   7.0e-77
E value
                   150
Match length
                   99
% identity
NCBI Description Homo sapiens chromosome 17 HSPC009 mRNA, complete cds
                   301324
 Seq. No.
                   ceu700421787.h1
 Seq. ID
                   BLASTX
Method
                   g1709848
NCBI GI
                   191
 BLAST score
                   7.0e-15
 E value
 Match length
                   78
                   53
 % identity
                   PHOTOSYSTEM II REACTION CENTRE W PROTEIN
 NCBI Description
                   >gi 2147936 pir__S73268 photosystem II protein W - Porphyra
```

protein W [Porphyra purpurea]

purpurea chloroplast >gi_1276813 (U38804) Photosystem II

```
301325
Seq. No.
Seq. ID
                  ceu700421808.hl
                  BLASTX
Method
NCBI GI
                  g2393722
BLAST score
                  180
                  9.0e-14
E value
                  36
Match length
                  97
% identity
                  (U90313) glutathione-S-transferase homolog [Homo sapiens]
NCBI Description
                  301326
Seq. No.
                   ceu700421842.hl
Seq. ID
                   BLASTN
Method
                   g3342001
NCBI GI
BLAST score
                   134
E value
                   1.0e-69
Match length
                   183
% identity
                   94
                  Homo sapiens hematopoietic cell derived zinc finger protein
NCBI Description
                   mRNA, complete cds
                   301327
Seq. No.
Seq. ID
                   ceu700421848.h1
                   BLASTX
Method
                   q4263831
NCBI GI
BLAST score
                   140
                   6.0e-09
E value
                   78
Match length
% identity
                   44
                   (AC006067) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
                   301328
Seq. No.
                   ceu700421861.hl
Seq. ID
                   BLASTX
Method
                   g4512018
NCBI GI
                   306
BLAST score
                   2.0e-28
E value
                   71
Match length
                   82
% identity
                   (AF106660) mRNA binding protein precursor [Lycopersicon
NCBI Description
                   esculentum]
                   301329
Seq. No.
                   ceu700421876.hl
 Seq. ID
                   BLASTN
Method
                   g3043569
NCBI GI
                   125
BLAST score
                   3.0e-64
E value
                   154
Match length
                   94
 % identity
```

NCBI Description Homo sapiens mRNA for KIAA0523 protein, partial cds

Seq. No. 301330

Seq. ID ceu700421973.h1

Method BLASTX



```
g3641252
NCBI GI
                  281
BLAST score
                  1.0e-25
E value
Match length
                  57
                  86
% identity
                  (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                  domestica]
                  301331
Seq. No.
                  ceu700422069.hl
Seq. ID
                  BLASTX
Method
                  g1001257
NCBI GI
                  235
BLAST score
                  5.0e-20
E value
Match length
                  84
% identity
                  51
                  (D64003) hypothetical protein [Synechocystis sp.]
NCBI Description
                  301332
Seq. No.
                  ceu700422087.h1
Seq. ID
Method
                  BLASTX
                  q4506883
NCBI GI
                  186
BLAST score
                  2.0e-14
E value
Match length
                  39
                  97
% identity
                  semenogelin I >gi_134426_sp_P04279_SEM1_HUMAN SEMENOGELIN I
NCBI Description
                  PROTEIN PRECURSOR (SGI) [CONTAINS: SEMINAL BASIC PROTEIN;
                  ALPHA-INHIBIN-92; ALPHA-INHIBIN-31] >gi_338019 (J04440)
                   semenogelin [Homo sapiens]
                   301333
Seq. No.
                   ceu700422091.h1
Seq. ID
                   BLASTN
Method
                   g2411434
NCBI GI
                   243
BLAST score
                   1.0e-134
E value
                   251
Match length
                   99
% identity
                   Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21)
NCBI Description
                   from the Roswell Park Cancer Institute, complete sequence
                   [Homo sapiens]
                   301334
Seq. No.
                   ceu700422165.h1
Seq. ID
                   BLASTX
Method
                   g4539355
NCBI GI
                   139
BLAST score
                   9.0e-09
E value
Match length
                   68
% identity
                   46
                  (AL049525) putative protein [Arabidopsis thaliana]
NCBI Description
```

301335 Seq. No.

Seq. ID ceu700422192.h1

Method BLASTX g4432825 NCBI GI



```
292
BLAST score
                  1.0e-26
E value
                  83
Match length
% identity
                  61
                  (ACO06593) putative SOP2p protein [Arabidopsis thaliana]
NCBI Description
                  301336
Seq. No.
                  ceu700422230.h1
Seq. ID
                  BLASTX
Method
                  g3212861
NCBI GI
                  195
BLAST score
                  2.0e-15
E value
Match length
                  46
                  78
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   301337
Seq. No.
                   ceu700422244.h1
Seq. ID
Method
                   BLASTN
                   g452340
NCBI GI
BLAST score
                   79
                   7.0e-37
E value
                   95
Match length
                   96
% identity
                   Z.mays mRNA for type II light-harvesting chlorophyll
NCBI Description
                   a/b-binding protein
                   301338
Seq. No.
                   ceu700422316.h1
Seq. ID
                   BLASTN
Method
                   q1684871
NCBI GI
BLAST score
                   159
                   1.0e-84
E value
                   163
Match length
                   99
% identity
                   Homo sapiens LPS-Induced TNF-Alpha Factor (LITAF) mRNA,
NCBI Description
                   complete cds
                   301339
Seq. No.
                   ceu700422377.h1
Seq. ID
                   BLASTX
Method
                   q82733
NCBI GI
                   190
BLAST score
                   6.0e-15
E value
                   39
Match length
                   90
 % identity
                   ubiquitin fusion protein UBF9 - maize >gi 168651 (M68937)
NCBI Description
                   ubiquitin fusion protein [Zea mays] >gi_902527 (U29161)
                   ubiquitin fusion protein [Zea mays]
                   >gi_1589388_prf__2211240B ubiquitin fusion protein [Zea
                   mays]
                   301340
 Seq. No.
                   ceu700422385.h1
 Seq. ID
                   BLASTX
 Method
```

g99758

159

NCBI GI

BLAST score



```
3.0e-11
E value
Match length
                  37
                  76
% identity
                  monosaccharid transport protein STP4 - Arabidopsis thaliana
NCBI Description
                  >gi_16524_emb_CAA47325_ (X66857) sugar transport protein
                  [Arabidopsis thaliana]
                  301341
Seq. No.
                  ceu700422424.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4567173
                  107
BLAST score
                  1.0e-53
E value
                   123
Match length
                   97
% identity
                  Homo sapiens chromosome 19, cosmid R34187, complete
NCBI Description
                   sequence
                   301342
Seq. No.
                   ceu700422426.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3914555
                   234
BLAST score
                   4.0e-20
E value
                   71
Match length
% identity
                   PUTATIVE RIBOSOME-BINDING FACTOR A, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_3096942_emb_CAA18852.1_ (AL023094) putative protein
                   [Arabidopsis thaliana]
                   301343
Seq. No.
                   ceu700422519.h1
Seq. ID
                   BLASTX
Method
                   g3941468
NCBI GI
                   259
BLAST score
                   8.0e-23
E value
Match length
                   55
                   78
% identity
                   (AF062888) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   301344
Seq. No.
                   ceu700422540.h1
 Seq. ID
                   BLASTX
Method
                   g1747296
NCBI GI
                   330
BLAST score
                   4.0e-31
 E value
                   70
Match length
                   97
 % identity
```

(D45384) vacuolar H+-pyrophosphatase [Oryza sativa] NCBI Description >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]

301345 Seq. No.

ceu700422613.h1 Seq. ID

BLASTN Method g405634 NCBI GI BLAST score 85



E value 2.0e-40 Match length 180 88

NCBI Description Z.mays zmcpt mRNA triose phosphate/phosphate translocator

Seq. No. 3

301346

Seq. ID

ceu700422631.h1

Method BLASTX
NCBI GI g2262136
BLAST score 159
E value 2.0e-11
Match length 31
% identity 94

NCBI Description (AC002330) predicted protein of unknown function

[Arabidopsis thaliana] >gi_4263520_gb_AAD15346_ (AC004044)

predicted protein of unknown function [Arabidopsis

thaliana]

Seq. No. 301347

Seq. ID ceu700422639.h1

Method BLASTX
NCBI GI g4506885
BLAST score 227
E value 3.0e-19
Match length 58
% identity 79

NCBI Description semenogelin II >gi 401079 sp 002383 SEM2 HUMAN SEMENOGELIN

II PRECURSOR (SGII) >gi 346359 pir A43412 semenogelin II precursor - human >gi 307418 (M81651) semenogelin II [Homo sapiens] >gi 338239 (M81652) semenogelin II [Homo sapiens] >gi 1147570 emb CAA87637 (Z47556) semenogelin II [Homo

sapiens]

Seq. No. 301348

Seq. ID ceu700422736.h1

Method BLASTX
NCBI GI g2832677
BLAST score 154
E value 2.0e-10
Match length 82
% identity 38

NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301349

Seg. ID ceu700422775.h1

Method BLASTN
NCBI GI g2984582
BLAST score 120
E value 4.0e-61
Match length 268
% identity 95

NCBI Description Homo sapiens chromosome 9, Pl clone 11659, complete

sequence [Homo sapiens]

Seq. No. 301350

Seq. ID ceu700422887.h1

Method BLASTX

```
q4455271
NCBI GI
                  240
BLAST score
                  1.0e-20
E value
                  81
Match length
                  56
% identity
                  (AL035527) serine protease-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  301351
Seq. No.
                  ceu700422908.h1
Seq. ID
                  BLASTX
Method
                  g2244940
NCBI GI
                   161
BLAST score
                   3.0e-11
E value
                  47
Match length
                   64
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301352
Seq. No.
                   ceu700422974.h1
Seq. ID
                   BLASTN
Method
                   g1663516
NCBI GI
                   172
BLAST score
                   4.0e-92
E value
                   234
Match length
                   94
% identity
                  Homo sapiens mRNA for membrane glycoprotein M6, complete
NCBI Description
                   cds
                   301353
Seq. No.
                   ceu700423143.h1
Seq. ID
                   BLASTN
Method
                   g2898171
NCBI GI
BLAST score
                   103
                   2.0e-51
E value
                   115
Match length
                   97
% identity
NCBI Description Homo sapiens microtubule-associated protein tau (tau) gene,
                   alternatively spliced products, exon 13/14 and complete cds
                   301354
Seq. No.
                   ceu700423146.h1
Seq. ID
                   BLASTX
Method
                   g3293031
NCBI GI
BLAST score
                   320
E value
                   6.0e-30
Match length
                   90
                   67
% identity
                  (AJ007574) amino acid carrier [Ricinus communis]
NCBI Description
```

Seq. No. 301355

Seq. ID ceu700423150.h1

Method BLASTX
NCBI GI g2494275
BLAST score 253
E value 4.0e-22
Match length 88

% identity NCBI Description ELONGATION FACTOR P (EF-P) >gi 1399829 (U59235) elongation factor P [Synechococcus PCC7942] 301356 Seq. No. ceu700423233.h1 Seq. ID BLASTX Method g2760327 NCBI GI 246 BLAST score 4.0e-21 E value 58 Match length 79 % identity (AC002130) F1N21.12 [Arabidopsis thaliana] NCBI Description Seq. No. 301357 ceu700423234.h1 Seq. ID BLASTX Method q1279876 NCBI GI 148 BLAST score 2.0e-14E value Match length 61 61 % identity (U52867) high affinity sulfate transporter HVST1 [Hordeum NCBI Description vulgare] 301358 Seq. No. ceu700423243.h1 Seq. ID BLASTN Method g1213279 NCBI GI 54 BLAST score 1.0e-21 E value 54 Match length 100 % identity NCBI Description Z.mays ZEMc gene 301359 Seq. No. ceu700423301.h1 Seq. ID

Method BLASTX
NCBI GI g231654
BLAST score 157
E value 5.0e-11
Match length 33
% identity 88

NCBI Description BRITTLE-1 PROTEIN PRECURSOR >gi_82676_pir__JQ1459 Bt1 protein precursor - maize >gi_168426 (M79333) brittle-1

protein [Zea mays]

Seq. No. 301360

Seq. ID ceu700423456.h1

Method BLASTX
NCBI GI g3193328
BLAST score 296
E value 4.0e-27
Match length 76
% identity 67

NCBI Description (AF069299) No definition line found [Arabidopsis thaliana]



```
301361
Seq. No.
                  ceu700423471.h1
Seq. ID
Method
                  BLASTN
                  g4240320
NCBI GI
BLAST score
                  275
                  1.0e-153
E value
                  287
Match length
                  99
% identity
NCBI Description Homo sapiens mRNA for KIAA0916 protein, partial cds
Seq. No.
                  301362
                  ceu700423583.hl
Seq. ID
                  BLASTN
Method
                  g4503872
NCBI GI
BLAST score
                  83
E value
                  2.0e-39
                   99
Match length
                   96
% identity
                  Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1)
NCBI Description
                   mRNA >gi_182935_gb_M81883_HUMGAD67A Human glutamate
                   decarboxylase (GAD67) mRNA, complete cds.
                   >gi_1408341_gb_G28526_G28526 human STS SHGC-31511
                   301363
Seq. No.
                   ceu700423665.hl
Seq. ID
                   BLASTX
Method
                   g3522947
NCBI GI
BLAST score
                   179
                   2.0e-13
E value
Match length
                   52
% identity
                   62
                  (AC004411) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301364
Seq. No.
                   ceu700423670.h1
Seq. ID
                   BLASTX
Method
                   g4510348
NCBI GI
                   148
BLAST score
                   8.0e-10
E value
                   57
Match length
% identity
                   60
                   (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   301365
Seq. No.
                   ceu700423689.h1
Seq. ID
                   BLASTX
Method
                   g419792
NCBI GI
                   419
BLAST score
                   1.0e-41
 E value
                   84
Match length
                   94
 % identity
                   alternative oxidase - voodoo lily >gi_21216_emb_CAA78823_
 NCBI Description
                   (Z15117) salicylic acid-inducible alternative oxidase
                   [Sauromatum guttatum]
```

301366

ceu700423711.h1

Seq. No.

Seq. ID



```
BLASTN
Method
NCBI GI
                  g733457
BLAST score
                  84
E value
                  6.0e-40
Match length
                  127
% identity
                  94
NCBI Description Zea mays chlorophyll a/b-binding apoprotein CP24 (Lhcb6-1)
                  mRNA, complete cds
Seq. No.
                  301367
Seq. ID
                  ceu700423717.h1
Method
                  BLASTX
NCBI GI
                  g2129628
BLAST score
                  154
E value
                  2.0e-10
Match length
                  92
% identity
                  43
NCBI Description ketoconazole resistent protein - Arabidopsis thaliana
                  >gi 928938 emb CAA61433 (X89036) ketoconazole resistent
                  protein [Arabidopsis thaliana]
                  301368
Seq. No.
                  ceu700423838.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206306
                  289
BLAST score
E value
                  2.0e-41
Match length
                  89
% identity
                  95
NCBI Description (AF049110) prpol [Zea mays]
Seq. No.
                  301369
Seq. ID
                  ceu700423847.h1
Method
                  BLASTN
NCBI GI
                  g387670
BLAST score
                  135
E value
                  2.0e-70
Match length
                  139
                  99
% identity
NCBI Description Human MG61 mRNA, partial cds
Seq. No.
                  301370
Seq. ID
                  ceu700423863.h1
Method
                  BLASTN
NCBI GI
                  q4507098
BLAST score
                  59
E value
                  8.0e-25
Match length
                  132
```

% identity 95

NCBI Description Homo sapiens synaptosomal-associated protein, 25kD (SNAP25)

mRNA >gi_2373387_dbj_D21267_D21267 Homo sapiens mRNA,

complete cds

Seq. No.

301371

Seq. ID

ceu700423877.h1

Method NCBI GI BLASTX q4467125



```
208
BLAST score
                  8.0e-17
E value
Match length
                  88
% identity
                  53
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                  301372
Seq. No.
                  ceu700423958.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2668747
BLAST score
                  61
                  7.0e-26
E value
Match length
                  61
                  100
% identity
NCBI Description Zea mays ribosomal protein L17 (rpl17) mRNA, complete cds
                  301373
Seq. No.
                  ceu700423967.h1
Seq. ID
                  BLASTN
Method
                  q3360421
NCBI GI
BLAST score
                  223
                   1.0e-122
E value
                   243
Match length
                   98
% identity
NCBI Description Homo sapiens clone 23887 mRNA sequence
                   301374
Seq. No.
                   ceu700424002.h1
Seq. ID
Method
                   BLASTX
                   g585574
NCBI GI
                   234
BLAST score
E value
                   4.0e-20
Match length
                   52
                   85
% identity
                  NEURONAL PROTEIN NP25 >gi_2119343_pir__I52644 neuronal
NCBI Description
                   protein - rat >gi_205755 (M84725) neuronal protein [Rattus
                   norvegicus]
                   301375
Seq. No.
                   ceu700424010.h1
Seq. ID
                   BLASTN
Method
                   q3097872
NCBI GI
BLAST score
                   120
                   4.0e-61
E value
                   245
Match length
                   97
% identity
                   Homo sapiens chromosome 17, clone HCIT305D20, complete
NCBI Description
                   sequence [Homo sapiens]
                   301376
Seq. No.
                   ceu700424017.h1
Seq. ID
Method
                   BLASTN
                   g1835730
NCBI GI
                   33
BLAST score
```

4.0e-09

33

100

E value

Match length

% identity



NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA,

complete cds

Seq. No. 301377

Seq. ID ceu700424046.h1

Method BLASTX
NCBI GI g2286121
BLAST score 144
E value 2.0e-09
Match length 42
% identity 69

NCBI Description (U88068) sec14 like protein [Oryza sativa]

Seq. No. 301378

Seq. ID ceu700424085.h1

Method BLASTN
NCBI GI g37967
BLAST score 198
E value 1.0e-107
Match length 254
% identity 94

NCBI Description H.sapiens WRS gene for tryptophanyl-tRNA synthetase, exon

Seq. No. 301379

Seq. ID ceu700424116.h1

Method BLASTN
NCBI GI g3413869
BLAST score 120
E value 5.0e-61
Match length 252
% identity 91

NCBI Description Homo sapiens mRNA for KIAA0454 protein, partial cds

Seq. No. 301380

Seq. ID ceu700424174.h1

Method BLASTX
NCBI GI g2815606
BLAST score 140
E value 1.0e-13
Match length 56
% identity 76

NCBI Description (AF025439) Opa-interacting protein OIP3 [Homo sapiens]

Seq. No. 301381

Seq. ID ceu700424195.h1

Method BLASTX
NCBI GI g461999
BLAST score 166
E value 1.0e-20
Match length 82
% identity 67

NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)

Seq. No. 301382

Seq. ID ceu700424281.h1

Method BLASTX NCBI GI g4510348



```
158
BLAST score
                  3.0e-11
E value
                  60
Match length
% identity
                  70
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                  301383
Seq. No.
                  ceu700424324.h1
Seq. ID
                  BLASTX
Method
                  g540450
NCBI GI
                  152
BLAST score
                  3.0e-10
E value
                  53
Match length
                  62
% identity
                  (M28584) MHC class II DR-beta [Homo sapiens]
NCBI Description
                  301384
Seq. No.
                  ceu700424327.h1
Seq. ID
Method
                  BLASTX
                  q4508068
NCBI GI
BLAST score
                  162
E value
                  2.0e-11
                  63
Match length
                  57
% identity
                  (AC005882) 3063 [Arabidopsis thaliana]
NCBI Description
                   301385
Seq. No.
                   ceu700424345.h1
Seq. ID
Method
                  BLASTX
                   q466160
NCBI GI
                   230
BLAST score
                   2.0e-19
E value
                   58
Match length
                   76
% identity
                  HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
NCBI Description
                   >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis
                   elegans >gi 289769 (L14429) putative [Caenorhabditis
                   elegans]
                   301386
Seq. No.
                   ceu700424359.h1
Seq. ID
                   BLASTX
Method
                   g2494849
NCBI GI
                   287
BLAST score
                   3.0e-26
E value
                   77
Match length
                   69
% identity
                   HYDROXYACYLGLUTATHIONE HYDROLASE (GLYOXALASE II) (GLX II)
NCBI Description
                   >qi 1237213 emb CAA62483_ (X90999) glyoxalase II [Homo
                   sapiens]
                   301387
Seq. No.
```

Seq. ID ceu700424413.h1

Method BLASTN NCBI GI g3582311 BLAST score 63

E value 2.0e-27



Match length 87
% identity 93
NCBI Description Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence [Homo sapiens]

Seq. No. 301388
Seq. ID ceu700424487.h1
Method BLASTN
NCBI GI g3005598

NCBI GI g3005598
BLAST score 79
E value 5.0e-37
Match length 87
% identity 98

NCBI Description Homo sapiens katanin p80 subunit mRNA, complete cds

Seq. No. 301389

Seq. ID ceu700424502.h1

Method BLASTX
NCBI GI g133978
BLAST score 255
E value 2.0e-22
Match length 75
% identity 73

NCBI Description 40S RIBOSOMAL PROTEIN S6 (PHOSPHOPROTEIN NP33)

>gi_70932_pir__R3RTS6 ribosomal protein S6 - rat
>gi_70933_pir__R3MS6 ribosomal protein S6 - mouse
>gi_319910_pir__R3HU6 ribosomal protein S6 - human

>gi_36148_emb_CAA47719_ (X67309) ribosomal protein S6 [Homo sapiens] >gi_54010_emb_CAA68430_ (Y00348) ribosomal protein S6 [Mus musculus] >gi_206747 (M29358) ribosomal protein S6 [Rattus norvegicus] >gi_307393 (M77232) ribosomal protein S6 [Homo sapiens] >gi_1177549_emb_CAA90936_ (Z54209) rpS6

[Mus musculus]

Seq. No. 301390

Seq. ID ceu700424520.h1

Method BLASTX
NCBI GI g3288881
BLAST score 292
E value 1.0e-26
Match length 88
% identity 77

NCBI Description (AF073839) bithoraxoid-like protein [Rattus norvegicus]

Seq. No. 301391

Seq. ID ceu700424560.h1

Method BLASTX
NCBI GI g4468986
BLAST score 176
E value 4.0e-13
Match length 66
% identity 44

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 301392

Seq. ID ceu700424624.hl

Method BLASTN



g4506044 NCBI GI BLAST score 105 3.0e-52 E value 173 Match length % identity Homo sapiens proteoglycan 1, secretory granule (PRG1) mRNA NCBI Description >gi_32432_emb_X17042_HSHPCP Human mRNA for hematopoetic proteoglycan core protein 301393 Seq. No. ceu700424638.h1 Seq. ID BLASTN Method g4090180 NCBI GI 85 BLAST score 2.0e-40 E value 120 Match length 93 % identity Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human NCBI Description BAC Library) complete sequence [Homo sapiens] 301394 Seq. No. ceu700424641.h1 Seq. ID BLASTN Method NCBI GI g181207 142 BLAST score 2.0e-74 E value 178 Match length 97 % identity Human Cu/Zn superoxide dismutase gene NCBI Description 301395 Seq. No. ceu700424686.h1 Seq. ID BLASTX Method q3287688 NCBI GI 148 BLAST score 5.0e-10 E value Match length 40 % identity 72 (AC003979) Contains similarity to ycf37 gene product NCBI Description gb 1001425 from Synechocystis sp. genome gb_D63999. ESTs gb_T43026, gb_R64902, gb_Z18169 and gb_N37374 come from this gene. [Arabidopsis thaliana] 301396 Seq. No. ceu700424714.h1 Seq. ID BLASTX Method g3006143 NCBI GI 164 BLAST score 1.0e-11 E value 42 Match length

69 % identity

(AL022299) hypothetical protein [Schizosaccharomyces pombe] NCBI Description

301397 Seq. No.

ceu700424732.hl Seq. ID

BLASTX Method g2244816 NCBI GI



```
BLAST score
                  2.0e-11
E value
                  67
Match length
                  40
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
                  301398
Seq. No.
                  ceu700424769.h1
Seq. ID
                  BLASTX
Method
                  g4115559
NCBI GI
                  238
BLAST score
                  2.0e-20
E value
                  82
Match length
                   50
% identity
                  (AB013596) UDP-glucose:anthocysnin 5-0-glucosyltransferase
NCBI Description
                   [Perilla frutescens]
                   301399
Seq. No.
                   ceu700424933.h1
Seq. ID
                   BLASTX
Method
                   g3779218
NCBI GI
                   142
BLAST score
                   3.0e-09
E value
                   36
Match length
                   72
% identity
                  (AF030879) protein kinase CPK1 [Solanum tuberosum]
NCBI Description
                 301400
Seq. No.
                   ceu700424993.h1
Seq. ID
                   BLASTX
Method
                   g1806192
NCBI GI
                   164
BLAST score
                   9.0e-12
E value
                   84
Match length
                   40
% identity
                  (Z84395) sppA [Mycobacterium tuberculosis]
NCBI Description
                   301401
Seq. No.
                   ceu700424996.h1
Seq. ID
                   BLASTN
Method
                   q3036778
NCBI GI
                   121
BLAST score
                   5.0e-62
E value
                   129
Match length
                   98
% identity
```

NCBI Description Human DNA sequence from cosmid 398G5 from a region of the tip of the short arm of chromosome 16, spanning 2Mb of

16p13.3. Contains RAR (RAS like GTPASE) like gene, an

anonymous gene and ESTs. Contains CpG island

Seq. No. 301402

Seq. ID ceu700425005.h1

Method BLASTX
NCBI GI g295855
BLAST score 313
E value 3.0e-29
Match length 64



```
% identity
                  (X15642) P-pyruvate carboxylase [Zea mays]
NCBI Description
Seq. No.
                  301403
                  ceu700425034.h1
Seq. ID
                  BLASTX
Method
                  q2979544
NCBI GI
                  320
BLAST score
                  7.0e-30
E value
Match length
                  93
% identity
                  60
                  (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]
NCBI Description
                  301404
Seq. No.
Seq. ID
                  ceu700425066.h1
Method
                  BLASTX
                  q4507065
NCBI GI
                  440
BLAST score
                  5.0e-44
E value
Match length
                  92
                  83
% identity
                  secretory leukocyte protease inhibitor
NCBI Description
                   (antileukoproteinase) >gi_113636_sp_P03973_ALK1_HUMAN
                  ANTILEUKOPROTEINASE 1 PRECURSOR (ALP) (HUSI-1) (SEMINAL
                  PROTEINASE INHIBITOR) (SECRETORY LEUKOCYTE PROTEASE
                  INHIBITOR) (BLPI) (MUCUS PROTEINASE INHIBITOR) (MPI)
                  >gi_1070529_pir__TIHUSP antileukoproteinase 1 precursor -
                  human >gi_28639_emb_CAA28158_ (X04470) precursor ALP [Homo
                   sapiens] >gi_36491_emb_CAA28188_ (X04503) SLPI-precursor
                   [Homo sapiens] >gi_758\overline{101}emb_CAA28187_ (X04502) secretory
                   leukocyte protease inhibitor (SLPI) [Homo sapiens]
                  >gi 4378759 gb_AAD19661_ (AF114471) secretory leukocyte
                  proteinase inhibitor precursor [Homo sapiens]
                   301405
Seq. No.
                   ceu700425119.hl
Seq. ID
                   BLASTN
Method
                   g3176654
NCBI GI
                   70
BLAST score
                   1.0e-31
E value
Match length
                   123
                   96
% identity
                  Homo sapiens chromosome 16, cosmid clone RT140 (LANL),
NCBI Description
                   complete sequence [Homo sapiens]
                   301406
Seq. No.
                   ceu700425120.h1
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI 94102582
BLAST score 163
E value 2.0e-11
Match length 63
% identity 52

NCBI Description (AF013115) CAO [Arabidopsis thaliana]

Seq. No.

Seq. ID ceu700425135.h1

301407



BLASTN Method q687589 NCBI GI BLAST score 163 E value 7.0e-87 Match length 187 97 % identity

Human (AF1q) mRNA, complete cds NCBI Description

Seq. No. Seq. ID

301408 ceu700425136.h1

BLASTN Method g285909 NCBI GI BLAST score 177 4.0e-95 E value Match length 212 % identity 97

Homo sapiens P2 mRNA for ATP synthase subunit c, complete NCBI Description

Seq. No.

301409

Seq. ID

ceu700425224.h1

Method BLASTX g4262242 NCBI GI BLAST score 148 1.0e-16 E value

Match length 52 % identity

(AC006200) NADC homolog [Arabidopsis thaliana] NCBI Description

301410 Seq. No.

ceu700425227.h1 Seq. ID BLASTN Method

q3550039 NCBI GI 114 BLAST score 7.0e-58 E value 121 Match length 99 % identity

Human DNA sequence from clone 333H23 on chromosome NCBI Description

22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold

alternatively spliced gene for Synaptogyrin 1A, 1B

301411 Seq. No.

ceu700425273.h1 Seq. ID

BLASTN Method g3281967 NCBI GI 142 BLAST score 2.0e-74 E value 169 Match length 96 % identity

NCBI Description Human DNA sequence from clone 425C14 on chromosome 6q22

Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar

to the placental protein DIFF33 gene. Contains

301412 Seq. No.

ceu700425274.h1 Seq. ID



```
BLASTN
Method
                  g1633547
NCBI GI
BLAST score
                  101
                  6.0e-50
E value
Match length
                  167
                  98
% identity
                  Human chromosome 12p13 sequence, complete sequence [Homo
NCBI Description
                  sapiens]
                  301413
Seq. No.
                  ceu700425276.h1
Seq. ID
                  BLASTN
Method
                  g3582736
NCBI GI
                  98
BLAST score
                   4.0e-48
E value
Match length
                   105
% identity
                   99
                   Homo sapiens putative holocytochrome c-type synthetase
NCBI Description
                   (HCCS) gene, nuclear gene encoding mitochondrial protein,
                   301414
Seq. No.
                   ceu700425315.h1
Seq. ID
                   BLASTX
Method
                   q3800742
NCBI GI
                   140
BLAST score
                   4.0e-09
E value
                   35
Match length
                   80
% identity
                  (AF036548) RGC-32 [Rattus norvegicus]
NCBI Description
                   301415
Seq. No.
Seq. ID
                   ceu700425331.h1
                   BLASTN
Method
                   q533965
NCBI GI
BLAST score
                   134
                   1.0e-69
E value
Match length
                   188
                   93
 % identity
 NCBI Description H.sapiens (xs99) mRNA, 344bp
                   301416
 Seq. No.
                   ceu700425370.h1
 Seq. ID
                   BLASTX
 Method
                   q3287693
 NCBI GI
                   210
 BLAST score
                   2.0e-22
 E value
 Match length
                   62
                   87
 % identity
                   (AC003979) Similar to LIM17 gene product gb 1653769 from
 NCBI Description
                   the genome of Synechocystis sp. gb_D90916. [Arabidopsis
```

Seq. No. 301417

Seq. ID ceu700425446.h1

thaliana]

Method BLASTN NCBI GI g1228046



BLAST score 130 E value 3.0e-67 Match length 150 % identity 97

NCBI Description Human mRNA for KIAA0199 gene, partial cds

Seq. No. 301418

Seq. ID ceu700425609.h1

Method BLASTX
NCBI GI g2832692
BLAST score 239
E value 2.0e-20
Match length 63
% identity 68

NCBI Description (AL021713) putative protein [Arabidopsis thaliana]

Seq. No. 301419

Seq. ID ceu700425688.h1

Method BLASTN
NCBI GI 94503012
BLAST score 195
E value 1.0e-106
Match length 218
% identity 97

NCBI Description Homo sapiens copine I (CPNE1) mRNA

>gi_1791256_gb_U83246_HSU83246 Homo sapiens copine I mRNA,

complete cds

Seq. No. 301420

Seq. ID ceu700425793.h2

Method BLASTX
NCBI GI g2244965
BLAST score 245
E value 3.0e-21
Match length 79
% identity 57

NCBI Description (Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No. 301421

Seq. ID ceu700425940.h1

Method BLASTN
NCBI GI g4185579
BLAST score 103
E value 3.0e-51
Match length 119
% identity 97

NCBI Description Homo sapiens p120E4F transcription factor mRNA, complete

cds

Seq. No. 301422

Seq. ID ceu700426046.h1

Method BLASTX
NCBI GI g282748
BLAST score 182
E value 9.0e-14
Match length 80
% identity 42

NCBI Description



```
gene coxII intron 2 protein - liverwort (Marchantia
NCBI Description
                  polymorpha) mitochondrion >gi_786218 (M68929) coxII intron2
                  ORF [Marchantia polymorpha]
Seq. No.
                  301423
                  ceu700426114.h1
Seq. ID
                  BLASTN
Method
                  g3851004
NCBI GI
BLAST score
                  36
                  2.0e-11
E value
                  52
Match length
                  92
% identity
                  Zea mays pyruvate dehydrogenase E1 alpha subunit RNA,
NCBI Description
                  nuclear gene encoding mitochondrial protein, complete cds
Seq. No.
                  301424
                  ceu700426128.h1
Seq. ID
Method
                  BLASTX
                  q3402713
NCBI GI
                   175
BLAST score
                   3.0e-13
E value
Match length
                   67
                   55
% identity
                   (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301425
Seq. No.
                   ceu700426176.h1
Seq. ID
                   BLASTN
Method
                   q4062855
NCBI GI
BLAST score
                   99
                   7.0e-49
E value
Match length
                   135
% identity
                   93
                  Homo sapiens mRNA for HIS1 protein, complete cds
NCBI Description
Seq. No.
                   301426
                   ceu700426183.h1
Seq. ID
                   BLASTX
Method
                   g1154954
NCBI GI
                   173
BLAST score
                   1.0e-12
E value
                   52
Match length
                   75
% identity
                  (X94693) histone H2A [Triticum aestivum]
NCBI Description
                   301427
Seq. No.
                   ceu700426184.h1
 Seq. ID
                   BLASTX
Method
                   g82466
NCBI GI
 BLAST score
                   160
                   3.0e-11
 E value
Match length
                   49
                   61
 % identity
```

42492

reductase enzyme [Oryza sativa]

probable ferredoxin--NADP+ reductase (EC 1.18.1.2) - rice

>gi_218163_dbj_BAA02248_ (D12815) ferredoxin-NADP+

```
Seq. No.
                   301428
Seq. ID
                  ceu700426186.h1
Method
                  BLASTX
NCBI GI
                  g2129698
BLAST score
                   158
E value
                   3.0e-11
Match length
                  53
% identity
                   64
                  protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                  >gi_1054633_emb_CAA63387_ (X92728) protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  301429
Seq. ID
                  ceu700426245.h1
Method
                  BLASTX
NCBI GI
                  q4263714
BLAST score
                  404
E value
                  1.0e-39
Match length
                  96
% identity
                  83
NCBI Description
                  (AC006223) putative integral membrane protein [Arabidopsis
                  thaliana]
Seq. No.
                  301430
Seq. ID
                  ceu700426343.h1
Method
                  BLASTX
NCBI GI
                  q115771
BLAST score
                  292
E value
                  1.0e-26
Match length
                  55
% identity
                  100
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-1) (LHCP) >gi_82682_pir_ S04453 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding
                  preprotein (AA 1 - 262) [Zea mays]
Seg. No.
                  301431
Seq. ID
                  ceu700426425.h1
Method
                  BLASTN
NCBI GI
                  q3108052
BLAST score
                  58
E value
                  2.0e-24
Match length
                  106
% identity
                  89
NCBI Description
                  Zea mays myo-inositol 1-phosphate synthase mRNA, complete
                  cds
Seq. No.
                  301432
Seq. ID
                  ceu700426431.h1
Method
                  BLASTN
```

NCBI GI g22396
BLAST score 43
E value 1.0e-15
Match length 107
% identity 85

NCBI Description Z.mays gene for phosphoenolpyruvate carboxylase (EC



4.1.1.31)

```
Seq. No.
                  301433
Seq. ID
                  ceu700426494.h1
Method
                  BLASTX
NCBI GI
                  g1086147
BLAST score
                  153
E value
                  1.0e-10
Match length
                  31
                  90
% identity
NCBI Description
                  protein S2 - Phalaris coerulescens >gi_556833_emb_CAA57520_
                   (X81992) S2 [Phalaris coerulescens]
Seq. No.
                  301434
Seq. ID
                  ceu700426584.h1
Method
                  BLASTX
NCBI GI
                  g2144902
BLAST score
                  190
E value
                  6.0e-15
Match length
                  39
                  100
% identity
NCBI Description
                  semenogelin I precursor - human >gi 487420 (M81650) SEMGI
                   [Homo sapiens] >gi_1147569 emb CAA8\overline{7}636 (Z47556)
                  semenogelin I [Homo sapiens]
Seq. No.
                  301435
Seq. ID
                  ceu700426592.h1
Method
                  BLASTN
NCBI GI
                  g4416300
BLAST score
                  51
E value
                  5.0e-20
Match length
                  63
                  32
% identity
NCBI Description
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
                  region, complete sequence
Seq. No.
                  301436
Seq. ID
                  ceu700426733.h1
Method
                  BLASTX
NCBI GI
                  g3402751
BLAST score
                  149
E value
                  1.0e-13
Match length
                  88
% identity
                  27
NCBI Description (AL031187) putative protein [Arabidopsis thaliana]
                  301437
Seq. No.
Seq. ID
                  ceu700426758.h1
Method
                  BLASTN
NCBI GI
                  q495268
BLAST score
                  92
E value
                  9.0e-45
Match length
                  112
% identity
```

Seq. No. 301438

NCBI Description R.norvegicus cox VIa gene (heart)



```
ceu700426791.h1
Seq. ID
                  BLASTN
Method
                  g168436
NCBI GI
BLAST score
                  33
                  1.0e-09
E value
Match length
                  33
                  100
% identity
NCBI Description Zea mays catalase (Cat3) gene, complete cds
                  301439
Seq. No.
                  ceu700426834.h1
Seq. ID
Method
                  BLASTN
                  g56669
NCBI GI
BLAST score
                  133
E value
                  5.0e-69
                  185
Match length
% identity
                  93
NCBI Description Rat mRNA for ventricular myosin light chain
                  301440
Seq. No.
                  ceu700426943.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567228
BLAST score
                  143
E value
                  3.0e-09
Match length
                  40
% identity
                  62
NCBI Description
                  (AC007119) unknown protein [Arabidopsis thaliana]
                  301441
Seq. No.
Seq. ID
                  ceu700426963.h1
Method
                  BLASTX
NCBI GI
                  g4503479
BLAST score
                  201
E value
                  3.0e-16
Match length
                  40
% identity
                  97
NCBI Description
                  eukaryotic translation elongation factor 1 delta (guanine
                  nucleotide exchange protein)
                  >gi_461994_sp_P29692_EF1D_HUMAN ELONGATION FACTOR 1-DELTA
                  (EF-1-DELTA) >gi_1085404_pir__S34626 translation elongation
                  factor eEF-1 delta chain - human >gi_38522_emb_CAA79716_
                  (Z21507) human elongation factor-1-delta [Homo sapiens]
Seq. No.
                  301442
Seq. ID
                  ceu700426984.h1
Method
                  BLASTX
NCBI GI
                  g559371
BLAST score
                  210
E value
                  3.0e-17
Match length
                  45
% identity
                  96
NCBI Description (D29766) Crk-associated substrate, p130 [Rattus norvegicus]
```

NOSE BESCHIPTION (B23700) CIR associated Sabbilate, p150 [lack

Seq. No.

301443

Seq. ID ceu700427158.h1

Method BLASTX

```
NCBI GI
                   q4105794
BLAST score
                  155
E value
                   1.0e-10
Match length
                   54
% identity
                   50
NCBI Description
                  (AF049928) PGP224 [Petunia x hybrida]
Seq. No.
                  301444
                  ceu700427161.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3047114
BLAST score
                  287
E value
                  5.0e-26
Match length
                  73
% identity
                  70
NCBI Description
                  (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                  301445
Seq. ID
                  ceu700427201.h1
Method
                  BLASTX
NCBI GI
                  g2385369
BLAST score
                  376
E value
                  2.0e-36
Match length
                  73
% identity
                  97
NCBI Description
                  (AJ001421) Rer1 protein [Homo sapiens]
Seq. No.
                  301446
Seq. ID
                  ceu700427203.h1
Method
                  BLASTN
NCBI GI
                  g203477
BLAST score
                  213
E value
                  1.0e-116
Match length
                  255
% identity
                  96
                  Rat skeletal muscle creatine kinase composite mRNA,
NCBI Description
                  complete cds
Seq. No.
                  301447
Seq. ID
                  ceu700427219.h1
Method
                  BLASTX
NCBI GI
                  q4406818
BLAST score
                  189
E value
                  1.0e-14
Match length
                  56
% identity
                  61
NCBI Description
                  (AC006201) putative transcription factor-like protein
                  [Arabidopsis thaliana]
```

Seq. No. 301448

Seq. ID ceu700427241.h1

Method BLASTX
NCBI GI g115793
BLAST score 172
E value 1.0e-12
Match length 33
% identity 94



```
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR
                   (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein
type III precursor - barley >gi_19023_emb_CAA44881_
                   (X63197) type III LHCII CAB precursor protein [Hordeum
                   vulgare]
                   301449
Seq. No.
Seq. ID
                   ceu700427273.h1
Method
                   BLASTN
NCBI GI
                   g20276
BLAST score
                   51
E value
                   7.0e-20
Match length
                   85
                   91
% identity
NCBI Description O.sativa oryzacystatin-II gene
                   301450
Seq. No.
Seq. ID
                   ceu700427302.h1
Method
                   BLASTN
NCBI GI
                   g203477
BLAST score
                   104
                   5.0e-52
E value
Match length
                   104
% identity
                   100
NCBI Description
                   Rat skeletal muscle creatine kinase composite mRNA,
                   complete cds
Seq. No.
                   301451
Seq. ID
                   ceu700427325.h1
Method
                   BLASTX
NCBI GI
                   g3688576
BLAST score
                   200
                   4.0e-16
E value
Match length
                   43
                   93
% identity
NCBI Description
                  (D00512) mitochondrial acetoacetyl-CoA thiolase precursor
                   [Rattus sp.]
                   301452
Seq. No.
Seq. ID
                   ceu700427336.h1
Method
                   BLASTX
NCBI GI
                   g4522011
BLAST score
                   194
                   2.0e-15
E value
Match length
                   59
% identity
                   54
NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   301453
Seq. ID
                   ceu700427394.hl
Method
                   BLASTX
NCBI GI
                   g2493493
BLAST score
                   147
E value
                   7.0e-10
Match length
                   32
% identity
                   78
```

NCBI Description SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1)



>gi_619352_bbs_153538 CP-MII.1=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324

Seq. No. 301454

Seq. ID ceu700427416.h1

Method BLASTN NCBI GI g1906603 BLAST score 54 E value 6.0e-22 Match length 54 % identity 100

NCBI Description Zea mays ACCase gene, intron containing colonist1 and

colonist2 retrotransposons and reverse transcriptase

pseudogene, complete sequence

Seq. No. 301455

Seq. ID ceu700427482.h1

Method BLASTX NCBI GI q4102839 BLAST score 139 E value 9.0e-09 Match length 72 % identity 42

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 301456

Seq. ID ceu700427617.h1

Method BLASTX NCBI GI q4512624 BLAST score 259 E value 9.0e-23 Match length 66 % identity 67

NCBI Description (AC004793) Strong similarity to gi 3033401 F19I3.29

putative potassium transporter from Arabidopsis thaliana

BAC gb_AC004238

Seq. No. 301457

Seq. ID ceu700427634.h1

Method BLASTX NCBI GI q3461821 BLAST score 153 E value 3.0e-10 Match length 82 % identity 44

NCBI Description (AC004138) putative nucleoside triphosphatase [Arabidopsis

thaliana]

Seq. No.

301458

Seq. ID ceu700427648.h1

Method BLASTN g168508 NCBI GI 110 BLAST score E value 4.0e-55 Match length 203 % identity 94

42498

Match length

45



```
NCBI Description Maize oleosin KD18 (KD18; L2) gene, complete cds
Seq. No.
                  301459
Seq. ID
                  ceu700427766.h1
Method
                  BLASTX
                  g3746903
NCBI GI
BLAST score
                  155
E value
                  8.0e-11
Match length
                  36
% identity
                  86
                  (AF089724) signal recognition particle 54 kDa subunit
NCBI Description
                  precursor [Pisum sativum]
Seq. No.
                  301460
                  ceu700428036.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586260
BLAST score
                  158
E value
                  3.0e-11
                  45
Match length
% identity
                  67
NCBI Description
                  (AL049640) putative protein [Arabidopsis thaliana]
                  301461
Seq. No.
Seq. ID
                  ceu700428060.h1
Method
                  BLASTN
NCBI GI
                  g4506236
BLAST score
                  88
E value
                  2.0e-42
Match length
                  100
                  98
% identity
NCBI Description
                  Homo sapiens proteasome (prosome, macropain) activator
                  subunit 2 (PA28 beta) (PSME2) mRNA
                  >gi_1008914_dbj D45248 HUMPHPA28A Human mRNA for proteasome
                  activator hPA28 subunit beta, complete cds
Seq. No.
                  301462
Seq. ID
                  ceu700428122.h1
Method
                  BLASTX
NCBI GI
                  g557474
BLAST score
                  143
E value
                  3.0e-09
Match length
                  74
% identity
                  41
NCBI Description
                  (U15179) ORF1 [Bacteroides ovatus]
                  301463
Seq. No.
Seq. ID
                  ceu700428144.h1
Method
                  BLASTX
NCBI GI
                  g1352410
BLAST score
                  157
E value
                  6.0e-11
```

% identity 62 NCBI Description ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR

>gi_484645_pir__JS0738 ATPase inhibitor protein precursor,
mitochondrial - rat >gi_286198_dbj_BAA02424_ (D13122)



ATPase inhibitor protein precursor [Rattus norvegicus] >gi_517226 (U12250) mitochondrial ATPase inhibitor [Rattus norvegicus]

Seq. No. 301464

Seq. ID ceu700428190.h1

Method BLASTN
NCBI GI g3150014
BLAST score 231
E value 1.0e-127
Match length 255
% identity 98

NCBI Description Human Chromosome 15q26.1 PAC clone pDJ443n8, complete

sequence [Homo sapiens]

Seq. No. 301465

Seq. ID ceu700428285.h1

Method BLASTX
NCBI GI g168586
BLAST score 248
E value 1.0e-21
Match length 79
% identity 98

NCBI Description (M58656) pyruvate, orthophosphate dikinase [Zea mays]

Seq. No. 301466

Seq. ID ceu700428329.h1

Method BLASTX
NCBI GI g133863
BLAST score 158
E value 4.0e-11
Match length 31
% identity 100

NCBI Description 40S RIBOSOMAL PROTEIN S24 (S19) >gi 71037 pir R3XL19

ribosomal protein S24 - African clawed frog

>gi_65054_emb_CAA24704 (V01443) ribsomal protein S19

[Xenopus laevis]

Seq. No. 301467

Seq. ID ceu700428531.h1

Method BLASTX
NCBI GI g2997589
BLAST score 154
E value 1.0e-10
Match length 40
% identity 75

NCBI Description (AF020813) glucose-6-phosphate/phosphate-translocator

precursor [Zea mays]

Seq. No. 301468

Seq. ID ceu700428610.h1

Method BLASTN
NCBI GI 98051606
BLAST score 112
E value 2.0e-56
Match length 210
% identity 88

42500



NCBI Description Homo sapiens glycophorin C (Gerbich blood group) (GYPC) mRNA >gi 36459 emb X12496 HSSIALOB Human mRNA for erythrocyte membrane sialoglycoprotein beta (glycophorin C) 301469 Seq. No. Seq. ID ceu700428741.h1 Method BLASTN NCBI GI q576644 BLAST score 249 1.0e-138 E value Match length 269 % identity 98 NCBI Description Human calmodulin-I (CALM1) mRNA, 3'UTR, partial sequence Seq. No. 301470 ceu700428751.h1 Seq. ID Method BLASTX NCBI GI q1168329 BLAST score 162 E value 7.0e-25 Match length 80 % identity 60 NCBI Description ACTIN-LIKE PROTEIN 3 (ACTIN-LIKE PROTEIN 66B) (ACTIN-2) >gi 558568 emb CAA50674 (X71789) actin related protein [Drosophila melanogaster] >gi 1096138 prf 2111232A actin-related protein [Drosophila melanogaster] Seq. No. 301471 Seq. ID ceu700428768.h1 Method BLASTX g3250693 NCBI GI BLAST score 223 1.0e-18 E value Match length 88 % identity 45 NCBI Description (AL024486) lectin like protein [Arabidopsis thaliana] Seq. No. 301472 Seq. ID ceu700428793.h1 Method BLASTX g4544383 NCBI GI BLAST score 168 4.0e-12 E value Match length 84 % identity 42 NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana] Seq. No. 301473 Seq. ID ceu700428822.h1 Method BLASTX

g3309565 NCBI GI BLAST score 315 E value 2.0e-29 Match length 83 % identity 78

NCBI Description (AF049460) nuclear DEAF-1 related transcriptional regulator

protein 8 [Homo sapiens]

42501



```
Seq. No.
                   301474
Seq. ID
                   ceu700428830.h1
Method
                   BLASTN
NCBI GI
                   g2588612
BLAST score
                   34
                   1.0e-09
E value
Match length
                   38
                   97
% identity
                   Human BAC clone RG326G04 from 7p21, complete sequence [Homo
NCBI Description
                   sapiens]
                   301475
Seq. No.
Seq. ID
                   ceu700428854.h1
Method
                   BLASTN
NCBI GI
                   g4508148
                   137
BLAST score
E value
                   2.0e-71
                   205
Match length
% identity
                   91
NCBI Description Homo sapiens clone DJ0747G18, complete sequence
Seq. No.
                   301476
Seq. ID
                   ceu700428927.h1
Method
                   BLASTN
NCBI GI
                   g3095110
BLAST score
                   222
E value
                   1.0e-122
                   250
Match length
% identity
                   98
NCBI Description Homo sapiens 15 kDa selenoprotein mRNA, complete cds
Seq. No.
                   301477
Seq. ID
                   ceu700429017.h1
Method
                   BLASTX
NCBI GI
                   g4506679
BLAST score
                   150
E value
                   3.0e-10
Match length
                   33
% identity
NCBI Description
                   ribosomal protein S10 >gi_1173177_sp_P46783_RS10_HUMAN 40S
                   RIBOSOMAL PROTEIN S10 >gi 1362933 pir S55918 ribosomal
                   protein S10 - human >gi 5\overline{5}0025 (\overline{U1}497\overline{2}) ribosomal protein
                   S10 [Homo sapiens] >gi 1096944 prf 2113200G ribosomal
                   protein S10 [Homo sapiens]
Seq. No.
                   301478
Seq. ID
                   ceu700429031.h1
Method
                   BLASTX
NCBI GI
                   g2760834
```

BLAST score 252 E value 6.0e-22 Match length 84

% identity 64

NCBI Description (AC003105) putative nitrate transporter [Arabidopsis

thaliana]

```
Seq. No.
                   301479
                  ceu700429060.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2055391
BLAST score
                  54
                   4.0e-22
E value
Match length
                  98
                  89
% identity
                  Rattus norvegicus transmembrane receptor Unc5H1 mRNA,
NCBI Description
                   complete cds
                   301480
Seq. No.
                   ceu700429079.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4416300
BLAST score
                   109
                   2.0e-54
E value
Match length
                   263
                   86
% identity
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
Seq. No.
                   301481
                   ceu700429156.h1
Seq. ID
Method
                   BLASTN
                   g2326946
NCBI GI
                   97
BLAST score
                   2.0e-47
E value
                   204
Match length
                   89
% identity
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29
                   301482
Seq. No.
                   ceu700429190.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1592832
BLAST score
                   233
                   9.0e-20
E value
                   50
Match length
% identity
                   86
                  (L36095) mipA [Mesembryanthemum crystallinum]
NCBI Description
                   301483
Seq. No.
                   ceu700429194.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3777601
BLAST score
                   43
```

E value

4.0e-15

Match length

139

% identity

83

NCBI Description

Oryza sativa clone LS195 50S ribosomal protein L10 (rpl10)

mRNA, nuclear gene encoding chloroplast protein, complete

cds

Seq. No.

301484

Seq. ID

ceu700429206.h1

Method

BLASTX



NCBI GI a2088647 BLAST score 220 6.0e-22 E value Match length 95 59 % identity

(AF002109) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi 3158394 (AF036340) LRR-containing F-box protein

[Arabidopsis thaliana]

301485 Seq. No.

Seq. ID ceu700429287.hl

Method BLASTX NCBI GI a4580468 150 BLAST score 5.0e-10 E value Match length 36 75 % identity

(AC006081) putative protein kinase; similar to human PKX1 NCBI Description

and Drosophila DC2 [Arabidopsis thaliana]

301486 Seq. No.

ceu700429293.h1 Seq. ID

Method BLASTX q3421413 NCBI GI 229 BLAST score 3.0e-19 E value 80 Match length 53 % identity

(AF081922) protein phosphatase 2A 55 kDa B regulatory NCBI Description

subunit [Oryza sativa] >gi 3421415 (AF081923) protein

phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

301487 Seq. No.

Seq. ID ceu700429295.h1

Method BLASTX NCBI GI q3287696 BLAST score 326 E value 1.0e-30 Match length 78 % identity 76

(AC003979) Strong similarity to phosphoribosylanthranilate NCBI Description

transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

301488 Seq. No.

Seq. ID ceu700429329.h1

Method BLASTX q3337367 NCBI GI BLAST score 151 4.0e-13 E value 86 Match length % identity 51

(AC004481) hypothetical protein [Arabidopsis thaliana] NCBI Description

301489 Seq. No.

ceu700429388.h1 Seq. ID



```
BLASTN
Method
NCBI GI
                  g3132309
BLAST score
                  47
                  1.0e-17
E value
Match length
                  82
                  90
% identity
                  Zea mays mRNA for phosphoenolpyruvate carboxylase, complete
NCBI Description
                  301490
Seq. No.
                  ceu700429408.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g452340
BLAST score
                  69
E value
                  4.0e-31
                  77
Match length
                  99
% identity
                  Z.mays mRNA for type II light-harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  301491
Seq. No.
Seq. ID
                   ceu700429511.h1
Method
                  BLASTX
NCBI GI
                  g2499987
BLAST score
                  147
E value
                   6.0e-10
Match length
                  54
                  56
% identity
NCBI Description PEPTIDYL-TRNA HYDROLASE (PTH) >gi 1870014 emb CAB06865_
                   (Z92539) pth [Mycobacterium tuberculosis]
                   301492
Seq. No.
                   ceu700429666.h1
Seq. ID
Method
                  BLASTX
                  g3057120
NCBI GI
BLAST score
                   294
                   7.0e-27
E value
Match length
                   64
% identity
                   78
NCBI Description
                  (AF023159) starch synthase DULL1 [Zea mays]
                   301493
Seq. No.
                   ceu700429691.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3510374
                   269
BLAST score
                   5.0e-24
E value
                   81
Match length
% identity
                   69
NCBI Description
                  (AB017188) antisecretory factor [Rattus norvegicus]
Seq. No.
                   301494
                   ceu700429707.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4416300
                   178
BLAST score
```

42505

7.0e-96

E value



```
Match length
                  182
% identity
                  99
NCBI Description
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
                  region, complete sequence
                  301495
Seq. No.
                  ceu700429724.h1
Seq. ID
Method
                  BLASTN
                  g3256174
NCBI GI
BLAST score
                  58
                  3.0e-24
E value
Match length
                  74
% identity
                  95
NCBI Description
                  Homo sapiens DNA sequence from PAC 168L15 on chromosome
                  6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase,
                  EST, GSS, STS. CpG island, complete sequence [Homo sapiens]
Seq. No.
                  301496
                  ceu700429786.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213558
                  137
BLAST score
                  1.0e-08
E value
Match length
                  51
% identity
                  47
                  (Z97052) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  301497
Seq. No.
                  ceu700429931.h1
Seq. ID
Method
                  BLASTX
                  g1658315
NCBI GI
BLAST score
                  268
E value
                  7.0e-24
Match length
                  47
% identity
                  94
NCBI Description (Y08988) osr40g3 [Oryza sativa]
Seq. No.
                  301498
                  ceu700429978.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3386565
BLAST score
                  277
                  6.0e-25
E value
Match length
                  62
% identity
                  85
                  (AF079588) 1-aminocyclopropane-1-carboxylate oxidase
NCBI Description
                  [Sorghum bicolor]
Seq. No.
                  301499
Seq. ID
                  ceu700430011.h1
```

Method BLASTX NCBI GI q3157946 BLAST score 228 E value 4.0e-19

Match length 92 53 % identity

NCBI Description (AC002131) Similar to salt-inducible membrane protein



```
EST gb F14010 comes from
                  gb U08285∝from Nicotiana tabacum.
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  301500
                  ceu700430046.h1
Seq. ID
                  BLASTX
Method
                  q951112
NCBI GI
                  178
BLAST score
                  3.0e-13
E value
Match length
                  79
% identity
                  43
                  (U22470) galactose-binding lectin precursor [Arachis
NCBI Description
                  hypogaea]
Seq. No.
                  301501
                  ceu700430049.h1
Seq. ID
Method
                  BLASTX
                  g2500139
NCBI GI
                  231
BLAST score
                  2.0e-19
E value
                  74
Match length
% identity
                  58
NCBI Description PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)
                   >gi_1653916_dbj_BAA18826_ (D90917) peptide chain release
```

factor [Synechocystis sp.] Seq. No. 301502 ceu700430064.h1 Seq. ID Method BLASTX

NCBI GI q4544418 BLAST score 150 3.0e-10 E value Match length 55 56 % identity

(AC006955) hypothetical protein [Arabidopsis thaliana] NCBI Description

301503 Seq. No. ceu700430093.h1 Seq. ID BLASTX Method g2055273 NCBI GI 156 BLAST score 9.0e-11 E value

Match length 43 60 % identity

(D85339) hydroxypyruvate reductase [Arabidopsis thaliana] NCBI Description

301504 Seq. No.

ceu700430292.h1 Seq. ID BLASTX Method

g3790581 NCBI GI 196 BLAST score 2.0e-15 E value Match length 54 50 % identity

(AF079179) RING-H2 finger protein RHBla [Arabidopsis NCBI Description

thaliana]



```
301505
Seq. No.
                  ceu700430339.h1
Seq. ID
Method
                  BLASTN
                  g3947780
NCBI GI
                  42
BLAST score
                  2.0e-14
E value
                  169
Match length
                  82
% identity
                  Human DNA sequence from clone 1118D24 on chromosome
NCBI Description
                  1p36.11-36.33. Contains part of a novel gene similar to
                  worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal
                  Protein L10 LIKE (pseudo)gene and two 3' exons of the
Seq. No.
                  301506
                  ceu700430501.h1
Seq. ID
                  BLASTX
Method
                  g4210330
NCBI GI
                  146
BLAST score
                   2.0e-09
E value
                   29
Match length
                   93
% identity
                   (AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit
NCBI Description
                   [Arabidopsis thaliana]
                   301507
Seq. No.
                   ceu700430575.h1
Seq. ID
                   BLASTX
Method
                   g3329368
NCBI GI
                   286
BLAST score
                   8.0e-26
E value
                   89
Match length
                   63
% identity
                   (AF031244) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   301508
Seq. No.
                   ceu700430656.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4506882
BLAST score
                   69
                   4.0e-31
E. value
Match length
                   105
                   91
% identity
                   Homo sapiens semenogelin I (SEMG1) mRNA
NCBI Description
                   >gi_338018_gb_J04440_HUMSEM Homo sapiens semenogelin
                   protein (SEMG) mRNA, complete cds
                   301509
Seq. No.
```

ceu700430776.h1 Seq. ID Method BLASTX

q3024122 NCBI GI BLAST score 373 4.0e-36 E value 94 Match length 81 % identity

S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE NCBI Description

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]



```
301510
Seq. No.
                  ceu700430813.h1
Seq. ID
                  BLASTX
Method
                  g2766450
NCBI GI
BLAST score
                  162
                  1.0e-11
E value
Match length
                   43
                  74
% identity
NCBI Description (AF029857) cytochrome P450 CYP99A1 [Sorghum bicolor]
Seq. No.
                   301511
                   ceu700430827.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1805654
                   170
BLAST score
                   4.0e-23
E value
Match length
                   92
                   71
% identity
                   (X99972) calmodulin-stimulated calcium-ATPase [Brassica
NCBI Description
                   oleracea]
Seq. No.
                   301512
Seq. ID
                   ceu700430866.hl
                   BLASTX
Method
                   q3337389
NCBI GI
                   292
BLAST score
                   1.0e-26
E value
Match length
                   95
                   56
% identity
                   (AC004682) pre-mRNA splicing factor (PRP16)(KIAA0224) [Homo
NCBI Description
                   sapiens]
                   301513
Seq. No.
Seq. ID
                   ceu700430881.hl
Method
                   BLASTX
NCBI GI
                   g3342734
BLAST score
                   206
E value
                   8.0e-17
Match length
                   44
                   93
% identity
                   (AC005329) NUKM_HUMAN, partial CDS; COMPLE; CI-20KD; PSST
NCBI Description
                   SUBUNIT [Homo sapiens]
                   301514
Seq. No.
                   ceu700431089.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1938424
BLAST score
                   167
                   3.0e-12
E value
                   44
Match length
                   68
% identity
                   (U97002) similar to acyl-CoA dehydrogenases and epoxide
NCBI Description
                   hydrolases [Caenorhabditis elegans]
```

301515

ceu700431138.hl

Seq. No.

Seq. ID

NCBI Description

sequence



```
Method
                  BLASTX
NCBI GI
                  g118104
                  325
BLAST score
                  2.0e-30
E value
                  66
Match length
                  92
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi_168461 (M55021) cyclophilin [Zea mays]
                  >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
Seq. No.
                  301516
                  ceu700431190.h1
Seq. ID
                  BLASTN
Method
                  a498145
NCBI GI
                   98
BLAST score
E value
                   6.0e-48
Match length
                   255
                   92
% identity
                  Human mRNA for HHR23A protein, complete cds
NCBI Description
                  >gi_1408335_gb_G28520_G28520 human STS SHGC-31478
Seq. No.
                   301517
                   ceu700431325.h1
Seq. ID
Method
                  BLASTN
                   q4505884
NCBI GI
BLAST score
                   116
E value
                   5.0e-59
                   120
Match length
                   99
% identity
                  Homo sapiens perilipin (PLIN) mRNA
NCBI Description
                   >gi 3041770 dbj AB005293 AB005293 Homo sapiens mRNA for
                   perilipin, complete cds
Seq. No.
                   301518
Seq. ID
                  ceu700431403.h1
Method
                   BLASTN
NCBI GI
                   q2979600
BLAST score
                   67
E value
                   2.0e-29
Match length
                   165
% identity
                   86
                   Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete
NCBI Description
                   sequence [Homo sapiens]
Seq. No.
                   301519
Seq. ID
                   ceu700431404.h1
Method
                   BLASTN
NCBI GI
                   g433039
BLAST score
                   61
                   4.0e-26
E value
Match length
                   129
% identity
                   87
```

Zea mays W-22 clone PREM-1 retroelement PREM-1, partial

```
301520
Seq. No.
                   ceu700431413.hl
Seq. ID
                  BLASTX
Method
                   g3549669
NCBI GI
                   195
BLAST score
E value
                   3.0e-15
Match length
                   61
                   64
% identity
                   (AL031394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                   ceu700431465.h1
Method
                   BLASTN
NCBI GI
                   g1098664
BLAST score
                   35
E value
                   2.0e-10
Match length
                   120
% identity
                   84
NCBI Description Zea mays phytoene synthase (Y1) gene, complete cds
Seq. No.
                   301522
Seq. ID
                   ceu700431489.h1
Method
                   BLASTN
NCBI GI
                   q4505578
BLAST score
                   222
                   1.0e-122
E value
                   254
Match length
                   97
% identity
NCBI Description
                   Homo sapiens paired basic amino acid cleaving enzyme
                   (furin, membrane associated receptor protein) (PACE) mRNA
                   >gi_31477_emb_X17094_HSFUR Human fur mRNA for furin
Seq. No.
                   301523
                   ceu700431556.h1
Seq. ID
Method
                   BLASTX
                   g3769549
NCBI GI
                   309
BLAST score
                   3.0e-38
E value
                   90
Match length
                   89
% identity
                   (AF089812) ubiquitin-conjugating enzyme HR6A [Mus musculus]
NCBI Description
                   301524
Seq. No.
Seq. ID
                   ceu700431616.h1
                   BLASTN
Method
                   q1754648
NCBI GI
BLAST score
                   48
E value
                   5.0e-18
                   60
Match length
% identity
                   95
                   Homo sapiens mRNA for HSM-2, complete cds
NCBI Description
                   301525
Seq. No.
```

Seq. ID ceu700431677.h1

Method BLASTX
NCBI GI g4406764
BLAST score 171

```
4.0e-21
E value
Match length
                  57
% identity
                  (AC006836) putative uridylyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                  301526
Seq. No.
                  ceu700431728.hl
Seq. ID
                  BLASTN
Method
                  g22378
NCBI GI
BLAST score
                  43
                  4.0e-15
E value
Match length
                  87
                  89
% identity
NCBI Description Z.mays gene for nucleic acid binding protein
                  301527
Seq. No.
                  ceu700431773.hl
Seq. ID
Method
                  BLASTX
                  g2465923
NCBI GI
BLAST score
                  193
                   5.0e-15
E value
                  89
Match length
```

% identity 46

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

301528 Seq. No. ceu700431776.h1 Seq. ID BLASTX Method g3935168 NCBI GI 169

BLAST score 3.0e-12 E value Match length 57 60 % identity

(AC004557) F17L21.11 [Arabidopsis thaliana] NCBI Description

301529 Seq. No.

ceu700431783.h1 Seq. ID

Method BLASTN q3819359 NCBI GI 53 BLAST score 5.0e-21E value

85 Match length % identity 91

Hordeum vulgare genomic DNA fragment; clone MWG0829.uni NCBI Description

301530 Seq. No.

ceu700431831.h1 Seq. ID

Method BLASTX NCBI GI g1293835 BLAST score 150 6.0e-12 E value Match length 72 % identity 47

(U56965) C15H9.5 gene product [Caenorhabditis elegans] NCBI Description

```
301531
Seq. No.
                  ceu700431853.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2135819
BLAST score
                  233
                  6.0e-20
E value
Match length
                  43
                  100
% identity
                  neuropolypeptide h3, brain - human (fragment)
NCBI Description
                  >gi_4261934_gb_AAD14234_S76773_1 (S76773) neuropolypeptide
                  h3 [Homo sapiens]
Seq. No.
                  301532
                  ceu700431858.hl
Seq. ID
                  BLASTN
Method
                  q4557252
NCBI GI
                   240
BLAST score
                   1.0e-132
E value
Match length
                   240
                   100
% identity
                  Homo sapiens disintegrin and metalloprotease domain 8
NCBI Description
                   (ADAM8) mRNA >gi 1864004_dbj_D26579_D26579 Homo sapiens
                  mRNA for transmembrane protein, complete cds
                   301533
Seq. No.
                   ceu700431906.hl
Seq. ID
                   BLASTN
Method
                   q950423
NCBI GI
BLAST score
                   88
                   2.0e-42
E value
                   116
Match length
                   95
% identity
                   Homo sapiens splicing factor, arginine/serine-rich 7
NCBI Description
                   (SFRS7) gene, complete cds
                   301534
Seq. No.
                   ceu700431946.hl
Seq. ID
                   BLASTN
Method
                   q285948
NCBI GI
                   91
BLAST score
                   4.0e-44
E value
                   103
Match length
                   97
% identity
                   Human mRNA for KIAA0106 gene, complete cds
NCBI Description
                   301535
Seq. No.
                   ceu700431967.h1
Seq. ID
Method
                   BLASTX
                   g1001355
NCBI GI
                   203
BLAST score
                   3.0e-16
E value
                   83
Match length
                   52
% identity
                   (D64006) auxin-induced protein [Synechocystis sp.]
NCBI Description
```

Seq. ID ceu700431983.h1



```
BLASTN
  Method
                     q3970875
  NCBI GI
  BLAST score
                     217
                     1.0e-119
  E value
                     273
* Match length
                     95
  % identity
  NCBI Description Homo sapiens HRIHFB2216 mRNA, partial cds
                     301537
  Seq. No.
  Seq. ID
                     ceu700432127.hl
  Method
                     BLASTN
  NCBI GI
                     g22239
  BLAST score
                     150
                     4.0e-79
  E value
                     181
  Match length
  % identity
                     96
                     Maize cytosolic mRNA for subunit A of chloroplast GAPDH
  NCBI Description
                     (GapA) glyceraldehyde-3-phosphate dehydrogenase
                     301538
  Seq. No.
                     ceu700432132.h1
  Seq. ID
  Method
                     BLASTN
                     g3599965
  NCBI GI
                     158
  BLAST score
                     7.0e-84
  E value
                     190
  Match length
  % identity
                     97
                     Homo sapiens h-scol (SCOl) mRNA, nuclear gene encoding
  NCBI Description
                     mitochondrial protein, complete cds
                     301539
  Seq. No.
                     ceu700432229.h1
  Seq. ID
                     BLASTN
  Method
                     g809120
  NCBI GI
  BLAST score
                     64
                     6.0e-28
  E value
  Match length
                     129
                     97
   % identity
                     Human DNA from cosmid DNA MMDB (f10080) and MMDC (f13544)
  NCBI Description
                     from chromosome 19q13.3 (obtained by automated sequence
                     analysis)
                     301540
   Seq. No. -
                     ceu700432248.hl
   Seq. ID
                     BLASTN
   Method
                     g4507812
   NCBI GI
   BLAST score
                      47
                     7.0e-18
   E value
                      63
   Match length
                      94
   % identity
                     Homo sapiens UDP-glucose dehydrogenase (UGDH) mRNA, and
   NCBI Description
                      translated products >gi_3127126_gb_AF061016_AF061016 Homo
                      sapiens UDP-glucose dehydrogenase (UGDH) mRNA, complete cds
```

Seq. ID ceu700432264.h1

Method BLASTX

```
g3688172
NCBI GI
                  204
BLAST score
                  1.0e-16
E value
Match length
                   60
% identity
                  63
                  (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                  301542
Seq. No.
                  ceu700432286.h1
Seq. ID
Method
                  BLASTN
                  g4500013
NCBI GI
                   104
BLAST score
                   1.0e-51
E value
Match length
                   188
% identity
                   88
                   Homo sapiens mRNA; cDNA DKFZp564F053 (from clone
NCBI Description
                   DKFZp564F053)
                   301543
Seq. No.
                   ceu700432287.h1
Seq. ID
Method
                   BLASTN
                   q4506606
NCBI GI
BLAST score
                   80
E value
                   1.0e-37
Match length
                   100
                   95
% identity
                   Homo sapiens ribosomal protein L18 (RPL18) mRNA
NCBI Description
                   >gi_337492_gb_L11566_HUMRPL18A Homo sapiens ribosomal
                   protein L18 (RPL18) mRNA, complete cds
                   301544
Seq. No.
                   ceu700432339.h1
Seq. ID
                   BLASTX
Method
                   g3786011
NCBI GI
                   147
BLAST score
                   8.0e-10
E value
Match length
                   51
                   67
% identity
                   (AC005499) putative elongation factor [Arabidopsis
NCBI Description
                   thaliana]
                   301545
Seq. No.
                   ceu700432432.h1
Seq. ID
                   BLASTX
Method
                   g3334667
NCBI GI
                   264
BLAST score
                   2.0e-23
E value
                   83
Match length
                   59
% identity
                   (Y10493) putative cytochrome P450 [Glycine max]
NCBI Description
```

Seq. ID ceu700432437.h1 Method BLASTN

Method BLASTN
NCBI GI g4416300
BLAST score 81
E value 8.0e-38



Match length 252 % identity 84 NCRI Description 7ea

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 301547

Seq. ID ceu700432474.h1

Method BLASTX
NCBI GI g4490314
BLAST score 361
E value 8.0e-35
Match length 82
% identity 78

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 301548

Seq. ID ceu700432509.h1

Method BLASTN
NCBI GI g2815550
BLAST score 241
E value 1.0e-133
Match length 273
% identity 97

NCBI Description Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete

sequence [Homo sapiens]

Seq. No. 301549

Seq. ID ceu700432533.h1

Method BLASTN
NCBI GI g3150016
BLAST score 76
E value 5.0e-35
Match length 160
% identity 87

NCBI Description Homo sapiens chromosome 7 clone NHGRI:yWSS1564 from

7p14-15, complete sequence [Homo sapiens]

Seq. No. 301550

Seq. ID ceu700432577.h1

Method BLASTX
NCBI GI g3406749
BLAST score 245
E value 2.0e-21
Match length 52
% identity 90

NCBI Description (AF068180) B cell linker protein BLNK [Homo sapiens]

Seq. No. 301551

Seq. ID ceu700432636.h1

Method BLASTX
NCBI GI g1076290
BLAST score 279
E value 4.0e-25
Match length 70
% identity 71

NCBI Description amino acid transporter AAP4 - Arabidopsis thaliana

>gi_608671_emb_CAA54631_ (X77500) amino acid transporter



[Arabidopsis thaliana]

```
301552
Seq. No.
                  ceu700432654.h1
Seq. ID
                  BLASTX
Method
                  q3252807
NCBI GI
                  155
BLAST score
                  8.0e-11
E value
                  45
Match length
% identity
                  64
NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]
                  301553
Seq. No.
                  ceu700432689.h1
Seq. ID
Method
                  BLASTN
                  g3135974
NCBI GI
BLAST score
                  109
                  7.0e-55
E value
                  125
Match length
                   97
% identity
                  Homo sapiens DNA sequence from PAC 422H11 on chromosome
NCBI Description
                   6p21.1-22.2. Contains the gene coding for two isoforms of a
                   known Serine Kinase. Contains ESTs, STSs and a GSS,
                   complete sequence [Homo sapiens]
Seq. No.
                   301554
                   ceu700432771.hl
Seq. ID
Method
                   BLASTX
                   g4510347
NCBI GI
BLAST score
                   141
                   5.0e-09
E value
Match length
                   66
                   48
% identity
                  (AC006921) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301555
Seq. No.
                   ceu700432778.h1
Seq. ID
                   BLASTX
Method
                   g1911166
NCBI GI
BLAST score
                   206
                   1.0e-16
E value
                   70
Match length
% identity
                   53
                  (X94400) soluble-starch-synthase [Solanum tuberosum]
NCBI Description
                   301556
Seq. No.
                   ceu700432807.h1
Seq. ID
                   BLASTX
Method
                   g3776082
NCBI GI
BLAST score
                   346
                   5.0e-33
E value
Match length
                   88
                   72
% identity
                   (Y18250) MtN30 [Medicago truncatula]
NCBI Description
```

42517

* 62

301557

ceu700432943.hl

Seq. No.

Seq. ID

```
BLASTX
Method
                  g3088575
NCBI GI
BLAST score
                  411
E value
                  1.0e-40
Match length
                  83
                  94
% identity
                   (AF059531) protein arginine N-methyltransferase 3 [Homo
NCBI Description
                  301558
Seq. No.
                   ceu700432978.h1
Seq. ID
Method
                  BLASTN
                   g1103627
NCBI GI
BLAST score
                  124
E value
                   1.0e-63
Match length
                   139
% identity
                   98
NCBI Description
                  Z.mays Ferl gene
                   301559
Seq. No.
                   ceu700433004.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3335345
BLAST score
                   412
E value
                   1.0e-40
Match length
                   91
% identity
                   87
                   (AC004512) Contains similarity to ABC transporter
NCBI Description
                   gb_1651790 from Synechocystis sp. gb_D90900. [Arabidopsis
                   thaliana]
                   301560
Seq. No.
                   ceu700433048.h1
Seq. ID
                   BLASTX
Method
                   g4587568
NCBI GI
BLAST score
                   206
                   1.0e-16
E value
                   51
Match length
                   69
% identity
                   (AC006550) Contains PF 00637 Clathrin 7-fold repeat. EST
NCBI Description
                   gb_AA721862 comes from this gene. [Arabidopsis thaliana]
                   301561
Seq. No.
                   ceu700433070.h1
Seq. ID
                   BLASTN
Method
                   g236729
NCBI GI
                   80
BLAST score
                   3.0e-37
E value
                   243
Match length
                   86
% identity
NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
```

301562

ceu700433077.hl Seq. ID

BLASTX Method g3047119 NCBI GI 235 BLAST score

```
5.0e-20
E value
Match length
                  86
                  49
% identity
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
                  301563
Seq. No.
                  ceu700433173.h1
Seq. ID
                  BLASTX
Method
                  g1574938
NCBI GI
                  244
BLAST score
                  4.0e-21
E value
                  47
Match length
                  100
% identity
NCBI Description (U34726) superoxide dismutase 4 [Zea mays]
                  301564
Seq. No.
                  ceu700433264.h1
Seq. ID
                  BLASTX
Method
                  g4580013
NCBI GI
BLAST score
                  162
E value
                  1.0e-11
Match length
                  46
% identity
                  65
NCBI Description (U83194) TRAF4-associated factor 2 [Homo sapiens]
                  301565
Seq. No.
                  ceu700433458.h1
Seq. ID
                  BLASTN
Method
                  g606814
NCBI GI
BLAST score
                  82
                  7.0e-39
E value
                   90
Match length
                   98
% identity
                  Zea mays Golden Bantam carbonic anhydrase mRNA, complete
NCBI Description
                   301566
Seq. No.
                   ceu700433528.h1
Seq. ID
Method
                   BLASTN
                   g609287
NCBI GI
BLAST score
                   51
                   7.0e-20
E value
                   262
Match length
% identity
                   81
NCBI Description Z.diploperennis Grandel gene
                   301567
Seq. No.
                   ceu700433555.h1
Seq. ID
Method
                   BLASTN
                   g56543
NCBI GI
BLAST score
                   67
                   2.0e-29
E value
Match length
                   262
                   82
```

NCBI Description Rat mRNA for lactate dehydrogenase

% identity

42519



```
ceu700433588.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4106342
BLAST score
                  371
E value
                   6.0e-36
Match length
                  85
% identity
                   (AF062076) palmitylated serine/threonine kinase [Mus
NCBI Description
                  musculus]
Seq. No.
                   301569
Seq. ID
                   ceu700433595.hl
Method
                  BLASTX
                   q4538934
NCBI GI
BLAST score
                   262
E value
                   4.0e-23
Match length
                   85
% identity
                   (AL049483) putative leucine-rich-repeat protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   301570
                   ceu700433642.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4539009
BLAST score
                   228
E value
                   2.0e-19
Match length
                   55
% identity
                   (AL049481) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   301571
                   ceu700433657.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2773156
BLAST score
                   252
E value
                   1.0e-31
Match length
                   75
                   91
% identity
                   (AF039574) serine/threonine protein kinase [Mus musculus]
NCBI Description
                   301572
Seq. No.
                   ceu700433658.h1
Seq. ID
                   BLASTX
Method
                   g1495804
NCBI GI
BLAST score
                   164
                   1.0e-11
E value
Match length
                   33
                   85
% identity
                   (X96406) 13-lipoxygenase [Solanum tuberosum]
NCBI Description
Seq. No.
                   301573
                   ceu700433713.h1
Seq. ID
                   BLASTX
Method
                   g2618721
NCBI GI
```

257

2.0e-22

BLAST score E value



```
Match length
                  70
% identity
                  (U49072) IAA16 [Arabidopsis thaliana]
NCBI Description
                  301574
Seq. No.
Seq. ID
                  ceu700433813.hl
                  BLASTX
Method
                  q3004565
NCBI GI
                  336
BLAST score
                  2.0e-32
E value
Match length
                  87
                  74
% identity
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]
                  301575
Seq. No.
Seq. ID
                  ceu700433822.h1
Method
                  BLASTX
                   g4503155
NCBI GI
BLAST score
                   452
                   2.0e-45
E value
                   89
Match length
                   93
% identity
                   cathepsin L >gi_115741_sp P07711 CATL_HUMAN CATHEPSIN L
NCBI Description
                   PRECURSOR (MAJOR EXCRETED PROTEIN) (MEP)
                   >gi_67649_pir__KHHUL cathepsin L (EC 3.4.22.15) precursor -
                   human >qi 29715 emb CAA30981 (X12451) pro-(cathepsin L)
                   [Homo sapiens] >gi 190418 (M20496) preprocathepsin L
                   precursor [Homo sapiens]
                   301576
Seq. No.
                   ceu700433827.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2058498
                   220
BLAST score
                   3.0e-18
E value
                   65
Match length
% identity
                   66
                   (U76029) hemoglobin 1 [Oryza sativa] >gi_2058500 (U76030)
NCBI Description
                   hemoglobin 1 [Oryza sativa]
                   301577
Seq. No.
Seq. ID
                   ceu700433829.h1
Method
                   BLASTN
NCBI GI
                   q2393736
BLAST score
                   38
                   4.0e-12
E value
                   38
Match length
                   100
% identity
                   Human BAC clone GS025M02 from 7q21-q22, complete sequence
NCBI Description
                   [Homo sapiens]
                   301578
```

Seq. ID ceu700433861.hl Method BLASTX

q3395426 NCBI GI BLAST score 315 2.0e-29 E value



65

74

Match length

NCBI Description

% identity

```
Match length
                   64
% identity
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                   301579
Seq. No.
                   ceu700433918.h2
Seq. ID
                   BLASTX
Method
                   q629602
NCBI GI
                   201
BLAST score
                   3.0e-16
E value
                   52
Match length
                   67
% identity
                   probable imbibition protein - wild cabbage
NCBI Description
                   >gi_488787_emb_CAA55893_ (X79330) putative imbibition
                   protein [Brassica oleracea]
                   301580
Seq. No.
Seq. ID
                   ceu700433935.h2
                   BLASTX
Method
NCBI GI
                   q3176726
BLAST score
                   315
                   2.0e-29
E value
                   73
Match length
                   75
% identity
                   (AC002392) putative serine proteinase [Arabidopsis
NCBI Description
                   thaliana]
                   301581
Seq. No.
                   ceu700433958.h2
Seq. ID
Method
                   BLASTN
                   q2121307
NCBI GI
                   69
BLAST score
E value
                   1.0e-30
                   157
Match length
% identity
                   Human DNA sequence from 4PTEL, Huntington's Disease Region,
NCBI Description
                   chromosome 4p16.3
                    301582
Seq. No.
Seq. ID
                    ceu700434008.h1
                    BLASTN
Method
NCBI GI
                    q4240216
BLAST score
                    120
                    5.0e-61
E value
                    253
Match length
                    98
 % identity
                   Homo sapiens mRNA for KIAA0864 protein, partial cds
NCBI Description
                    301583
 Seq. No.
                    ceu700434206.h1
 Seq. ID
                    BLASTX
 Method
                    q3128173
 NCBI GI
 BLAST score
                    209
                    7.0e-17
 E value
```

42522

(AC004521) hypothetical protein [Arabidopsis thaliana]



99

% identity

```
Seq. No.
                  301584
Seq. ID
                  ceu700434343.hl
Method
                  BLASTN
NCBI GI
                  g1835730
BLAST score
                  55
                  2.0e-22
E value
                  82
Match length
                  93
% identity
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
NCBI Description
                  complete cds
                  301585
Seq. No.
                  ceu700434376.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2501620
BLAST score
                  185
E value
                  2.0e-14
                  51
Match length
                  71
% identity
NCBI Description UREASE (UREA AMIDOHYDROLASE) >gi 1944148_dbj_BAA19550
                   (AB002590) Urelp [Schizosaccharomyces pombe]
                   301586
Seq. No.
                  ceu700434382.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2529562
                  135
BLAST score
                   3.0e-70
E value
Match length
                   175
% identity
NCBI Description Homo sapiens TRAIL receptor 2 mRNA, complete cds
                   301587
Seq. No.
                   ceu700434393.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076791
BLAST score
                   224
                   6.0e-19
E value
Match length
                   42
                   98
% identity
                   calcium-binding protein - maize >gi_2119370_pir__S58170
NCBI Description
                   Calreticulin precursor - maize >gi_577612_emb_CAA86728_
                   (Z46772) calcium-binding protein [\overline{Z}ea\ mays]
                   >gi_927572_emb_CAA61939_ (X89813) Calreticulin precursor
                   [Zea mays] >gi_1587033_prf__2205314A calreticulin [Zea
                   mays]
                   301588
Seq. No.
                   ceu700434408.h1
Seq. ID
Method
                   BLASTN
                   g4503100
NCBI GI
BLAST score
                   173
                   7.0e-93
E value
                   180
Match length
```

NCBI Description Homo sapiens cysteine and glycine-rich protein 2 (LIM

NCBI Description



domain only, smooth muscle) (CSRP2) mRNA

```
301589
Seq. No.
Seq. ID
                  ceu700434483.h1
Method
                  BLASTN
NCBI GI
                  q436123
                  100
BLAST score
E value
                  2.0e-49
                  147
Match length
                  93
% identity
NCBI Description M.musculus mRNA for phosphorylase kinase
                  301590
Seq. No.
                  ceu700434492.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2459446
BLAST score
                  147
                  6.0e-10
E value
Match length
                  57
                   47
% identity
NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
                  thaliana]
                   301591
Seq. No.
                  ceu700434619.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4506655
BLAST score
                   315
                   1.0e-35
E value
                   90
Match length
                   90
% identity
                  ribosomal protein L5 >gi_1173054_sp_P46777_RL5_HUMAN 60S
NCBI Description
                   RIBOSOMAL PROTEIN L5 >gi 1362932 pir S55912 ribosomal
                   protein L5 - human >gi_550013 (U14966) ribosomal protein L5
                   [Homo sapiens] >gi_1096938 prf__2113200A ribosomal protein
                   L5 [Homo sapiens]
Seq. No.
                   301592
                   ceu700434640.hl
Seq. ID
                   BLASTX
Method
                   g3063448
NCBI GI
BLAST score
                   194
E value
                   3.0e-15
Match length
                   87
% identity
NCBI Description (AC003981) F22013.10 [Arabidopsis thaliana]
                   301593
Seq. No.
                   cjh700192904.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168681
BLAST score
                   234
E value
                   1.0e-129
Match length
                   260
                   74
% identity
                   Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
```

>gi 270686 gb I03333_ Sequence 8 from Patent US



```
301594
Seq. No.
Seq. ID
                  cjh700192964.h1
Method
                  BLASTN
NCBI GI
                  q3015620
BLAST score
                  101
                  9.0e-50
E value
                  101
Match length
                  100
% identity
                  Zea mays low molecular weight heat shock protein precursor
NCBI Description
                  (hsp22) mRNA, nuclear gene encoding mitochondrial protein,
                  complete cds
                  301595
Seq. No.
                  cjh700193222.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82654
BLAST score
                  208
                  6.0e-17
E value
                  55
Match length
                  69
% identity
                  10K zein precursor - maize >gi 22541_emb CAA30409_ (X07535)
NCBI Description
                  10kDa zein (AA 1 - 150) [Zea mays]
                  301596
Seq. No.
                  cjh700193275.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g136757
                  252
BLAST score
                  3.0e-36
E value
Match length
                  81
% identity
                  100
                  GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
NCBI Description
                  >qi 100881 pir S07314 UDPqlucose--starch
                  glucosyltransferase (EC 2.4.1.11) precursor - maize
                  >gi 168653 (M24258) amyloplast-specific transit protein
                  [Zea mays] >gi 1644339 emb CAA27574 (X03935) glucosyl
                  transferase [Zea mays]
                  301597
Seq. No.
Seq. ID
                  cjh700193292.h1
                  BLASTX
Method
NCBI GI
                  q82660
BLAST score
                  211
E value
                  3.0e-17
Match length
                  58
% identity
                  76
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi 809117_emb_CAA24720 (V01473) zein [Zea mays]
                  301598
Seq. No.
                  cjh700193306.hl
Seq. ID
```

Method BLASTN
NCBI GI g22514
BLAST score 209
E value 1.0e-114

Match length 252



```
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                  301599
Seq. No.
Seq. ID
                  cjh700193374.h1
Method
                  BLASTN
NCBI GI
                  g340933
BLAST score
                  124
                  1.0e-63
E value
                  124
Match length
% identity
                  100
NCBI Description Zea mays 10-kDa zein gene, complete cds
                  301600
Seq. No.
Seq. ID
                  cjh700193403.h1
Method
                  BLASTN
NCBI GI
                  q168669
BLAST score
                  88
                   5.0e-42
E value
                   100
Match length
                   97
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19A2, partial cds
                   301601
Seq. No.
Seq. ID
                   cjh700193418.h1
                  BLASTN
Method
NCBI GI
                   q625147
BLAST score
                   128
                   4.0e-66
E value
Match length
                   148
                   97
% identity
                   Zea mays protein disulfide isomerase (pdi) mRNA, complete
NCBI Description
Seq. No.
                   301602
Seq. ID
                   cjh700193595.h1
Method
                   BLASTX
NCBI GI
                   g2832247
BLAST score
                   353
                   7.0e-34
E value
Match length
                   86
% identity
                   86
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
                   301603
Seq. No.
                   cjh700193609.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g121472
                   139
BLAST score
                   2.0e-12
E value
                   77
Match length
                   61
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
```

[Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea



```
mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
```

.

301604 Seq. No.

Seq. ID cjh700193621.h1

Method BLASTN NCBI GI g463151 BLAST score 77 2.0e-35 E value 123 Match length 90 % identity

NCBI Description Zea mays high sulfur zein gene, complete cds

301605 Seq. No.

Seq. ID cjh700193677.h1

BLASTX Method NCBI GI g224514 BLAST score 191 E value 6.0e-15 39 Match length 97 % identity

zein M8 [Zea mays] NCBI Description

301606 Seq. No.

cjh700193680.h1 Seq. ID

BLASTN Method g1864000 NCBI GI BLAST score 132 2.0e-68 E value 205 Match length % identity 32

NCBI Description Maize DNA for Fd III, complete cds

Seq. No.

301607 cjh700193736.h1 Seq. ID

Method BLASTN NCBI GI g4416300 BLAST score 41 6.0e-14 E value

Match length 129 % identity 83

Zea mays chromosome 4 22 kDa zein-associated intercluster NCBI Description region, complete sequence

301608 Seq. No.

cjh700193770.h1 Seq. ID Method BLASTN

NCBI GI g22100 BLAST score 33 3.0e-09 E value Match length 61 89 % identity

NCBI Description Z.mays 27kDa zein locus DNA

301609 Seq. No.

cjh700193786.h1 Seq. ID

Method BLASTN NCBI GI g168398

42527

```
BLAST score
                  1.0e-39
E value
Match length
                  92
% identity
                  98
                  Zea mays auxin-binding protein (abp4) gene, exons 1-5 and
NCBI Description
                  complete cds
                  301610
Seq. No.
                  cjh700193992.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1314391
BLAST score
                   77
                   8.0e-36
E value
Match length
                   116
                   93
% identity
                   Zea mays ssp. mays USDA PI 214195 ITS1, 5.8S ribosomal RNA,
NCBI Description
Seq. No.
                   301611
                   cjh700194040.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q141616
BLAST score
                   264
E value
                   2.0e-23
Match length
                   57
% identity
                   ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                   >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
Seq. No.
                   301612
                   cjh700194170.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168681
BLAST score
                   186
                   1.0e-100
E value
Match length
                   220
% identity
                   54
                   Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                   >gi 270686 gb I03333_ Sequence 8 from Patent US
Seq. No.
                   301613
Seq. ID
                   cjh700194189.hl
Method
                   BLASTN
                   g3452306
NCBI GI
BLAST score
                   38
                   3.0e-12
E value
Match length
                   66
% identity
                   91
                   Zea mays retrotransposon Opie-3 5' LTR, partial sequence
NCBI Description
                   301614
Seq. No.
                   cjh700194192.h1
Seq. ID
                   {\tt BLASTX}
Method
                   g1632831
NCBI GI
BLAST score
                   141
```

4.0e-09

54

E value Match length

```
50
% identity
NCBI Description (Z49698) orf [Ricinus communis]
Seq. No.
                  301615
                  cjh700194216.h1
Seq. ID
Method
                  BLASTX
                  g2982289
NCBI GI
BLAST score
                  469
                  2.0e-47
E value
                  91
Match length
% identity
                  99
NCBI Description (AF051229) 60S ribosomal protein L17 [Picea mariana]
                  301616
Seq. No.
Seq. ID
                  cjh700194226.h1
Method
                  BLASTX
NCBI GI
                  g4206196
BLAST score
                  147
E value
                  1.0e-09
Match length
                  49
% identity
                  53
                  (AF071527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  301617
Seq. No.
                  cjh700194250.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4325341
BLAST score
                  368
E value
                   1.0e-35
Match length
                  85
% identity
                  74
                   (AF128393) similar to the Drosophila DES-1 protein
NCBI Description
                   (GB:X94180) [Arabidopsis thaliana]
                  301618
Seq. No.
                   cjh700194263.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q168701
BLAST score
                  336
                   8.0e-32
E value
Match length
                   91
                  76
% identity
                  (M60837) zein [Zea mays]
NCBI Description
                   301619
Seq. No.
                   cjh700194320.h1
Seq. ID
Method
                  BLASTX
                   g509810
NCBI GI
                   193
BLAST score
```

4.0e-15 E value 84 Match length % identity 44

(L08468) envelope Ca2+-ATPase [Arabidopsis thaliana] NCBI Description

Seq. No.

301620

cjh700194440.h1 Seq. ID

BLASTX Method

NCBI GI

BLAST score

g121472

182

```
g2832247
NCBI GI
BLAST score
                  322
                  2.0e-30
E value
Match length
                  83
                  83
% identity
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
Seq. No.
                  301621
                  cjh700194482.hl
Seq. ID
Method
                  BLASTN
                  g22548
NCBI GI
BLAST score
                  76
                  6.0e-35
E value
Match length
                  76
% identity
                  100
                  Maize chimeric zein/beta-phaseolin gene 3'end region
NCBI Description
Seq. No.
                   301622
                  cjh700194549.h1
Seq. ID
Method
                  BLASTX
                   g121472
NCBI GI
BLAST score
                   154
                   1.0e-16
E value
Match length
                   86
                   60
% identity
                  GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
                  mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
                   301623
Seq. No.
                   cjh700194632.h1
Seq. ID
Method
                   BLASTX
                   g4006921
NCBI GI
BLAST score
                   367
E value
                   2.0e-35
Match length
                   84
                   83
% identity
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   301624
                   cjh700194690.h1
Seq. ID
Method
                   BLASTN
                  g287829
NCBI GI
BLAST score
                   118
                   6.0e-60
E value
                   194
Match length
% identity
                   90
NCBI Description Z.mays gene for polygalacturonase
                   301625
Seq. No.
                   cjh700194701.h1
Seq. ID
Method
                   BLASTX
```



70

% identity

NCBI Description

```
4.0e-25
E value
                   85
Match length
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >gi_\overline{2}251\overline{7}_emb_CAA\overline{3}7594_ (X53514) zein Zc2 [Zea
                   mays] >gi 1684\overline{8}5 (M1\overline{6}066) glutelin-2 [Zea mays]
                   301626
Seq. No.
Seq. ID
                   cjh700194747.h1
                   BLASTX
Method
                   g141617
NCBI GI
                   226
BLAST score
                   5.0e-19
E value
Match length
                   56
                   77
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi 100941 pir S12140 zein Zc1 - maize
                   >gi 100945 pir B29017 zein 2 - maize
                   >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                   301627
Seq. No.
                   cjh700194753.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2243118
                   257
BLAST score
                   1.0e-22
E value
Match length
                   71
% identity
                   (Y10984) glutathione synthetase [Brassica juncea]
NCBI Description
                   301628
Seq. No.
                   cjh700194828.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q100812
                   245
BLAST score
                   3.0e-21
E value
                   48
Match length
% identity
NCBI Description
                   ubiquitin precursor - wheat (fragment)
                   >gi_21816_emb_CAA40138 (X56803) ubiquitin [Triticum
                   aestivum] >qi 21900 emb CAA39938 (X56601) ubiquitin
                    [Triticum aestivum]
                   301629
Seq. No.
Seq. ID
                   cjh700194857.h1
                   BLASTX
Method
NCBI GI
                   g4185308
BLAST score
                   185
E value
                    1.0e-22
Match length
                    82
```

(AF090446) 22-kDa alpha zein protein 21 [Zea mays]

BLAST score

E value

161 2.0e-11

```
301630
Seq. No.
                   cjh700194908.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3560243
BLAST score
                   144
E value
                   2.0e-09
                   85
Match length
                   35
% identity
                  (AL031532) putative hydrolase [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                   301631
                   cjh700195039.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4581149
BLAST score
                   212
E value
                   2.0e-17
Match length
                   69
% identity
                   59
                   (AC006919) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301632
Seq. No.
Seq. ID
                   cjh700195051.h1
Method
                   BLASTX
                   q511870
NCBI GI
                   220
BLAST score
                   3.0e-18
E value
Match length
                   53
                   77
% identity
                   (M23537) zein protein [Zea mays]
NCBI Description
                   301633
Seq. No.
Seq. ID
                   cjh700195155.h1
Method
                   BLASTN
NCBI GI
                   q22514
BLAST score
                   146
E value
                   1.0e-76
Match length
                   245
% identity
                   90
NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)
Seq. No.
                   301634
Seq. ID
                   cjh700195156.h1
Method
                   BLASTX
                   g3445212
NCBI GI
                   315
BLAST score
                   2.0e-29
E value
                   80
Match length
                   78
% identity
                   (AC004786) putative chloroplast envelope Ca2+-ATPase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   301635
                   cjh700195169.h1
Seq. ID
Method
                   BLASTX
                   g141616
NCBI GI
```



```
Match length 40
% identity 78
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 301636
Seq. ID cjh700195179.h1
Method BLASTN
NCBI GI g1129085
```

NCBI GI g1129085
BLAST score 33
E value 4.0e-09
Match length 53
% identity 91

NCBI Description Wheat mRNA for protein H2A, complete cds, clone wcH2A-9

Seq. No. 301637

Seq. ID cjh700195210.hl

Method BLASTX
NCBI GI g4544430
BLAST score 175
E value 3.0e-13
Match length 51
% identity 63

NCBI Description (AC006955) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 301638

Seq. ID cjh700195247.h1

Method BLASTN
NCBI GI g602605
BLAST score 37
E value 1.0e-11
Match length 64
% identity 91

NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No. 301639

Seq. ID cjh700195351.h1

Method BLASTN
NCBI GI g168681
BLAST score 128
E value 7.0e-66
Match length 260
% identity 72

NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.

>gi_270686_gb_I03333_ Sequence 8 from Patent US

Seq. No. 301640

Seq. ID cjh700195381.h1

Method BLASTN
NCBI GI g1244652
BLAST score 171
E value 2.0e-91
Match length 243
% identity 93

NCBI Description Zea mays copia-type retroelement PREM-2 gag gene, complete

cds



```
301641
Seq. No.
                  cjh700195392.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q168681
BLAST score
                  163
E value
                   9.0e-87
Match length
                   235
                   92
% identity
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                   >gi_270686_gb_I03333_ Sequence 8 from Patent US
                   301642
Seq. No.
Seq. ID
                   cjh700195401.h1
Method
                  BLASTX
NCBI GI
                   g3914899
BLAST score
                   249
                   7.0e-22
E value
Match length
                   59
                   86
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 2331301 (AF013487) ribosomal
                  protein S4 type I [Zea mays]
                   301643
Seq. No.
Seq. ID
                   cjh700195522.h1
                   BLASTN
Method
NCBI GI
                   g4416300
BLAST score
                   47
E value
                   2.0e-17
Match length
                   71
                   54
% identity
                   Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
                   301644
Seq. No.
Seq. ID
                   cjh700195531.h1
Method
                   BLASTX
NCBI GI
                   q82654
BLAST score
                   208
E value
                   7.0e-17
Match length
                   55
% identity
NCBI Description
                   10K zein precursor - maize >gi 22541 emb CAA30409 (X07535)
                   10kDa zein (AA 1 - 150) [Zea mays]
Seq. No.
                   301645
Seq. ID
                   cjh700195562.h1
Method
                   BLASTN
NCBI GI
                   g432367
BLAST score
                   96
                   9.0e-47
E value
Match length
                   252
% identity
NCBI Description
                  Rice mRNA for elongation factor 1 beta, complete cds
```

301646

cjh700195573.h1

Seq. No.

Seq. ID

Seq. ID

Method NCBI GI BLASTX

g2641619



```
BLASTX
Method
                  q1685003
NCBI GI
BLAST score
                  151
E value
                  3.0e-10
Match length
                  75
% identity
                  37
                  (U32643) immediate-early salicylate-induced
NCBI Description
                  glucosyltransferase [Nicotiana tabacum]
                  301647
Seq. No.
                  cjh700195582.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q322641
BLAST score
                  289
                   3.0e-26
E value
Match length
                  83
% identity
                   59
                  beta-1,3-glucanase homolog (clone A6) - rape (fragment)
NCBI Description
                   >qi 17738 emb CAA49513 (X69887) beta-1,3-glucanase
                  homologue [Brassica napus]
Seq. No.
                   301648
                   cjh700195669.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1706327
BLAST score
                   252
E value
                   2.0e-31
                   81
Match length
% identity
                   PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
NCBI Description
                   >gi_551261_emb_CAA57447_ (X81854) pyruvate decarboxylase
                   [Nicotiana tabacum]
                   301649
Seq. No.
                   cjh700195717.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g507844
BLAST score
                   37
                   1.0e-11
E value
                   213
Match length
% identity
                   79
                   Zea mays A188 retrotransposon gag gene, complete cds
NCBI Description
                   301650
Seq. No.
                   cjh700195786.h1
Seq. ID
                   BLASTN
Method
                   g3452299
NCBI GI
BLAST score
                   69
                   1.0e-30
E value
                   159
Match length
                   94
% identity
                  Zea mays retrotransposon Ji-6 3' LTR, partial sequence
NCBI Description
                   301651
Seq. No.
                   cjh700195788.h1
```

```
BLAST score
                   4.0e-11
E value
Match length
                  29
% identity
                  97
                   (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea
NCBI Description
                  301652
Seq. No.
                  cjh700195796.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738306
BLAST score
                   230
                   2.0e-19
E value
Match length
                   57
% identity
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   301653
                   cjh700195877.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q168703
BLAST score
                   381
E value
                   4.0e-37
Match length
                   85
% identity
NCBI Description
                   (M86591) 22 kDa zein protein [Zea mays]
Seq. No.
                   301654
Seq. ID
                   cjh700195921.h1
Method
                   BLASTX
NCBI GI
                   g4039155
BLAST score
                   158
E value
                   5.0e-11
Match length
                   80
% identity
                   41
                   (AF104258) putative copper-inducible 35.6 kDa protein
NCBI Description
                   [Festuca rubra]
                   301655
Seq. No.
                   cjh700196001.h1
Seq. ID
Method
                   BLASTX
                   q511870
NCBI GI
BLAST score
                   225
                   8.0e-19
E value
                   54
Match length
                   78
% identity
                   (M23537) zein protein [Zea mays]
NCBI Description
```

Seq. No.

301656

Seq. ID cjh700196114.h1

Method BLASTX
NCBI GI g4063760
BLAST score 208
E value 7.0e-17
Match length 57
% identity 67

NCBI Description (AC005561) putative POL3 protein [Arabidopsis thaliana]



```
301657
Seq. No.
                  cjh700196130.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3367520
BLAST score
                  214
                  1.0e-17
E value
                  77
Match length
% identity
                  (AC004392) Similar to protein kinase APK1A,
NCBI Description
                  tyrosine-serine-threonine kinase gb D12522 from A.
                  thaliana. [Arabidopsis thaliana]
                  301658
Seq. No.
Seq. ID
                  cjh700196136.hl
Method
                  BLASTX
NCBI GI
                  g4574406
BLAST score
                  257
                  1.0e-22
E value
                  75
Match length
% identity
                   (AF121139) RIM2 protein [Oryza sativa]
NCBI Description
                   301659
Seq. No.
                   cjh700196144.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q121472
                   142
BLAST score
                   3.0e-12
E value
Match length
                   50
                   75
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
                   mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
                   301660
Seq. No.
                   cjh700196335.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g433044
BLAST score
                   69
                   1.0e-30
E value
Match length
                   97
                   93
% identity
                   Zea mays W-22 clone PREM-1D retroelement PREM-1, partial
NCBI Description
                   sequence
                   301661
Seq. No.
                   cjh700196383.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1076678
BLAST score
                   350
```

42537

1.0e-33

70

100

E value

Match length % identity

Method

NCBI GI

BLASTX

g4582456



```
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
                  301662
Seq. No.
Seq. ID
                  cjh700196412.h1
                  BLASTN
Method
NCBI GI
                  g22514
BLAST score
                  111
                  8.0e-56
E value
                  175
Match length
                  91
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.
                  301663
                  cjh700196414.h1
Seq. ID
                  BLASTX
Method
                  g419803
NCBI GI
BLAST score
                  154
E value
                   1.0e-10
Match length
                   75
                   49
% identity
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
                   301664
Seq. No.
Seq. ID
                   cjh700196449.h1
                   BLASTN
Method
NCBI GI
                   g22514
BLAST score
                   288
                   1.0e-161
E value
                   311
Match length
                   98
% identity
                  Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
NCBI Description
                   301665
Seq. No.
                   cjh700196485.h1
Seq. ID
                   BLASTX
Method
                   g468516
NCBI GI
BLAST score
                   246
                   4.0e-21
E value
                   108
Match length
% identity
                   56
                   (X55724) zein [Zea mays]
NCBI Description
Seq. No.
                   301666
                   cjh700196511.h1
Seq. ID
                   BLASTX
Method
                   q4587589
NCBI GI
BLAST score
                   271
E value
                   3.0e-24
Match length
                   80
% identity
                   (AC007232) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   301667
                   cjh700196512.hl
Seq. ID
```

42538

```
BLAST score
                   4.0e-10
E value
Match length
                   64
                   55
% identity
                   (AC007071) putative trithorax protein [Arabidopsis
NCBI Description
                   301668
Seq. No.
                   cjh700196515.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q511870
BLAST score
                   225
                   8.0e-19
E value
                   54
Match length
% identity
NCBI Description
                   (M23537) zein protein [Zea mays]
Seq. No.
                   301669
                   cjh700196549.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q168586
BLAST score
                   228
                   7.0e-27
E value
                   67
Match length
% identity
                   (M58656) pyruvate, orthophosphate dikinase [Zea mays]
NCBI Description
                   301670
Seq. No.
                   cjh700196620.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q511870
BLAST score
                   211
E value
                   3.0e-17
Match length
                   51
                   76
% identity
                   (M23537) zein protein [Zea mays]
NCBI Description
                   301671
Seq. No.
                   cjh700196669.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2842744
BLAST score
                   173
                   9.0e-13
E value
                   39
Match length
                   77
% identity
                   ENHANCER OF RUDIMENTARY HOMOLOG >gi 1595812 (U67398)
NCBI Description
                   enhancer of rudimentary homolog ATER [Arabidopsis thaliana]
                   301672
Seq. No.
                   cjh700196675.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4432861
                   237
BLAST score
                   3.0e-20
E value
                   68
Match length
```

42539

(AC006300) hypothetical protein [Arabidopsis thaliana]

63

% identity

NCBI Description

```
Seq. No.
                  301673
Seq. ID
                  cjh700196910.h1
Method
                  BLASTX
NCBI GI
                  g121472
BLAST score
                  142
                  5.0e-25
E value
Match length
                  84
                  80
% identity
                  GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                  (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                  >gi 72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                  maize >qi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                  [Zea mays] >qi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
                  mays] >gi_168485 (M16066) glutelin-2 [Zea mays]
Seq. No.
                  301674
Seq. ID
                  cjh700196943.h1
Method
                  BLASTX
NCBI GI
                  g4206306
BLAST score
                  339
E value
                  3.0e-32
                  82
Match length
                  83
% identity
                  (AF049110) prpol [Zea mays]
NCBI Description
Seq. No.
                  301675
                  cjh700196991.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  q168703
BLAST score
                  219
E value
                  3.0e-18
Match length
                  50
                   90
% identity
                  (M86591) 22 kDa zein protein [Zea mays]
NCBI Description
Seq. No.
                  301676
Seq. ID
                  cjh700197014.h1
Method
                  BLASTX
NCBI GI
                   g1669599
BLAST score
                   196
E value
                   2.0e-15
Match length
                  87
% identity
                   43
                  (D88746) AR791 [Arabidopsis thaliana]
NCBI Description
                   301677
Seq. No.
                   cjh700197143.hl
Seq. ID
                  BLASTX
Method
                   g4544383
NCBI GI
                   192
BLAST score
E value
                   4.0e-15
Match length
                   64
% identity
                   61
```

Seq. No. 301678

NCBI Description

(AC007047) hypothetical protein [Arabidopsis thaliana]

```
cjh700197152.h1
Seq. ID
                  BLASTX
Method
                  q4539460
NCBI GI
                  172
BLAST score
                  1.0e-12
E value
Match length
                  85
% identity
                  (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
                  301679
Seq. No.
Seq. ID
                  cjh700197248.h1
                  BLASTN
Method
NCBI GI
                  g4140643
BLAST score
                  53
                  4.0e-21
E value
                  93
Match length
% identity
                  89
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                  complete sequence
                  301680
Seq. No.
Seq. ID
                  cjh700197404.h1
Method
                  BLASTN
                  q3282440
NCBI GI
BLAST score
                  220
                  1.0e-120
E value
                  261
Match length
                  96
% identity
                  Zea mays subsp. mexicana internal transcribed spacer 1,
NCBI Description
                   5.8S ribosomal RNA gene, and internal transcribed spacer 2,
                   complete sequence
                   301681
Seq. No.
Seq. ID
                   cjh700197413.h1
                  BLASTX
Method
                   g1174780
NCBI GI
                   254
BLAST score
E value
                   3.0e-22
                   51
Match length
% identity
                   TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR (ORANGE PERICARP
NCBI Description
                   2) >gi_320135_pir__PQ0450 tryptophan synthase (EC 4.2.1.20)
                   beta-2 chain precursor - maize (fragment) >gi_168574
                   (M76685) tryptophan synthase beta-subunit [Zea mays]
                   301682
Seq. No.
                   cjh700197414.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g169818
BLAST score
                   64
E value
                   1.0e-27
Match length
                   80
                   95
% identity
NCBI Description
                  Rice 25S ribosomal RNA gene
```

42541

301683

cjh700197434.h1

Seq. No.

Seq. ID

E value

Match length

3.0e - 31

70



```
BLASTN
Method
NCBI GI
                   g168704
BLAST score
                   83
                   5.0e-39
E value
Match length
                  197
% identity
                   93
                  Zea mays zein protein gene, complete cds
NCBI Description
                   301684
Seq. No.
Seq. ID
                   cjh700197452.h1
Method
                  BLASTX
NCBI GI
                   q2829923
                   291
BLAST score
E value
                   1.0e-26
Match length
                   84
                   69
% identity
                   (AC002291) Similar to uridylyl transferases [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   301685
Seq. ID
                   cjh700197463.h1
                   BLASTX
Method
NCBI GI
                   g4432825
                   141
BLAST score
E value
                   5.0e-09
                   58
Match length
% identity
NCBI Description (AC006593) putative SOP2p protein [Arabidopsis thaliana]
                   301686
Seq. No.
Seq. ID
                   cjh700197482.h1
Method
                   BLASTX
NCBI GI
                   g1915974
BLAST score
                   147
                   9.0e-10
E value
                   57
Match length
                   47
% identity
NCBI Description
                   (U62329) fructokinase [Lycopersicon esculentum] >gi_2102693
                   (U64818) fructokinase [Lycopersicon esculentum]
                   301687
Seq. No.
Seq. ID
                   cjh700197611.h1
Method
                   BLASTN
NCBI GI
                   g168665
BLAST score
                   198
E value
                   1.0e-107
Match length
                   256
                   95
% identity
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
Seq. No.
                   301688
Seq. ID
                   cjh700197639.h1
Method
                   BLASTX
NCBI GI
                   g141605
BLAST score
                   331
```



```
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  301689
                  cjh700197640.h1
Seq. ID
                  BLASTX
Method
                  q2832246
NCBI GI
                  233
BLAST score
E value
                  8.0e-20
Match length
                  66
                  79
% identity
                  (AF031569) 22-kDa alpha zein 8 [Zea mays]
NCBI Description
                  301690
Seq. No.
Seq. ID
                  cjh700197644.h1
                  BLASTN
Method
NCBI GI
                  g1244652
                  125
BLAST score
                  4.0e-64
E value
                  241
Match length
                  88
% identity
                  Zea mays copia-type retroelement PREM-2 gag gene, complete
NCBI Description
                  301691
Seq. No.
Seq. ID
                  cjh700197646.h1
                  BLASTX
Method
NCBI GI
                  g4507857
BLAST score
                  155
E value
                  1.0e-10
Match length
                  75
% identity
                  43
                  Herpes virus-associated ubiquitin-specific protease
NCBI Description
                  >qi 2501460 sp Q93009 UBPH HUMAN PROBABLE UBIQUITIN
                  CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE
                  HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP)
                   (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED
                  UBIQUITIN-SPECIFIC PROTEASE) >gi 1545952 emb CAA96580
                   (Z72499) herpesvirus associated ubiquitin-specific protease
                   (HAUSP) [Homo sapiens]
Seq. No.
                  301692
Seq. ID
                  cih700197716.h1
```

Method BLASTX NCBI GI q3264767

BLAST score 237 E value 3.0e-20 Match length 68 % identity

(AF071893) AP2 domain containing protein [Prunus armeniaca] NCBI Description

Seq. No. 301693 cjh700197718.h1 Seq. ID Method BLASTN

g22437

NCBI GI

42543

```
BLAST score
                   6.0e-16
E value
Match length
                   71
                   92
% identity
NCBI Description Maize pML1 gene for zein
Seq. No.
                   301694
                   cjh700197723.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2982459
BLAST score
                   255
                   2.0e-22
E value
                   80
Match length
                   66
% identity
                   (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                   301695
Seq. No.
                   cjh700197738.hl
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22514
                   206
BLAST score
                   1.0e-112
E value
                   233
Match length
                   97
% identity
NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)
                   301696
Seq. No.
                   cjh700197747.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g168701
BLAST score
                   187
E value
                   2.0e-14
                   62
Match length
% identity
                   68
                   (M60837) zein [Zea mays]
NCBI Description
                   301697
Seq. No.
Seq. ID
                   cjh700197752.h1
                   BLASTN
Method
                   g1840117
NCBI GI
                   311
BLAST score
                   1.0e-175
E value
Match length
                   334
% identity
                   99
                   Zea mays PIF-12 transposable element in r-1 (r-p) locus,
NCBI Description
                   complete sequence
                   301698
Seq. No.
Seq. ID
                   cjh700197762.h1
                   BLASTX
Method
```

g2642159 NCBI GI BLAST score 183 E value 5.0e-22 Match length 65 % identity 78

(AC003000) putative mannose-1-phosphate guanyltransferase NCBI Description



pyrophosphorylase [Arabidopsis thaliana] >gi_4151925
(AF108660) CYT1 protein [Arabidopsis thaliana]

301699 Seq. No. Seq. ID cjh700197860.h1 Method BLASTN g793901 NCBI GI 91 BLAST score 9.0e-44 E value Match length 111 95 % identity Z.mays mRNA for ZEMa protein (ZEM1 gene) NCBI Description 301700 Seq. No. ckd700461145.hl Seq. ID Method BLASTX NCBI GI g3135543 267 BLAST score 9.0e-24 E value Match length 65 83 % identity (AF062393) aquaporin [Oryza sativa] NCBI Description 301701 Seq. No. ckd700461156.h1 Seq. ID BLASTX Method NCBI GI g515377 251 BLAST score 8.0e-22 E value Match length 51 100 % identity (X79715) histone H4 [Lolium temulentum] NCBI Description 301702 Seq. No. ckd700461234.h1 Seq. ID Method BLASTN NCBI GI g473602 BLAST score 67 E value 2.0e-29 Match length 167 86 % identity NCBI Description Zea mays W-22 histone H2A mRNA, complete cds Seq. No. 301703 Seq. ID ckd700461283.h1 Method BLASTN NCBI GI q168484 BLAST score 161 E value 2.0e-85 Match length 257 91 % identity

Seq. No. 301704

NCBI Description

Seq. ID ckd700461290.h1

Method BLASTN NCBI GI g22324

Maize endosperm glutelin-2 gene, complete cds

```
BLAST score
                  5.0e-36
E value
                  134
Match length
                  90
% identity
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)
Seq. No.
                  301705
                  clt700041505.fl
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3212861
BLAST score
                  381
                  4.0e-37
E value
                  90
Match length
                  78
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                  301706
Seq. No.
Seq. ID
                  clt700041585.f1
Method _
                  BLASTN
NCBI GI
                  g733457
                  85
BLAST score
                  3.0e-40
E value
                  169
Match length
                  96
% identity
                  Zea mays chlorophyll a/b-binding apoprotein CP24 (Lhcb6-1)
NCBI Description
                  mRNA, complete cds
                   301707
Seq. No.
                  clt700041682.fl
Seq. ID
                  BLASTX
Method
NCBI GI
                  g543938
BLAST score
                   302
                   7.0e-28
E value
Match length
                   68
                   88
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB48) (LHCP) >gi 82681 pir S22497 chlorophyll
                   a/b-binding protein precursor (cab-48) - maize
                   >qi 22228 emb CAA44888 (X63205) chlorophyll a /b binding
                   protein [Zea mays]
                   301708
Seq. No.
Seq. ID
                   clt700041776.f1
Method
                   BLASTX
NCBI GI
                   q3024871
                   234
BLAST score
                   7.0e-20
E value
                   86
Match length
```

% identity 59

HYPOTHETICAL 77.3 KD PROTEIN SLL0005 NCBI Description

>gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis

sp.]

Seq. No. 301709

Seq. ID clt700041813.f1

BLASTN Method NCBI GI q22223



```
BLAST score
                      1.0e-57
    E value
                      226
    Match length
                      89
    % identity
    NCBI Description Maize cab-1 gene for chlorophyll a/b-binding protein
    Seq. No.
                      301710
                      clt700041814.f1
    Seq. ID
                      BLASTX
    Method
                      g115771
    NCBI GI
                      257
    BLAST score
                      2.0e-26
    E value
                      66
    Match length
    % identity
                      89
                      CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
    NCBI Description
                      (CAB-1) (LHCP) >gi 82682_pir__S04453 chlorophyll
                      a/b-binding protein precursor - maize
                      >gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding
                      preprotein (AA 1 - 262) [Zea mays]
                      301711
    Seq. No.
                      clt700041878.fl
    Seq. ID
                      BLASTX
    Method
                      g2275204
    NCBI GI
    BLAST score
                      206
    E value
                      1.0e-16
                      67
    Match length
    % identity
                      61
                      (AC002337) DNA binding protein isolog [Arabidopsis
    NCBI Description
                      thaliana]
                      301712
    Seq. No.
                      clt700041959.fl
    Seq. ID
    Method
                      BLASTX
    NCBI GI
                      q3618312
    BLAST score
                      212
                      3.0e-17
    E value
                      51
    Match length
    % identity
                      69
    NCBI Description (AB001884) zinc finger protein [Oryza sativa]
                      301713
    Seq. No.
    Seq. ID
                      clt700042043.f1
                      BLASTX
    Method
    NCBI GI
                      q115813
    BLAST score
                      167
                       5.0e-12
    E value
                      51
    Match length
                       69
    % identity
                      CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR
    NCBI Description
                       (CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                       chlorophyll a/b-binding protein [Lycopersicon esculentum]
                       301714
    Seq. No.
                       clt700042078.f1
```

Seq. ID

BLASTX Method NCBI GI g1172704

42547



201 6.0e-16

69

E value Match length

```
BLAST score
                  3.0e-11
E value
Match length
                  66
% identity
                  50
NCBI Description
                  PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN)
                  >qi 633940 (L39082) transport protein [Arabidopsis
                  thaliana] >gi 4406786 gb AAD20096 (AC006532) histidine
                  transport protein PTR2-B [Arabidopsis thaliana]
Seq. No.
                  301715
Seq. ID
                  clt700042104.f1
                  BLASTX
Method
                  g309673
NCBI GI
BLAST score
                  141
E value
                  5.0e-09
Match length
                  43
% identity
                  65
NCBI Description
                  (L19651) light harvesting protein [Pisum sativum]
                  301716
Seq. No.
Seq. ID
                  clt700042105.f1
Method
                  BLASTX
NCBI GI
                  g4589961
BLAST score
                  292
                  1.0e-26
E value
                  88
Match length
% identity
                   61
NCBI Description (AC007169) unknown protein [Arabidopsis thaliana]
                  301717
Seq. No.
Seq. ID
                  clt700042126.f1
Method
                  BLASTX
NCBI GI
                  q2864617
BLAST score
                  160
                  3.0e-11
E value
Match length
                  45
                  71
% identity
NCBI Description
                  (AL021811) H+-transporting ATP synthase chain9 - like
                  protein [Arabidopsis thaliana]
Seq. No.
                  301718
Seq. ID
                  clt700042138.f1
Method
                  BLASTX
NCBI GI
                  q1063400
BLAST score
                  211
E value
                  3.0e-17
Match length
                  51
                  82
% identity
NCBI Description
                  (X92888) glycolate oxidase [Lycopersicon esculentum]
Seq. No.
                  301719
                  clt700042166.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2655098
BLAST score
```

Seq. ID

```
% identity
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]
                  301720
Seq. No.
                  clt700042248.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567248
BLAST score
                  294
                  6.0e-27
E value
Match length
                  84
% identity
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
                  301721
Seq. No.
Seq. ID
                  clt700042302.f1
Method
                  BLASTX
NCBI GI
                  q168586
BLAST score
                  201
E value
                  3.0e - 34
Match length
                  81
% identity
NCBI Description (M58656) pyruvate, orthophosphate dikinase [Zea mays]
Seq. No.
                  301722
Seq. ID
                  clt700042339.f1
Method
                  BLASTN
NCBI GI
                  q4160401
BLAST score
                  85
E value
                  3.0e-40
Match length
                  133
% identity
                  91
NCBI Description Zea mays eIF-5 gene, exons 1-2
Seq. No.
                  301723
Seq. ID
                  clt700042342.f1
Method
                  BLASTX
NCBI GI
                  g4006855
BLAST score
                  282
E value
                  2.0e-25
Match length
                  87
% identity
                  62
NCBI Description
                  (Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  301724
Seq. ID
                  clt700042415.f1
Method
                  BLASTX
                  g3641252
NCBI GI
BLAST score
                  201
E value
                  6.0e-16
Match length
                  78
% identity
                  51
NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus
                  domestica]
Seq. No.
                  301725
```

42549

clt700042425.f1

BLAST score

E value

103

6.0e-51



```
Method
                  BLASTX
NCBI GI
                  g4115388
BLAST score
                  297
E value
                  3.0e-27
Match length
                  92
% identity
                  59
NCBI Description
                  (AC005967) putative prolylcarboxypeptidase [Arabidopsis
Seq. No.
                  301726
Seq. ID
                  clt700042433.f1
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  311
E value
                  7.0e-29
Match length
                  87
% identity
                  71
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  301727
Seq. ID
                  clt700042435.f1
Method
                  BLASTN
NCBI GI
                  g168527
BLAST score
                  61
E value
                  8.0e-26
Match length
                  81
% identity
                  94
NCBI Description Maize NADP-dependent malic enzyme (Me1) mRNA, complete cds
Seq. No.
                  301728
Seq. ID
                  clt700042440.f1
Method
                  BLASTX
NCBI GI
                  q482445
BLAST score
                  216
                  5.0e-18
E value
Match length
                  61
% identity
                  69
                  chlorophyll a/b-binding protein precursor - swollen
NCBI Description
                  duckweed >gi 168296 (M29334) light-harvesting chlorophyll
                  a/b protein precursor [Lemna gibba]
                  301729
Seq. No.
                  clt700042446.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q606815
BLAST score
                  199
E value
                  9.0e-16
Match length
                  88
% identity
                  56
NCBI Description
                  (U08403) carbonic anhydrase [Zea mays]
Seq. No.
                  301730
Seq. ID
                  clt700042486.f1
Method
                  BLASTN
NCBI GI
                  g3450841
```

Match length 135
% identity 94
NCBI Description Oryza sativa mitogen activated protein kinase kinase (MEK1) mRNA, complete cds

Seq. No. 301731
Seq. ID clt700042501.f1

Method BLASTX
NCBI GI g1154889
BLAST score 351
E value 1.0e-33
Match length 72
% identity 94

NCBI Description (Z68504) 3-hydroxy-3-methylglutaryl-CoA reductase [Oryza sativa] >gi 1171364 (U43961) 3-hydroxy-3-methylglutaryl=CoA

reductase [Oryza sativa]

Seq. No. 301732

Seq. ID clt700042502.f1

Method BLASTX
NCBI GI g3402713
BLAST score 249
E value 1.0e-21
Match length 84
% identity 55

NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301733

Seq. ID clt700042578.f1

Method BLASTX
NCBI GI g3914465
BLAST score 143
E value 8.0e-17
Match length 50
% identity 98

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR

(LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)

>gi_2981207 (AF052076) photosystem I complex PsaH subunit

precursor [Zea mays]

Seq. No. 301734

Seq. ID clt700042586.f1

Method BLASTX
NCBI GI g120657
BLAST score 198
E value 2.0e-20
Match length 56
% identity 95

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi 66024 pir DEZMG3

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - maize >gi_168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi_763035 emb CAA33455 (X15408)

glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

grycerataenyae o phosphaec denyarogenase (zea maye

Seq. No. 301735



```
clt700042626.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2130042
BLAST score
                  286
E value
                   6.0e-26
Match length
                   92
                   72
% identity
                  Mg-chelatase chain Xantha-f - barley >gi 861199 (U26916)
NCBI Description
                  protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
Seq. No.
                   301736
Seq. ID
                   clt700042631.f1
Method
                   BLASTX
NCBI GI
                   g4099835
BLAST score
                   162
E value
                   2.0e-11
Match length
                   58
% identity
NCBI Description
                  (U90266) bifunctional nuclease [Zinnia elegans]
Seq. No.
                   301737
                   clt700042682.f1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3955064
BLAST score
                   65
E value
                   2.0e-28
Match length
                   191
                   85
% identity
NCBI Description
                  Zea mays PHYT I gene for acidic phytase
Seq. No.
                   301738
                   clt700042683.f1
Seq. ID
Method
                   BLASTN
                   g733457
NCBI GI
BLAST score
                   52
E value
                   1.0e-20
Match length
                   117
% identity
                   97
                   Zea mays chlorophyll a/b-binding apoprotein CP24 (Lhcb6-1)
NCBI Description
                   mRNA, complete cds
                   301739
Seq. No.
                   clt700042768.f1
Seq. ID
Method
                   BLASTX
                   g4455331
NCBI GI
BLAST score
                   222
                   2.0e-18
E value
Match length
                   68
                   56
% identity
```

(AL035525) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 301740

clt700042773.f1 Seq. ID

Method BLASTX g606811 NCBI GI BLAST score 155

```
E value
Match length
                  38
% identity
                  79
NCBI Description
                  (U08401) carbonic anhydrase [Zea mays]
Seq. No.
                  301741
                  clt700042785.f1
Seq. ID
                  BLASTX
Method
                  q1653089
NCBI GI
                  193
BLAST score
E value
                  4.0e-15
                  86
Match length
% identity
                  47
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]
                  301742
Seq. No.
Seq. ID
                  clt700042807.f1
Method
                  BLASTN
NCBI GI
                  g1906603
BLAST score
                  152
E value
                  4.0e-80
Match length
                  263
% identity
                  89
                  Zea mays ACCase gene, intron containing colonist1 and
NCBI Description
                  colonist2 retrotransposons and reverse transcriptase
                  pseudogene, complete sequence
Seq. No.
                  301743
                  clt700042844.f1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22328
BLAST score
                  268
E value
                  1.0e-149
                  268
Match length
% identity
                  100
NCBI Description Maize mRNA for a high mobility group protein
Seq. No.
                  301744
Seq. ID
                  clt700042853.f1
Method
                  BLASTN
NCBI GI
                  q2661765
BLAST score
                  244
E value
                  1.0e-135
Match length
                  280
% identity
                  97
NCBI Description
                  Zea mays mRNA for putative porphobilinogen deaminase
Seq. No.
                  301745
Seq. ID
                  clt700042863.f1
```

68

Method BLASTX NCBI GI g119961 BLAST score 176 E value 5.0e-13 Match length 50

% identity

NCBI Description FERREDOXIN V PRECURSOR (FD V) >gi 168475 (M73828) ferredoxin [Zea mays] >gi 444684 prf 1907324A



ferredoxin:ISOTYPE=V [Zea mays]

```
301746
Seq. No.
Seq. ID
                  clt700042904.f1
Method
                  BLASTN
NCBI GI
                  g2239259
BLAST score
                  36
                  2.0e-11
E value
                  88
Match length
                   87
% identity
NCBI Description
                  Zea mays mRNA for cinnamoyl CoA reductase
                   301747
Seq. No.
Seq. ID
                  clt700042989.fl
Method
                  BLASTN
NCBI GI
                   g312289
BLAST score
                   33
                   4.0e-09
E value
Match length
                  33
                   100
% identity
                  O.sativa short highly repeated, interspersed DNA
NCBI Description
                   301748
Seq. No.
Seq. ID
                   clt700043027.f1
                  BLASTX
Method
NCBI GI
                   g68029
BLAST score
                   149
                   7.0e-10
E value
                   64
Match length
                   48
% identity
                  phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize
NCBI Description
                   >gi_22408_emb_CAA33317 (X15239) PEP carboxylase [Zea mays]
                   >gi 228619 prf 1807332A phosphoenolpyruvate carboxylase
                   [Zea mays]
                   301749
Seq. No.
                   clt700043163.f1
Seq. ID
Method
                   BLASTN
                   g4176423
NCBI GI
BLAST score
                   43
                   4.0e-15
E value
Match length
                   51
% identity
                  Oryza sativa rpl12-2 gene for chloroplast ribosomal protein
NCBI Description
                   L12, complete cds
Seq. No.
                   301750
Seq. ID
                   clt700043272.f1
Method
                   BLASTX
NCBI GI
                   g312179
BLAST score
                   427
E value
                   1.0e-42
Match length
                   85
% identity
                   (X73151) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
```

(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

Match length

NCBI Description

% identity

Seq. No.

66

100

301756



>gi_1185554 (U45858) glyceraldehyde-3-phosphate
dehydrogenase [Zea mays]

Seq. No. 301751 Seq. ID clt700043329.fl Method BLASTX NCBI GI q2244925 BLAST score 151 E value 4.0e-10 Match length 44 % identity (Z97339) glutaredoxin [Arabidopsis thaliana] NCBI Description 301752 Seq. No. clt700043330.f1 Seq. ID Method BLASTX g4107009 NCBI GI BLAST score 233 8.0e-20 E value Match length 48 % identity NCBI Description (D82039) OSK1 [Oryza sativa] 301753 Seq. No. clt700043341.f1 Seq. ID BLASTX Method NCBI GI g1854376 BLAST score 444 2.0e-44 E value Match length 86 % identity 100 (AB001337) Sucrose-Phosphate Synthase [Saccharum NCBI Description officinarum] Seq. No. 301754 Seq. ID clt700043358.f1 Method BLASTX NCBI GI g82080 BLAST score 179 E value 2.0e-13 Match length 53 % identity 70 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi 226872 prf 1609235A³chlorophyll a/b binding protein [Lycopersicon esculentum] Seq. No. 301755 Seq. ID clt700043362.f1 Method BLASTX NCBI GI g1673456 BLAST score 336 E value 8.0e-32

42555

(Y09214) rubisco small subunit [Zea mays]



```
Seq. ID
                  clt700043422.f1
Method
                  BLASTX
                  g1176689
NCBI GI
BLAST score
                  266
E value
                  1.0e-23
Match length
                  89
% identity
                  61
                  HYPOTHETICAL PROTEIN IN PETB 5'REGION >gi 97579 pir S18125
NCBI Description
                  hypothetical protein - Synechococcus sp. (PCC 7002)
                  >gi_38965_emb_CAA44776_ (X63049) orf [Synechococcus
                  PCC7002]
                  301757
Seq. No.
                  clt700043431.f1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2326946
BLAST score
                  241
E value
                  1.0e-133
Match length
                  255
                  99
% identity
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29
Seq. No.
                  301758 \
                  clt700043447.fl
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2326947
BLAST score
                  228
                  4.0e-25
E value
Match length
                  60
% identity
                  100
                  (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                   [Zea mays]
                  301759
Seq. No.
                  clt700043463.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2654226
BLAST score
                  243
E value
                  7.0e-21
Match length
                  61
                  77
% identity
                   (AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  301760
Seq. ID
                  clt700043468.f1
Method
                  BLASTX
NCBI GI
                  g4538939
BLAST score
                  210
```

E value 5.0e-17 Match length 45 84 % identity

(AL049483) Col-O casein kinase I-like protein [Arabidopsis NCBI Description

thaliana]

301761 Seq. No.

clt700043496.f1 Seq. ID

42556

```
Method BLASTN
NCBI GI g2326946
BLAST score 153
E value 9.0e-81
Match length 160
% identity 99
```

NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29

 Seq. No.
 301762

 Seq. ID
 clt700043623.f1

 Method
 BLASTX

 NCBI GI
 g2500959

 BLAST score
 248

 E value
 2.0e-21

BLAST score 248
E value 2.0e-21
Match length 90
% identity 56

NCBI Description ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS) >gi_1653611_dbj_BAA18523_ (D90915) alanyl-tRNA synthetase

[Synechocystis sp.]

Seq. No. 301763

Seq. ID clt700043633.f1

Method BLASTX
NCBI GI g1076685
BLAST score 160
E value 3.0e-11
Match length 45
% identity 34

NCBI Description SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_

(D30038) SPF1 protein [Ipomoea batatas]

Seq. No. 301764

Seq. ID clt700043642.f1

Method BLASTX
NCBI GI g115772
BLAST score 387
E value 1.0e-37
Match length 89
% identity 84

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi 82460 pir _S03705 chlorophyll

a/b-binding protein 1R precursor - rice

>gi 20178 emb CAA32108 (X13908) chlorophyll a/b-binding

preprotein (AA -31 to 235) [Oryza sativa]

Seq. No. 301765

Seq. ID clt700043679.f1

Method BLASTX
NCBI GI g4455364
BLAST score 144
E value 2.0e-09
Match length 39
% identity 72

NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis

thaliana]

Seq. No. 301766



```
Seq. ID
                  clt700043753.f1
                  BLASTX
Method
NCBI GI
                  g2326947
BLAST score
                  224
                  3.0e-31
E value
Match length
                  70
                  100
% identity
                  (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                  [Zea mays]
Seq. No.
                  301767
Seq. ID
                  clt700043761.f1
Method
                  BLASTX
NCBI GI
                  q2130091
BLAST score
                  356
E value
                  3.0e-34
Match length
                  68
% identity
                  97
NCBI Description
                  aspartate aminotransferase - proso millet
                  >gi_633095 dbj_BAA08106_ (D45076) plastidic aspartate
                  aminotransferase [Panicum miliaceum]
Seq. No.
                  301768
Seq. ID
                  clt700043884.f1
Method
                  BLASTX
NCBI GI
                  g2459411
BLAST score
                  265
E value
                  1.0e-23
Match length
                  83
% identity
                  59
                  (AC002332) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  301769
Seq. No.
                  clt700043901.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  173
                  1.0e-12
E value
Match length
                  52
% identity
                  69
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                  301770
Seq. No.
Seq. ID
                  clt700043923.fl
Method
                  BLASTX
NCBI GI
                  g4539404
BLAST score
                  205
E value
                  2.0e-16
                  58
Match length
% identity
                  67
```

NCBI Description (AL049524) putative protein [Arabidopsis thaliana]

Seq. No. 301771

Seq. ID clt700044039.f1

Method BLASTN

42558



```
g3885895
NCBI GI
BLAST score
                  46
E value
                  7.0e-17
Match length
                  182
% identity
                  81
                  Oryza sativa plastocyanin precursor, mRNA, complete cds
NCBI Description
                  301772
Seq. No.
Seq. ID
                  clt700044109.r1
Method
                  BLASTX
NCBI GI
                  g2213632
BLAST score
                  228
E value
                  3.0e~19
Match length
                  72
% identity
                  60
                  (AC000103) F21J9.24 [Arabidopsis thaliana]
NCBI Description
                  301773
Seq. No.
Seq. ID
                  clt700044167.f1
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  180
E value
                  1.0e-13
                  54
Match length
% identity
                  69
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
Seq. No.
                  301774
Seq. ID
                  clt700044356.f1
Method
                  BLASTX
NCBI GI
                  q4581162
BLAST score
                  208
E value
                  8.0e-17
Match length
                  49
                  82
% identity
NCBI Description
                  (AC006220) putative symbiosis-related protein [Arabidopsis
                  thaliana]
Seq. No.
                  301775
                  clt700044358.f1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2326946
BLAST score
                  229
E value
                  1.0e-126
Match length
                  247
% identity
                  99
                  Z.mays mRNA for chlorophyll a/b-binding protein CP29
NCBI Description
                  301776
Seq. No.
Seq. ID
                  clt700044368.f1
```

Method BLASTX NCBI GI g1176505 BLAST score 162 E value 2.0e-11 Match length 80

% identity

NCBI Description

74

thaliana]



```
% identity
                  42
                  HYPOTHETICAL 47.8 KD PROTEIN B0280.9 IN CHROMOSOME III
NCBI Description
                  >gi 500770 (U10438) B0280.9 gene product [Caenorhabditis
                  elegans]
                  301777
Seq. No.
                  clt700044383.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2326352
BLAST score
                  312
E value
                  5.0e-29
                  89
Match length
                  71
% identity
NCBI Description (Y11156) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  301778
                  clt700044389.fl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3482914
BLAST score
                  211
E value
                  3.0e-17
                  88
Match length
                  47
% identity
NCBI Description (AC003970) Similar to nodulins and lipase [Arabidopsis
                  thaliana]
Seq. No.
                  301779
Seq. ID
                  clt700044401.f1
Method
                  BLASTX
NCBI GI
                  g2462833
BLAST score
                  200
E value
                  8.0e-16
                  82
Match length
                  49
% identity
NCBI Description
                  (AF000657) highly similar to froha and frohb, potential
                  frohc [Arabidopsis thaliana]
                  301780
Seq. No.
Seq. ID
                  clt700044527.f1
Method
                  BLASTX
NCBI GI
                  q3885896
BLAST score
                  187
                  2.0e-14
E value
                  73
Match length
                  53
% identity
NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]
Seq. No.
                  301781
Seq. ID
                  clt700044539.f1
                  BLASTX
Method
NCBI GI
                  q3269291
BLAST score
                  318
E value
                  1.0e-29
Match length
                  82
```

(AL030978) putative receptor protein kinase [Arabidopsis



Seq. No.

Seq. ID

301782

clt700044544.f1

```
Method
                  BLASTX
                  q2326947
NCBI GI
                  199
BLAST score
                  2.0e-28
E value
Match length
                  66
% identity
                  100
NCBI Description
                   (Z50801) Chlorophyll a/b-binding protein CP29 precursor
                   [Zea mays]
                  301783
Seq. No.
Seq. ID
                  clt700044557.f1
Method
                  BLASTX
                  g4585882
NCBI GI
BLAST score
                  221
E value
                  2.0e-18
                   46
Match length
                   93
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  301784
                  clt700044585.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3450842
BLAST score
                  262
E value
                   2.0e-34
Match length
                  84
                  85
% identity
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                  sativa]
Seq. No.
                   301785
Seq. ID
                  clt700044619.f1
Method
                  BLASTX
NCBI GI
                   g2244910
BLAST score
                   142
E value
                  2.0e-09
Match length
                   44
% identity
                   66
                  (Z97339) unnamed protein product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  301786
Seq. ID
                  clt700044733.f1
Method
                  BLASTX
NCBI GI
                  g2623295
BLAST score
                  334
                  1.0e-31
E value
Match length
                  79
% identity
                  76
NCBI Description
                  (AC002409) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  301787
                  clt700044778.f1
Seq. ID
Method
                  BLASTX
```

Match length

NCBI Description

% identity

59

59

```
NCBI GI
                  q3341648
BLAST score
                  455
E value
                  8.0e-46
Match length
                  84
% identity
                  100
                  (AJ005343) DNA directed RNA polymerase [Zea mays]
NCBI Description
Seq. No.
                  301788
                  clt700044784.f1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22204
BLAST score
                  46
E value
                  6.0e-17
                  117
Match length
                  93
% identity
                  Maize Bz-McC gene for UDPglucose flavonoid
NCBI Description
                  glycosyl-transferase
Seq. No.
                  301789
Seq. ID
                  clt700044801.f1
Method
                  BLASTX
NCBI GI
                  q3337361
BLAST score
                  146
                  1.0e-09
E value
Match length
                  52
                   48
% identity
NCBI Description
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                  301790
                  clt700044864.f1
Seq. ID
                  BLASTX
Method
                  q4220517
NCBI GI
BLAST score
                  301
                  1.0e-27
E value
Match length
                  89
% identity
                  63
                  (AL035356) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301791
Seq. No.
Seq. ID
                  clt700044891.f1
Method
                  BLASTX
NCBI GI
                  g1814401
BLAST score
                   377
E value
                  1.0e-36
Match length
                  85
% identity
                  84
NCBI Description
                  (U84888) phosphoglucomutase [Mesembryanthemum crystallinum]
Seq. No.
                  301792
Seq. ID
                  clt700044894.f1
Method
                  BLASTX
NCBI GI
                  g4567283
BLAST score
                  168
                  3.0e-12
E value
```

42562

(AC006841) unknown protein [Arabidopsis thaliana]

Match length

% identity

68

81



```
301793
Seq. No.
                  clt700044936.f1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g100880
BLAST score
                  190
E value
                  6.0e-15
                  58
Match length
                  71
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
NCBI Description
                   (phosphorylating) (EC 1.2.1.13) A, chloroplast - maize
                  301794
Seq. No.
Seq. ID
                  clt700044960.fl
                  BLASTX
Method
                  g115815
NCBI GI
BLAST score
                  327
                  9.0e-31
E value
Match length
                  69
% identity
                  88
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-M9) (LHCP) >gi 100866 pir S13098 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi_22355_emb_CAA39376_ (X55892) light-harvesting
                  chlorophyll a/b binding protein [Zea mays]
                  301795
Seq. No.
Seq. ID
                  clt700044991.f1
Method
                  BLASTN
NCBI GI
                  g2773153
                   67
BLAST score
                   2.0e-29
E value
Match length
                   79
% identity
                   96
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
Seq. No.
                   301796
Seq. ID
                   clt700045013.f1
                   BLASTX
Method
                   g3004564
NCBI GI
BLAST score
                   282
E value
                   1.0e-25
Match length
                   82
                   63
% identity
                   (AC003673) putative receptor Ser/Thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   301797
                   clt700045074.f1
Seq. ID
Method
                   BLASTX
                   g115786
NCBI GI
BLAST score
                   266
E value
                   1.0e-23
```

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR



(CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]

::

 Seq. No.
 301798

 Seq. ID
 clt700045077.f1

 Method
 BLASTN

NCBI GI g21843
BLAST score 37
E value 1.0e-11
Match length 59
% identity 92

NCBI Description Wheat PsbO mRNA for 33kDa oxygen evolving protein of

photosystem II

Seq. No. 301799

Seq. ID clt700045136.f1

Method BLASTX
NCBI GI g1673456
BLAST score 278
E value 4.0e-25
Match length 55
% identity 100

NCBI Description (Y09214) rubisco small subunit [Zea mays]

Seq. No. 301800

Seq. ID clt700045148.f1

Method BLASTN
NCBI GI g168470
BLAST score 172
E value 4.0e-92
Match length 250
% identity 93

NCBI Description Maize ferredoxin I (Fd) isoprotein mRNA, pFD1'

Seq. No. 301801

Seq. ID clt700045162.f1

Method BLASTX
NCBI GI g4006835
BLAST score 177
E value 4.0e-13
Match length 91
% identity 36

NCBI Description (AC005970) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301802

Seq. ID clt700045182.f1

Method BLASTN
NCBI GI g168529
BLAST score 57
E value 2.0e-23
Match length 57
% identity 100

NCBI Description Zea mays opaque2 heterodimerizing protein 1 (OHP1) mRNA,

complete cds

Seq. No. 301803

42564



clt700045259.f1 Seq. ID Method BLASTX NCBI GI g131197 BLAST score 141 2.0e-15 E value Match length 51 % identity 88 PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR NCBI Description (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) (GOS5 PROTEIN) >gi 72679 pir A1RZH photosystem I protein psaH precursor - rice >gi_20240_emb_CAA36191_ (X51911) GOS5 [Oryza sativa] 301804 Seq. No. Seq. ID clt700045263.f1 BLASTX Method g4468984 NCBI GI BLAST score 213 1.0e-17 E value 73 Match length % identity (AL035605) putative protein [Arabidopsis thaliana] NCBI Description 301805 Seq. No. clt700045305.f1 Seq. ID BLASTN Method NCBI GI g2981206 BLAST score 198 1.0e-107 E value 220 Match length 98 % identity Zea mays photosystem I complex PsaH subunit precursor NCBI Description (psaH) mRNA, nuclear gene encoding chloroplast protein, complete cds 301806 Seq. No. clt700045321.f1 Seq. ID Method BLASTX NCBI GI g2326947 BLAST score 184 E value 4.0e-20 Match length 54 98 % identity NCBI Description [Zea mays]

(Z50801) Chlorophyll a/b-binding protein CP29 precursor

301807 Seq. No.

Seq. ID clt700045373.f1

Method BLASTX NCBI GI q4263711 BLAST score 337 E value 5.0e-32 Match length 81 % identity 79

(AC006223) putative CCR4-associated transcription factor NCBI Description

[Arabidopsis thaliana]

Seq. No. 301808 Seq. ID clt700045406.f1 Method BLASTX NCBI GI g462195 BLAST score 417 E value 3.0e-41 Match length 86 % identity 92 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi 100682 pir S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi 3789950 (AF094774) translation initiation factor [Oryza satīva] Seq. No. 301809 Seq. ID clt700045417.f1 Method BLASTX

NCBI GI g543938
BLAST score 268
E value 5.0e-24
Match length 57
% identity 95

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB48) (LHCP) >gi_82681_pir__S22497 chlorophyll a/b-binding protein precursor (cab-48) - maize

>gi_22228 emb CAA44888 (X63205) chlorophyll a /b binding

protein [Zea mays]

Seq. No. 301810

Seq. ID clt700045431.f1

Method BLASTN
NCBI GI g2326946
BLAST score 68
E value 2.0e-30
Match length 80
% identity 96

NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29

Seq. No.

301811

Seq. ID clt700045434.f1

Method BLASTX
NCBI GI g115786
BLAST score 277
E value 6.0e-25
Match length 74
% identity 74

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea

mays]

Seq. No. 301812

Seq. ID clt700045462.f1

Method BLASTX
NCBI GI g3913239
BLAST score 504
E value 2.0e-51



Match length 100 % identity 95

NCBI Description PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP

SYNTHASE) >gi 2612941 (AF024512) CLA1 transketolase-like

protein [Oryza sativa]

Seq. No. 301813

Seq. ID clt700045527.f1

Method BLASTX
NCBI GI g543938
BLAST score 262
E value 4.0e-23
Match length 62
% identity 85

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB48) (LHCP) >gi_82681_pir__\$22497 chlorophyll

a/b-binding protein precursor (cab-48) - maize

>gi_22228_emb_CAA44888_ (X63205) chlorophyll a /b binding

protein [Zea mays]

Seq. No. 301814

Seq. ID clt700045543.f1

Method BLASTX
NCBI GI g3789954
BLAST score 398
E value 3.0e-39
Match length 78
% identity 92

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No. 301815

Seq. ID clt700045579.f1

Method BLASTX
NCBI GI g2446998
BLAST score 219
E value 4.0e-18
Match length 45
% identity 96

NCBI Description (D63954) fatty acid desaturase [Zea mays]

Seq. No. 301816

Seq. ID clt700045586.f1

Method BLASTX
NCBI GI g3093410
BLAST score 323
E value 2.0e-30
Match length 84
% identity 75

NCBI Description (AJ225107) protoporphyrinogen oxidase [Solanum tuberosum]

Seq. No. 301817

Seq. ID clt700045623.f1

Method BLASTN
NCBI GI g2326946
BLAST score 237
E value 1.0e-131



```
Match length
% identity
                  99
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29
                  301818
Seq. No.
Seq. ID
                  clt700045655.f1
Method
                  BLASTX
NCBI GI
                  g534982
BLAST score
                  155
E value
                  1.0e-10
Match length
                  38
                  68
% identity
NCBI Description
                 (X75898) phosphoglucomutase [Spinacia oleracea]
                  301819
Seq. No.
Seq. ID
                  clt700045658.f1
Method
                  BLASTX
NCBI GI
                  g2914693
BLAST score
                  159
E value
                  5.0e-11
Match length
                  78
% identity
                  42
NCBI Description
                  (AC003974) putative protein kinase [Arabidopsis thaliana]
                  301820
Seq. No.
Seq. ID
                  clt700045665.f1
Method
                  BLASTX
NCBI GI
                  g2245087
BLAST score
                  190
                  1.0e-14
E value
Match length
                  50
% identity
                  64
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  301821
Seq. ID
                  clt700045738.f1
Method
                  BLASTX
NCBI GI
                  g115786
BLAST score
                  198
                  8.0e-16
E value
Match length
                  63
% identity
                  65
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB) (LHCP) >gi 82680 pir A29119 chlorophyll a/b-binding
                  protein - maize >gi 22357 emb CAA68451 (Y00379) LHCP [Zea
                  mays]
Seq. No.
                  301822
Seq. ID
                  clt700045842.f1
Method
                  BLASTX
NCBI GI
                  g115815
```

Method BLASTX
NCBI GI g115815
BLAST score 204
E value 2.0e-16
Match length 62
% identity 66

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll



a/b-binding protein precursor - maize
>gi_22355_emb_CAA39376_ (X55892) light-harvesting
chlorophyll a/b binding protein [Zea mays]

Seq. No. 301823

Seq. ID clt700045910.f1

Method BLASTX
NCBI GI g1673456
BLAST score 376
E value 2.0e-36
Match length 74
% identity 100

NCBI Description (Y09214) rubisco small subunit [Zea mays]

Seq. No. 301824

Seq. ID clt700045928.f1

Method BLASTX
NCBI GI g3885328
BLAST score 180
E value 1.0e-22
Match length 94
% identity 57

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 301825

Seq. ID clt700045986.f1

Method BLASTN
NCBI GI g21843
BLAST score 48
E value 4.0e-18
Match length 106
% identity 88

NCBI Description Wheat PsbO mRNA for 33kDa oxygen evolving protein of

photosystem II

Seq. No. 301826

Seq. ID clt700046012.f1

Method BLASTX
NCBI GI g729478
BLAST score 304
E value 5.0e-28
Match length 61
% identity 97

NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)

>gi 442481 dbj BAA04616 (D17790) ferredoxin-NADP+

reductase [Oryza sativa]

Seq. No. 301827

Seq. ID clt700046014.f1

Method BLASTX
NCBI GI g3421413
BLAST score 226
E value 7.0e-19
Match length 45
% identity 93

NCBI Description (AF081922) protein phosphatase 2A 55 kDa B regulatory



subunit [Oryza sativa] >gi_3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No. 301828

Seq. ID clt700046030.f1

Method BLASTX
NCBI GI g1488043
BLAST score 173
E value 1.0e-12
Match length 47
% identity 70

NCBI Description (U63784) PAPS-reductase-like protein [Catharanthus roseus]

Seq. No. 301829

Seq. ID clt700046032.f1

Method BLASTN
NCBI GI g2326946
BLAST score 237
E value 1.0e-131
Match length 255
% identity 99

NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29

Seq. No. 301830

Seq. ID clt700046060.f1

Method BLASTN
NCBI GI g22292
BLAST score 178
E value 1.0e-95
Match length 279
% identity 98

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 301831

Seq. ID clt700046066.f1

Method BLASTX
NCBI GI g1673456
BLAST score 239
E value 5.0e-32
Match length 75
% identity 100

NCBI Description (Y09214) rubisco small subunit [Zea mays]

Seq. No. 301832

Seq. ID clt700046073.f1

Method BLASTX
NCBI GI g115815
BLAST score 271
E value 4.0e-24
Match length 65

Match length 65 % identity 77

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll

a/b-binding protein precursor - maize

>qi 22355 emb CAA39376 (X55892) light-harvesting

chlorophyll a/b binding protein [Zea mays]

NCBI GI

BLAST score



```
301833
Seq. No.
Seq. ID
                  clt700046077.f1
                  BLASTN
Method
                   g3420038
NCBI GI
                   40
BLAST score
                   3.0e-13
E value
                   52
Match length
% identity
                   49
                   Zea mays gypsy/Ty3-type retrotransposon Tekay, complete
NCBI Description
                   sequence
                   301834
Seq. No.
                   clt700046241.f1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2739008
BLAST score
                   191
                   6.0e-15
E value
                   76
Match length
% identity
                   55
                   (AF022463) CYP78A3p [Glycine max]
NCBI Description
Seq. No.
                   301835
                   clt700046406.fl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3283026
BLAST score
                   184
                   6.0e-14
E value
                   92
Match length
                   38
% identity
                  (AF051562) putative transposase [Arabidopsis thaliana]
NCBI Description
                   301836
Seq. No.
                   clt700046458.f1
Seq. ID
                   BLASTX
Method
                   g4335735
NCBI GI
                   151
BLAST score
                   4.0e-10
E value
                   35
Match length
% identity
                  (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   301837
Seq. No.
Seq. ID
                   clt700046489.f1
                   BLASTN
Method
NCBI GI
                   g861198
BLAST score
                   63
                   2.0e-27
E value
                   87
Match length
                   93
% identity
                   Hordeum vulgare protoporphyrin IX Mg-chelatase subunit
NCBI Description
                   precursor (Xantha-f) gene, complete cds
                   301838
Seq. No.
Seq. ID
                   cyk700047301.fl
Method
                   BLASTX
```

42571

g2618691 287



```
7.0e-26
E value
                  107
Match length
% identity
                   (AC002510) putative chloroplast envelope Ca2+-ATPase
NCBI Description
                   [Arabidopsis thaliana]
                  301839
Seq. No.
Seq. ID
                  cyk700047370.f1
                  BLASTX
Method
                  g4006915
NCBI GI
BLAST score
                  159
                   6.0e-11
E value
                  74
Match length
                   41
% identity
NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   301840
Seq. ID
                   cyk700047402.f1
                   BLASTX
Method
                   q3023932
NCBI GI
                   211
BLAST score
                   4.0e-17
E value
Match length
                   78
                   51
% identity
NCBI Description HISTONE DEACETYLASE 3 (HD3) >gi_2791688 (AF039753) histone
                   deacetylase-3; HD-3 [Gallus gallus]
Seq. No.
                   301841
                   cyk700047429.f1
Seq. ID
Method
                   BLASTN
                   q559535
NCBI GI
                   309
BLAST score
E value
                   1.0e-174
                   335
Match length
% identity
                   99
NCBI Description Z.mays mRNA for metallothionein
Seq. No.
                   301842
Seq. ID
                   cyk700047456.fl
                   BLASTX
Method
                   g4039155
NCBI GI
BLAST score
                   169
E value
                   3.0e-12
Match length
                   79
% identity
                   (AF104258) putative copper-inducible 35.6 kDa protein
NCBI Description
                   [Festuca rubra]
Seq. No.
                   301843
Seq. ID
                   cyk700047539.f1
Method
                   BLASTX
                   g2499946
NCBI GI
BLAST score
                   299
E value
                   2.0e-27
Match length
                   96
% identity
                   66
```

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

% identity

NCBI Description



PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

```
Seq. No. Seq. ID
                   301844
                   cyk700047591.f1
                   BLASTX
Method
NCBI GI
                   g2213594
                   378
BLAST score
                   1.0e-36
E value
                   110
Match length
                   69
% identity
                  (AC000348) T7N9.14 [Arabidopsis thaliana]
NCBI Description
                   301845
Seq. No.
                   cyk700047652.fl
Seq. ID
Method
                   BLASTX
                   q4008406
NCBI GI
BLAST score
                   200
                   9.0e-16
E value
                   58
Match length
% identity
                   60
                   (Z82286) predicted using Genefinder [Caenorhabditis
NCBI Description
                   elegans]
                   301846
Seq. No.
                   cyk700047710.f1
Seq. ID
Method
                   BLASTX
                   g4580398
NCBI GI
                   226
BLAST score
                   8.0e-19
E value
                   52
Match length
% identity
                   (AC007171) putative protein kinase APK1A [Arabidopsis
NCBI Description
                   thaliana]
                   301847
Seq. No.
Seq. ID
                   cyk700047769.f1
Method
                   BLASTN
NCBI GI
                   g4140643
BLAST score
                   201
                   1.0e-109
E value
Match length
                   310
% identity
                   92
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   301848
Seq. No.
Seq. ID
                   cyk700047815.f1
                   BLASTX
Method
NCBI GI
                   g3366659
BLAST score
                   163
E value
                   2.0e-11
Match length
                   54
```

(AF036763) P-ATPase [Emericella nidulans]

NCBI Description



```
301849
Seq. No.
                  cyk700047828.fl
Seq. ID
                  BLASTX
Method
                  g584861
NCBI GI
                  153
BLAST score
                  3.0e-10
E value
Match length
                  56
% identity
                  CYTOCHROME P450 71A2 (CYPLXXIA2) (P-450EG4)
NCBI Description
                  >gi 480396_pir__S36806 cytochrome P450 71A2 - eggplant
                  >gi_408140_emb_CAA50645_ (X71654) P450 hydroxylase [Solanum
                  melongena] >gi_441185_dbj_BAA03635_ (D14990) Cytochrome
                  P-450EG4 [Solanum melongena]
                  301850
Seq. No.
Seq. ID
                  cyk700047850.fl
                  BLASTX
Method
NCBI GI
                  g4206114
                  389
BLAST score
                  6.0e-38
E value
Match length
                  78
                  92
% identity
                   (AF097663) cytoplasmic glucose-6-phosphate 1-dehydrogenase
NCBI Description
                   [Mesembryanthemum crystallinum]
                   301851
Seq. No.
                  cyk700047889.f1
Seq. ID
                  BLASTX
Method
                   g3168840
NCBI GI
BLAST score
                  183
                   8.0e-14
E value
Match length
                   51
% identity
                  (U88711) copper homeostasis factor [Arabidopsis thaliana]
NCBI Description
                   301852
Seq. No.
                   cyk700047924.f1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2981287
BLAST score
                   56
                   9.0e-23
E value
Match length
                   128
% identity
                   86
NCBI Description Bos taurus histone H4.1 mRNA, complete cds
                   301853
Seq. No.
                   cyk700047958.f1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1351136
BLAST score
                   439
                   1.0e-43
E value
                   88
Match length
                   100
% identity
```

42574

sucrose synthase 2 [Zea mays]

>gi 514946 (L22296) UDP-glucose:D-fructose

SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)

2-glucosyl-transferase [Zea mays] >gi_533252 (L33244)

NCBI Description



```
301854
Seq. No.
                  cyk700048174.f1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3025299
BLAST score
                  291
E value
                  2.0e-26
                  93
Match length
                  57
% identity
                  HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi 2088660
NCBI Description
                   (AF002109) ABC1 isolog [Arabidopsis thaliana]
                  301855
Seq. No.
Seq. ID
                  cyk700048179.f1
                  BLASTX
Method
NCBI GI
                  g1620986
BLAST score
                  154
E value
                  2.0e-10
Match length
                  35
                  89
% identity
                  (Y08858) 40S ribosomal protein S17 [Nicotiana
NCBI Description
                  plumbaginifolia]
                  301856
Seq. No.
Seq. ID
                  cyk700048210.f1
                  BLASTX
Method
                   g3121951
NCBI GI
BLAST score
                  168
                   6.0e-12
E value
                  109
Match length
                  36
% identity
                  CH-TOG PROTEIN (COLONIC AND HEPATIC TUMOR OVER-EXPRESSED
NCBI Description
                   PROTEIN) (KIAA0097) >gi 603951 dbj BAA07892 (D43948) This
                   gene is novel. [Homo sapiens]
                   301857
Seq. No.
                   cyk700048223.f1
Seq. ID
Method
                   BLASTX
                   q3868800
NCBI GI
BLAST score
                   365
                   5.0e-35
E value
Match length
                   103
% identity
                  (AB013603) topoisomerase III beta [Mus musculus]
NCBI Description
                   301858
Seq. No.
                   cyk700048234.fl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3122388
BLAST score
                   203
E value
                   5.0e-16
Match length
                   67
% identity
```

WD-40 protein MSI2 [Arabidopsis thaliana]
42575

repeat protein [Arabidopsis thaliana]

WD-40 REPEAT PROTEIN MSI2 >gi 2394231 (AF016847) WD-40

>gi 4581121_gb_AAD24611.1_AC005825_18 (AC005825) putative



```
301859
Seq. No.
Seq. ID
                  cyk700048266.f1
                  BLASTX
Method
NCBI GI
                  g4539383
BLAST score
                  169
E value
                   4.0e-12
Match length
                  91
                   41
% identity
                   (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                   301860
Seq. No.
Seq. ID
                   cyk700048267.fl
Method
                  BLASTN
NCBI GI
                   g433040
BLAST score
                   54
                   1.0e-21
E value
Match length
                  170
% identity
                   84
                  Zea mays W-22 clone PREM-1A retroelement PREM-1, partial
NCBI Description
                   sequence
                   301861
Seq. No.
Seq. ID
                   cyk700048271.f1
                  BLASTX
Method
NCBI GI
                   g1076353
BLAST score
                   421
E value
                   9.0e-42
Match length
                   97
% identity
                  myosin heavy chain PCR11 - Arabidopsis thaliana (fragment)
NCBI Description
                   301862
Seq. No.
Seq. ID
                   cyk700048315.f1
Method
                   BLASTX
NCBI GI
                   g3687469
BLAST score
                   178
E value
                   1.0e-13
Match length
                   51
% identity
NCBI Description
                   (AL031798) putative diphthine synthase [Schizosaccharomyces
                   pombe]
Seq. No.
                   301863
Seq. ID
                   cyk700048318.f1
Method
                   BLASTX
NCBI GI
                   g3176715
BLAST score
                   241
E value
                   1.0e-20
Match length
                   96
% identity
                   52
```

Seq. No. 301864

NCBI Description

Seq. ID cyk700048365.f1

[Arabidopsis thaliana]

(AC002392) putative receptor-like protein kinase

NCBI Description



```
Method
NCBI GI
                  g3242783
BLAST score
                  229
                  3.0e-19
E value
Match length
                  67
% identity
                  60
                  (AF055354) respiratory burst oxidase protein B [Arabidopsis
NCBI Description
                  thaliana]
                  301865
Seq. No.
Seq. ID
                  cyk700048446.f1
Method
                  BLASTX
NCBI GI
                  g1350595
BLAST score
                  228
E value
                  2.0e-19
Match length
                  49
% identity
                  84
                  RHO2 PROTEIN >gi 1076923 pir JC4045 Rho2 protein - fission
NCBI Description
                  yeast (Schizosaccharomyces pombe) >gi 1064858 dbj BAA07378
                  (D38181) Rho 2 [Schizosaccharomyces pombe]
Seq. No.
                  301866
Seq. ID
                  cyk700048453.f1
Method
                  BLASTX
NCBI GI
                  q4377999
BLAST score
                  393
E value
                  2.0e-38
Match length
                  99
                  69
% identity
                  (AF076951) Cu-Zn superoxide dismutase [Glomerella
NCBI Description
                  cingulata]
Seq. No.
                  301867
Seq. ID
                  cyk700048471.f1
Method
                  BLASTX
NCBI GI
                  q2129559
BLAST score
                  228
E value
                  5.0e-19
                  80
Match length
% identity
                  cellulase homolog OR16pep - Arabidopsis thaliana
NCBI Description
                  >gi 1022807 (U37702) cellulase [Arabidopsis thaliana]
                  >qi 3493633 (AF074092) cellulase [Arabidopsis thaliana]
                  >qi 3598956 (AF074375) cellulase [Arabidopsis thaliana]
                  >qi 3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
                  [Arabidopsis thaliana]
Seq. No.
                  301868
Seq. ID
                  cyk700048478.f1
Method
                  BLASTX
NCBI GI
                  g2275211
BLAST score
                  290
E value
                  2.0e-26
Match length
                  66
% identity
```

(AC002337) RNA helicase isolog [Arabidopsis thaliana]



301869 Seq. No. Seq. ID

cyk700048479.f1

BLASTX Method q3776573 NCBI GI BLAST score 236 E value 2.0e-20 Match length 61 67 % identity

(ACO05388) Similar to nodulins and lipase homolog F14J9.5 NCBI Description

gi 3482914 from Arabidopsis thaliana BAC gb AC003970. Alternate first exon from 72258 to 72509. [Arabidopsis

thaliana]

Seq. No.

301870 cyk700048492.f1 Seq. ID

Method BLASTX NCBI GI g585165 BLAST score 291 E value 2.0e-26 80

Match length 70 % identity

GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM NCBI Description

(G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato

>gi 471345 emb CAA52442 (X74421) glucose-6-phosphate

1-dehydrogenase [Solanum tuberosum]

Seq. No. 301871

Seq. ID cyk700048502.fl

BLASTX Method g2293566 NCBI GI BLAST score 369 E value 1.0e-35 Match length 73 % identity 100

(AF012896) ADP-ribosylation factor 1 [Oryza sativa] NCBI Description

Seq. No. 301872

cyk700048605.f1 Seq. ID

BLASTX Method q4455232 NCBI GI BLAST score 262 E value 2.0e-24 Match length 88 % identity

(AL035523) putative protein [Arabidopsis thaliana] NCBI Description

301873 Seq. No.

Seq. ID cyk700048636.f1

Method BLASTX NCBI GI g2980798 BLAST score 187 E value 3.0e-14 Match length 63 % identity

(AL022197) putative protein [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                  301874
                  cyk700048650.f1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22185
BLAST score
                  33
E value
                  4.0e-09
Match length
                  53
                  91
% identity
                  Z.mays mRNA for b-32 protein, putative regulatory factor of
NCBI Description
                  zein expression (clone b-32.120)
Seq. No.
                  301875
Seq. ID
                  cyk700048662.f1
                  BLASTN
Method
NCBI GI
                  g2288968
BLAST score
                  54
                   6.0e-22
E value
Match length
                  85
                   91
% identity
                  Zea mays mRNA for glutathione transferase
NCBI Description
                  301876
Seq. No.
Seq. ID
                  cyk700048675.f1
Method
                  BLASTX
NCBI GI
                  g3738308
BLAST score
                  204
                   3.0e-16
E value
Match length
                  100
% identity
                   47
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                   301877
Seq. ID
                   cyk700048691.f1
                  BLASTX
Method
NCBI GI
                   q4138179
BLAST score
                   263
E value
                   3.0e-23
Match length
                   77
                   69
% identity
NCBI Description
                   (AJ223969) elongation factor 1 alpha subunit [Malus
                  domestica]
Seq. No.
                   301878
Seq. ID
                   cyk700048747.f1
Method
                   BLASTX
NCBI GI
                   q4105798
BLAST score
                   229
```

E value 2.0e-25 Match length 73 % identity 71

(AF049930) PGP237-11 [Petunia x hybrida] NCBI Description

Seq. No. 301879

cyk700048751.fl Seq. ID

Method BLASTX g2130023 NCBI GI BLAST score 169

```
E value 5.0e-12

Match length 82
% identity 57

NCBI Description DNA-binding protein ABF1 - wild oat (fragment)
>gi_1159877_emb_CAA88326_ (Z48429) DNA-binding protein
```

[Avena fatua]

Method BLASTN
NCBI GI g3320103
BLAST score 35

E value 1.0e-10
Match length 55
% identity 91

NCBI Description Zea mays mRNA for calcium-dependent protein kinase

Seq. No. 301881 Seq. ID cyk700

Seq. ID cyk700048805.f1
Method BLASTX
NCBI GI q82696

NCBI GI g82696
BLAST score 283
E value 5.0e-29
Match length 80
% identity 88

NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_

(X61121) glycine-rich protein [Zea mays]

Seq. No. 301882

Seq. ID cyk700048818.f1

Method BLASTX

NCBI GI g542058

BLAST score 150

E value 5.0e-10

Match length 39

% identity 67

NCBI Description HSR203J protein - common tobacco >gi_444002_emb_CAA54393_

(X77136) HSR203J [Nicotiana tabacum]

Seq. No. 301883

Seq. ID cyk700048838.f1

Method BLASTX
NCBI GI g4454043
BLAST score 258
E value 1.0e-22
Match length 69
% identity 67

% identity 67 NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 301884

Seq. ID cyk700048876.f1

Method BLASTN
NCBI GI g998429
BLAST score 53
E value 4.0e-21

Match length 77 % identity 92



```
GRF1=general regulatory factor [Zea mays, XL80, Genomic,
NCBI Description
                  5348 nt]
Seq. No.
                  301885
                  cyk700048896.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980767
BLAST score
                  182
E value
                   6.0e-14
Match length
                  77
% identity
                   48
                   (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                   301886
Seq. No.
Seq. ID
                  cyk700048904.f1
Method
                  BLASTX
NCBI GI
                   q4582461
BLAST score
                   364
E value
                   5.0e-35
Match length
                   101
                   71
% identity
                   (AC007071) putative triacylglycerol lipase [Arabidopsis
NCBI Description
                   thaliana]
                   301887
Seq. No.
Seq. ID
                   cyk700048929.f1
Method
                   BLASTX
NCBI GI
                   a2541876
BLAST score
                   168
                   5.0e-12
E value
                   79
Match length
                   43
% identity
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                   301888
Seq. ID
                   cyk700048931.fl
Method
                   BLASTN
                   q1408221
NCBI GI
BLAST score
                   71
E value
                   9.0e-32
                   201
Match length
                   91
% identity
                   Sorghum bicolor pathogenesis-related protein (PR-10) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   301889
Seq. ID
                   cyk700048934.f1
Method
                   BLASTN
NCBI GI
                   q4240538
```

BLAST score 258

E value 1.0e-143

Match length 265 99 % identity

Zea mays knotted class 1 homeodomain protein liguleless3 NCBI Description

(1g3) mRNA, complete cds

NCBI GI

BLAST score

q603189



```
301890
Seq. No.
 Seq. ID
                   cyk700048973.f1
Method
                   BLASTX
NCBI GI
                   g1353193
 BLAST score
                   176
                   6.0e-13
E value
                   50
Match length
 % identity
                   64
                   O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268
NCBI Description
                   O-methyltransferase (EC 2.1.1.-) - maize >gi 404070
                   (L14063) O-methyltransferase [Zea mays]
                   301891
 Seq. No.
                   cyk700048987.f1
 Seq. ID
                   BLASTX
 Method
                   g4585972
 NCBI GI
                   277
 BLAST score
                   8.0e-25
 E value
Match length
                   96
 % identity
                   51
 NCBI Description (AC005287) Putative ATPase [Arabidopsis thaliana]
                   301892
 Seq. No.
                   cyk700049013.f1
 Seq. ID
 Method
                   BLASTX
                   q2058311
 NCBI GI
 BLAST score
                   186
                   4.0e-14
 E value
 Match length
                   40
 % identity
                   85
                   (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]
 NCBI Description
                   301893
 Seq. No.
 Seq. ID
                   cyk700049102.f1
                   BLASTX
 Method
 NCBI GI
                   g4588906
 BLAST score
                   305
                   5.0e-28
 E value
 Match length
                   67
                   88
 % identity
 NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]
                   301894
 Seq. No.
 Seq. ID
                   cyk700049141.f1
 Method
                   BLASTN
 NCBI GI
                   g559535
                   252
 BLAST score
                   1.0e-140
 E value
 Match length
                   294
                   96
 % identity
 NCBI Description Z.mays mRNA for metallothionein
 Seq. No.
                   301895
 Seq. ID
                   cyk700049142.f1
 Method
                   BLASTN
```



```
4.0e-12
E value
Match length
                  81
% identity
                  86
                  Zea mays translation initiation factor eIF-4A mRNA,
NCBI Description
                  complete cds
Seq. No.
                  301896
Seq. ID
                  cyk700049168.f1
Method
                  BLASTX
NCBI GI
                  g1313909
BLAST score
                  198
E value
                  8.0e-16
                  76
Match length
                  61
% identity
                  (D84508) CDPK-related protein kinase [Zea mays]
NCBI Description
                  301897
Seq. No.
Seq. ID
                  cyk700049175.fl
Method
                  BLASTN
NCBI GI
                  g4582786
BLAST score
                  40
                  3.0e-13
E value
Match length
                  40
                  100
% identity
                  Zea mays mRNA for adenosine kinase, putative
NCBI Description
                  301898
Seq. No.
Seq. ID
                  cyk700049210.f1
                  BLASTN
Method
NCBI GI
                  g1747295
BLAST score
                  86
E value
                  8.0e-41
Match length
                  165
                  89
% identity
                  Oryza sativa mRNA for vacuolar H+-pyrophosphatase, complete
NCBI Description
Seq. No.
                  301899
Seq. ID
                  cyk700049214.f1
                  BLASTX
Method
                  g3885334
NCBI GI
BLAST score
                  297
E value
                   4.0e-27
Match length
                  88
% identity
                   67
                   (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  301900
Seq. ID
                  cyk700049247.f1
Method
                  BLASTX
NCBI GI
                  g1706260
BLAST score
                  283
E value
                  1.0e-25
Match length
                  76
% identity
                  74
NCBI Description
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597
```



cysteine proteinase 1 precursor - maize
>gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No. 301901

Seq. ID cyk700049294.f1

Method BLASTX
NCBI GI g2190553
BLAST score 178
E value 7.0e-18
Match length 97
% identity 47

NCBI Description (AC001229) Strong similarity to Arabidopsis

zeta-crystallin-like protein (gb Z49268). [Arabidopsis

thaliana]

Seq. No. 301902

Seq. ID cyk700049352.f1

Method BLASTX
NCBI GI g4115559
BLAST score 229
E value 4.0e-19
Match length 104
% identity 46

NCBI Description (AB013596) UDP-glucose:anthocysnin 5-O-glucosyltransferase

[Perilla frutescens]

Seq. No. 301903

Seq. ID cyk700049357.f1

Method BLASTN
NCBI GI g1042260
BLAST score 42
E value 2.0e-14
Match length 54
% identity 94

NCBI Description {Mul element insertion site, clone 10} [maize, Transposon,

285 nt]

Seq. No. 301904

Seq. ID cyk700049422.f1

Method BLASTX
NCBI GI g2130024
BLAST score 155
E value 1.0e-10
Match length 66
% identity 55

NCBI Description DNA-binding protein ABF2 - wild oat

>gi_1159879 emb CAA88331 (Z48431) DNA-binding protein

[Avena fatua]

Seq. No. 301905

Seq. ID cyk700049454.f1

Method BLASTX
NCBI GI g444344
BLAST score 235
E value 7.0e-24
Match length 70

E value Match length

% identity

53



```
% identity
NCBI Description
                    thaumatin-like protein [Zea mays]
                    301906
  Seq. No.
  Seq. ID
                    cyk700049460.f1
 Method
                    BLASTX
 NCBI GI
                    g3367568
 BLAST score
                    177
 E value
                    5.0e-13
 Match length
                    39
  % identity
                    79
 NCBI Description
                    (AL031135) protein kinase - like protein [Arabidopsis
                    thaliana]
  Seq. No.
                    301907
 Seq. ID
                    cyk700049493.f1
 Method
                    BLASTX
 NCBI GI
                    g3913366
 BLAST score
                    175
                    7.0e-13
 E value
 Match length
                    96
                    47
 % identity
 NCBI Description
                    PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR
                    >gi 1597723 (U67422) CRINKLY4 precursor [Zea mays]
 Seq. No.
                    301908
  Seq. ID
                    cyk700049530.f1
 Method
                    BLASTX
 NCBI GI
                    g549597
 BLAST score
                    217
                    8.0e-18
 E value
 Match length
                    88
  % identity
                    48
 NCBI Description
                    ATP-DEPENDENT RNA HELICASE DBP7 >gi 539330 pir S38093
                    probable purine nucleotide-binding protein YKR024c - yeast
                    (Saccharomyces cerevisiae) >gi_486449_emb_CAA82096
                    (Z28249) ORF YKR024c [Saccharomyces cerevisiae]
 Seq. No.
                    301909
 Seq. ID
                    cyk700049532.f1
 Method
                    BLASTX
 NCBI GI
                    q3360289
BLAST score
                    150
 E value
                    5.0e-10
 Match length
                    40
 % identity
 NCBI Description
                    (AF023164) leucine-rich repeat transmembrane protein kinase
                    1 [Zea mays]
 Seq. No.
                    301910
                    cyk700049560.f1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2980781
 BLAST score
                    214
                    2.0e-17
```



NCBI Description (AL022198) putative protein [Arabidopsis thaliana] Seq. No. 301911 Seq. ID cyk700049654.f1

Method BLASTN NCBI GI g168654 BLAST score 34 1.0e-09 E value Match length 94 % identity 84

NCBI Description Zea mays ADP glucose pyrophosphorylase (shrunken-2) gene,

complete cds

Seq. No. 301912

Seq. ID cyk700049692.f1

Method BLASTN NCBI GI g1945282 BLAST score 37 2.0e-11 E value Match length 61 % identity 90

NCBI Description O.sativa mRNA for myb factor, 1402 bp

Seq. No. 301913

Seq. ID cyk700049694.f1

Method BLASTX NCBI GI q585876 BLAST score 232 E value 1.0e-19 Match length 81

% identity 62

NCBI Description 60S RIBOSOMAL PROTEIN L23A (L25) >qi 1084424 pir S48026

ribosomal protein L25 - common tobacco >qi 310935 (L18908)

60S ribosomal protein L25 [Nicotiana tabacum]

Seq. No. 301914

Seq. ID cyk700049731.fl

Method BLASTN NCBI GI g1906603 BLAST score 226 E value 1.0e-124 Match length 277 % identity 96

NCBI Description Zea mays ACCase gene, intron containing colonist1 and

colonist2 retrotransposons and reverse transcriptase

pseudogene, complete sequence

Seq. No. 301915

Seq. ID cyk700049738.f1

Method BLASTX NCBI GI g2570047 BLAST score 222 E value 2.0e-18 Match length 87 % identity 41

NCBI Description (Y09234) MSTK2S kinase-like protein [Mus musculus]

Method

BLASTX



```
Seq. No.
                  301916
Seq. ID
                  cyk700049749.f1
Method
                  BLASTX
NCBI GI
                  g3805964
BLAST score
                  306
E value
                  1.0e-28
Match length
                  64
% identity
                  86
                  (Y13773) laccase [Populus balsamifera subsp. trichocarpa]
NCBI Description
                  301917
Seq. No.
Seq. ID
                  cyk700049772.f1
Method
                  BLASTX
NCBI GI
                  g2244855
BLAST score
                  261
                  6.0e-23
E value
                  100
Match length
% identity
                  54
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  301918
Seq. ID
                  cyk700049805.f1
Method
                  BLASTX
NCBI GI
                  q4378178
BLAST score
                  181
E value
                  5.0e-16
                  89
Match length
                  56
% identity
NCBI Description
                  (AF102543) unknown [Zymomonas mobilis]
                  301919
Seq. No.
Seq. ID
                  cyk700049823.f1
Method
                  BLASTX
NCBI GI
                  g128185
BLAST score
                  235
                  3.0e-26
E value
Match length
                  75
% identity
                  NITRATE REDUCTASE (NR) >gi 66208 pir RDBHNH nitrate
NCBI Description
                  reductase (NADH) (EC 1.6.6.1) - barley (cv. Himalaya)
                  >gi_18994_emb_CAA40976_ (X57845) nitrate reductase [Hordeum
                  vulgare]
Seq. No.
                  301920
Seq. ID
                  cyk700049824.f1
                  BLASTX
Method
NCBI GI
                  q1491929
BLAST score
                  415
                  5.0e-41
E value
Match length
                  89
                  89
% identity
NCBI Description
                  (U51272) 1,3-beta-D-glucan synthase catalytic subunit
                  [Emericella nidulans]
Seq. No.
                  301921
Seq. ID
                  cyk700049833.f1
```



```
q4467126
NCBI GI
                  226
BLAST score
                  6.0e-19
E value
Match length
                  63
                  71
% identity
NCBI Description
                  (AL035538) guanine nucleotide-exchange protein-like
                  [Arabidopsis thaliana]
                  301922
Seq. No.
Seq. ID
                  cyk700049887.f1
Method
                  BLASTX
NCBI GI
                  g2598037
BLAST score
                  291
                  2.0e-26
E value
                  98
Match length
                  54
% identity
                  (AJ001272) manganese resistance 1 protein [Saccharomyces
NCBI Description
                  cerevisiae]
                  301923
Seq. No.
Seq. ID
                  cyk700049888.f1
                  BLASTN
Method
NCBI GI
                  q1657759
BLAST score
                  80
                  1.0e-37
E value
                  88
Match length
                  98
% identity
                  Zea mays retrotransposon Fourf 5' LTR and primer binding
NCBI Description
                  site DNA sequence
Seq. No.
                  301924
                  cyk700049907.f1
Seq. ID
Method
                  BLASTX
                  q2293566
NCBI GI
                  378
BLAST score
                   9.0e-37
E value
                  75
Match length
% identity
                  100
                  (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
NCBI Description
                   301925
Seq. No.
Seq. ID
                  cyk700049910.f1
Method
                  BLASTX
NCBI GI
                  q3522929
BLAST score
                   407
                   5.0e-40
E value
Match length
                   80
% identity
                   (AC002535) putative dTDP-glucose 4-6-dehydratase
NCBI Description
```

[Arabidopsis thaliana] >gi 3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 301926

Seq. ID cyk700049953.f1

BLASTX Method g100490 NCBI GI BLAST score 402



```
E value
                   2.0e-39
                  103
Match length
                   23
% identity
                  polyubiquitin - garden snapdragon (fragment)
NCBI Description
                  >gi 16071 emb CAA48140 (X67957) ubiquitin [Antirrhinum
                  majus]
Seq. No.
                   301927
Seq. ID
                   cyk700049964.fl
Method
                  BLASTX
                   q1076641
NCBI GI
BLAST score
                   208
                   8.0e-17
E value
Match length
                   40
                   97
% identity
                  tau-protein kinase (EC 2.7.1.135) homolog - common tobacco
NCBI Description
                   >gi 456356 emb CAA54803 (X77763) shaggy like protein
                   kinase [Nicotiana tabacum] >gi 1094395 prf 2106142A
                   Ser/Thr protein kinase [Nicotiana tabacum]
                   301928
Seq. No.
Seq. ID
                   cyk700050015.f1
Method
                  BLASTX
NCBI GI
                   q4539399
BLAST score
                   184
E value
                   6.0e-14
Match length
                   38
                   100
% identity
                   (AL035526) ras-like GTP-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   301929
Seq. No.
Seq. ID
                   cyk700050036.f1
Method
                   BLASTX
NCBI GI
                   g1209756
BLAST score
                   254
                   3.0e-22
E value
                  91
Match length
% identity
                  (U43629) integral membrane protein [Beta vulgaris]
NCBI Description
                   301930
Seq. No.
Seq. ID
                   cyk700050061.f1
Method
                   BLASTX
NCBI GI
                   g1076685
BLAST score
                   300
                   2.0e-27
E value
                   90
Match length
% identity
                   34
NCBI Description
                   SPF1 protein - sweet potato >gi 484261 dbj BAA06278
                   (D30038) SPF1 protein [Ipomoea batatas]
                   301931
Seq. No.
```

Seq. ID cyk700050077.f1

Method BLASTX NCBI GI g902586 BLAST score 438



```
E value
                  8.0e-44
Match length
                  88
% identity
NCBI Description
                  (U29162) ubiquitin [Zea mays]
Seq. No.
                  301932
Seq. ID
                  cyk700050123.f1
                  BLASTX
Method
                  g2894569
NCBI GI
BLAST score
                  186
E value
                  2.0e-14
Match length
                  50
% identity
NCBI Description
                  (AL021890) putative protein [Arabidopsis thaliana]
Seq. No.
                  301933
Seq. ID
                  cyk700050135.f1
Method
                  BLASTX
NCBI GI
                  g422029
BLAST score
                  312
E value
                  6.0e-29
Match length
                  99
% identity
                  69
NCBI Description
                  transcription factor OBF3.2, ocs element-binding - maize
                  >gi_297018 emb CAA48904 (X69152) ocs-element binding
                  factor 3.2 [Zea mays]
Seq. No.
                  301934
Seq. ID
                  cyk700050162.f1
Method
                  BLASTX
NCBI GI
                  g1708073
BLAST score
                  242
E value
                  1.0e-20
Match length
                  103
% identity
                  51
NCBI Description
                  GMP SYNTHASE (GLUTAMINE-HYDROLYSING) (GLUTAMINE
                  AMIDOTRANSFERASE) (GMP SYNTHETASE) >gi 1077145 pir S55099
                  GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) - yeast
                  (Saccharomyces cerevisiae) >gi 854469 emb CAA89932
                  (Z49809) Gualp [Saccharomyces cerevisiae]
Seq. No.
                  301935
Seq. ID
                  cyk700050189.f1
Method
                  BLASTX
NCBI GI
                  g2129587
BLAST score
                  187
E value
                  3.0e-14
Match length
                  83
% identity
NCBI Description
                  gamma-glutamyltransferase (EC 2.3.2.2) - Arabidopsis
                  thaliana >gi_928934 emb CAA89206 (Z49240) gamma-glutamyl
```

transpeptidase [Arabidopsis thaliana]

>gi 1585436 prf 2124427C gamma-Glu transpeptidase

[Arabidopsis thaliana]

Seq. No. 301936

Seq. ID cyk700050204.f1

```
Method BLASTX
NCBI GI g542157
BLAST score 177
E value 2.0e-13
Match length 52
% identity 67
NCBI Description ribesom
```

NCBI Description ribosomal 5S RNA-binding protein - Rice

 Seq. No.
 301937

 Seq. ID
 cyk700050222.f1

 Method
 BLASTX

 NCBI GI
 g2702268

 BLAST score
 161

 E value
 2.0e-11

E value 2.0 Match length 49 % identity 61

NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]

 Seq. No.
 301938

 Seq. ID
 cyk700050241.f1

 Method
 BLASTX

 NCBI GI
 g4558552

 BLAST score
 280

 E value
 3.0e-25

 Match length
 65

Match length 65 % identity 41 NCRI Description (A)

NCBI Description (AC007138) putative P-glycoprotein-like protein

[Arabidopsis thaliana]

Seq. No. 301939

Seq. ID cyk700050275.f1

Method BLASTN
NCBI GI g2668743
BLAST score 41
E value 8.0e-14
Match length 73
% identity 89

NCBI Description Zea mays ubiquitin conjugating enzyme (UBC) mRNA, complete

cds

Seq. No. 301940

Seq. ID cyk700050285.f1

Method BLASTX
NCBI GI g2281085
BLAST score 215
E value 2.0e-17
Match length 61
% identity 64

NCBI Description (AC002333) CTR1 protein kinase isolog [Arabidopsis

thaliana]

Seq. No. 301941

Seq. ID cyk700050290.f1

Method BLASTX
NCBI GI g673433
BLAST score 288
E value 4.0e-26

against a second

```
Match length
                   82
 % identity
                   68
                   (X56953) protein synthesis initiation factor 4A [Mus
NCBI Description
                   musculus]
 Seq. No.
                   301942
 Seq. ID
                   cyk700050349.fl
Method
                   BLASTN
NCBI GI
                   g4206307
BLAST score
                   57
                   1.0e-23
E value
                   154
Match length
 % identity
                   86
                   Zea mays retrotransposon Cinful-2
NCBI Description
                   301943
 Seq. No.
 Seq. ID
                   cyk700050391.f1
Method
                   BLASTN
NCBI GI
                   g499013
BLAST score
                   82
                   1.0e-38
E value
                   114
Match length
                   93
 % identity
                   T.aestivum (Capitole) mitochondrial orf240 gene
 NCBI Description
                   301944
 Seq. No.
 Seq. ID
                   cyk700050395.f1
                   BLASTX
Method
                   g1335862
 NCBI GI
 BLAST score
                   154
 E value
                   1.0e-10
Match length
                   51
 % identity
 NCBI Description (U42608) clathrin heavy chain [Glycine max]
                   301945
 Seq. No.
 Seq. ID
                   cyk700050474.f1
 Method
                   BLASTX
 NCBI GI
                   g3482915
 BLAST score
                   315
 E value
                    2.0e-29
 Match length
                   77
 % identity
                    71
 NCBI Description
                    (AC003970) Similar to 12-oxophytodienoate reductase,
                   gi 2765083 and old-yellow-enzyme homolog, gi 2232254
                    [Arabidopsis thaliana]
 Seq. No.
                    301946
                    cyk700050518.f1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g266578
 BLAST score
                   244
                    2.0e-22
 E value
 Match length
                   55
 % identity
                   METALLOTHIONEIN-LIKE PROTEIN 1 >qi 100898 pir S17560
 NCBI Description
                   metallothionein-like protein - maize >gi_\bar{2}367\bar{30}\text{bbs}_57629
```



(S57628) metallothionein homologue [Zea mays, Peptide, 76 aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186) metallothionein- like protein [Zea mays]

>gi_228095_prf__1717215A metallothionein-like protein [Zea mays]

Seq. No. 301947

Seq. ID cyk700050539.f1

Method BLASTX
NCBI GI g3128218
BLAST score 302
E value 1.0e-27
Match length 64
% identity 91

NCBI Description (AC004077) putative end13 protein [Arabidopsis thaliana]

Seq. No. 301948

Seq. ID cyk700050604.f1

Method BLASTX
NCBI GI g629688
BLAST score 353
E value 1.0e-33
Match length 100
% identity 68

NCBI Description dehydroquinase shikimate dehydrogenase - Common tobacco

>gi 535771 (L32794) dehydroquinate dehydratase/shikimate

dehydrogenase [Nicotiana tabacum]

Seq. No. 301949

Seq. ID cyk700050630.f1

Method BLASTX
NCBI GI g4467359
BLAST score 361
E value 9.0e-35
Match length 87
% identity 76

NCBI Description (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis

thaliana]

Seq. No. 301950

Seq. ID cyk700050635.f1

Method BLASTX
NCBI GI g66009
BLAST score 216
E value 3.0e-26
Match length 73
% identity 88

NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,

cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH

(AA 1-337) [Zea mays]

Seq. No. 301951

Seq. ID cyk700050649.f1

Method BLASTX
NCBI GI g4539676
BLAST score 217
E value 9.0e-18



101 Match length % identity 53

(AF061282) patatin-like protein [Sorghum bicolor] NCBI Description

301952 Seq. No.

Seq. ID cyk700050660.fl

BLASTX Method NCBI GI g586324 397 BLAST score E value 7.0e-39 Match length 101 67 % identity

TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT NCBI Description

> (TAFII-90) >gi_419854_pir__S34023 TATA box-binding protein-associated factor chain TAFII90 - yeast (Saccharomyces cerevisiae) >gi_311674_emb CAA79685

(Z21487) unknown [Saccharomyces cerevisiae] >gi_536569_emb_CAA85160_ (Z36067) ORF YBR198c

[Saccharomyces cerevisiae] >gi_1091232_prf__2020425A TATA box-binding protein-associated factor [Saccharomyces

cerevisiae]

Seq. No. 301953

Seq. ID cyk700050733.f1

Method BLASTX NCBI GI g2226329 BLAST score 274 E value 2.0e-24 Match length 71 % identity 72

(AF001634) physical impedance induced protein [Zea mays] NCBI Description

301954 Seq. No.

Seq. ID cyk700050743.f1

Method BLASTX g3868853 NCBI GI BLAST score 186 5.0e-14 E value Match length 47 68 % identity

NCBI Description (AB013853) GPI-anchored protein [Vigna radiata]

Seq. No. 301955

Seq. ID cyk700050750.f1

Method BLASTN NCBI GI g1185553 BLAST score 188 1.0e-101 E value 287 Match length % identity 99

Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2) NCBI Description

gene, complete cds

301956 Seq. No.

Seq. ID cyk700050754.f1

Method BLASTX NCBI GI q1667389 4



BLAST score 403 E value 1.0e-39 Match length 94 % identity 87

NCBI Description (Y09238) 3-hydroxy-3-methylglutaryl coenzyme A reductase

[Zea mays]

Seq. No. 301957

Seq. ID cyk700050762.f1

Method BLASTX
NCBI GI g1277236
BLAST score 228
E value 3.0e-19
Match length 56
% identity 75

NCBI Description (U52430) Sec13p [Pichia pastoris]

Seq. No. 301958

Seq. ID cyk700050787.f1

Method BLASTX NCBI GI g3885968 BLAST score 307 E value 2.0e-28

Match length 72 % identity 83

NCBI Description (AF100985) phosphopyruvate hydratase [Penaeus monodon]

Seq. No. 301959

Seq. ID cyk700050801.f1

Method BLASTX
NCBI GI g2129552
BLAST score 256
E value 2.0e-22
Match length 76

% identity 64

NCBI Description calcium-dependent protein kinase 19 - Arabidopsis thaliana

(fragment)

Seq. No. 301960

Seq. ID cyk700050833.f1

Method BLASTX
NCBI GI g417578
BLAST score 287
E value 4.0e-26
Match length 57
% identity 91

NCBI Description RAS-RELATED PROTEIN RAC1 >gi 345368 pir A45324 ras-related

GTP-binding protein - Caenorhabditis elegans

>gi_6829_emb_CAA48506_ (X68492) small ras-related protein
[Caenorhabditis elegans] >gi_156424 (L03711) rac1 protein
[Caenorhabditis elegans] >gi_156426 (L04287) rac1 protein

[Caenorhabditis elegans]

Seq. No. 301961

Seq. ID cyk700050885.f1

Method BLASTN NCBI GI g4115614



BLAST score E value 8.0e-26 Match length 250 86 % identity

NCBI Description Zea mays mRNA for root cap-specific glycine-rich protein,

complete cds

Seq. No. 301962

Seq. ID cyk700050896.f1

Method BLASTN NCBI GI g3294466 BLAST score 106 E value 8.0e-53 Match length 210 89 % identity

NCBI Description Zea mays phosphoglucomutase 1 mRNA, complete cds

Seq. No. 301963

Seq. ID cyk700050923.f1

Method BLASTX NCBI GI g1706956 BLAST score 442 E value 3.0e-44Match length 90

% identity 91

NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]

Seq. No. 301964

Seq. ID cyk700050989.f1

Method BLASTX NCBI GI g1723440 BLAST score 189 E value 4.0e-19 Match length 89 % identity 54

HYPOTHETICAL 35.9 KD PROTEIN C56F8.08 IN CHROMOSOME I NCBI Description

>gi 1204230 emb CAA93579 (Z69728) unknown

[Schizosaccharomyces pombe]

Seq. No. 301965

Seq. ID cyk700051004.f1

Method BLASTX g1255728 NCBI GI BLAST score 249 E value 1.0e-21 Match length 94 49 % identity

(U33265) complement fixation antigen [Coccidioides immitis] NCBI Description

>gi 1256769 (U51271) complement-fixation antigen

[Coccidioides immitis]

Seq. No. 301966

Seq. ID cyk700051023.f1

Method BLASTX NCBI GI g1170092 BLAST score 327 E value 9.0e-31



Match length % identity 88 GLUTATHIONE S-TRANSFERASE IV (GST-IV) (GST-27) (CLASS PHI) NCBI Description >gi 1076807 pir S52037 glutathione transferase (EC 2.5.1.18) 27K chain - maize >gi_529015 (U12679) glutathione S-transferase IV [Zea mays] >gi_695789_emb_CAA56047_ (X79515) glutathione transferase [Zea mays] >gi_1094866_prf__2106424A glutathione S-transferase: ISOTYPE=IV [Zea mays] Seq. No. 301967 Seq. ID cyk700051056.f1 Method BLASTX NCBI GI q3695403 BLAST score 188 E value 2.0e-14 Match length 51 % identity 82 NCBI Description (AF096373) contains similarity to the pfkB family of carbohydrate kinases (Pfam: PF00294, E=1.6e-75) [Arabidopsis thaliana] >gi_4538955_emb_CAB39779.1 (AL049488) fructokinase-like protein [Arabidopsis thaliana] Seq. No. 301968 Seq. ID cyk700051060.f1 Method BLASTX NCBI GI q4006920 BLAST score 223 E value 2.0e-18 Match length 62 % identity NCBI Description (Z99708) actin interacting protein [Arabidopsis thaliana] 301969 Seq. No. Seq. ID cyk700051071.f1 Method BLASTX NCBI GI g4204259 BLAST score 167 E value 6.0e-12 Match length 90 % identity 39 (AC005223) 18074 [Arabidopsis thaliana] NCBI Description Seq. No. 301970 Seq. ID cyk700051096.f1 Method BLASTX

NCBI GI g1621465 BLAST score 354 E value 8.0e-34 Match length 70 % identity 87

NCBI Description (U73105) laccase [Liriodendron tulipifera]

301971 Seq. No.

Seq. ID cyk700051130.f1

Method BLASTX NCBI GI g1172836

```
BLAST score
                  1.0e-27
E value
Match length
                  65
                  86
% identity
NCBI Description
                  GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)
                  small ras-related protein [Nicotiana tabacum]
Seq. No.
                  301972
Seq. ID
                  cyk700051155.fl
Method
                  BLASTX
NCBI GI
                  q4588012
BLAST score
                  235
E value
                  2.0e-20
Match length
                  101
% identity
                   46
NCBI Description
                   (AF085717) putative callose synthase catalytic subunit
                   [Gossypium hirsutum]
Seq. No.
                  301973
Seq. ID
                  cyk700051203.f1
Method
                  BLASTX
NCBI GI
                  q3292826
BLAST score
                   377
E value
                  2.0e-36
Match length
                  95
                  72
% identity
NCBI Description
                  (AL031018) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  301974
                  cyk700051224.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1346485
BLAST score
                   253
                  5.0e-22
E value
Match length
                  55
                  89
% identity
                  MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT
NCBI Description
                  MALIC ENZYME) (NADP-ME) >qi 20469 emb CAA39690 (X56233)
                  malic enzyme [Populus balsamifera subsp. trichocarpa]
Seq. No.
                  301975
Seq. ID
                  cyk700051225.f1
Method
                  BLASTX
                  g2252830
NCBI GI
BLAST score
                  383
E value
                  3.0e-37
Match length
                  101
% identity
                  81
NCBI Description
                   (AF013293) weak similarity to receptor protein kinase
                   [Arabidopsis thaliana]
```

Seq. No. 301976 Seq. ID cyk700051236.f1

Method BLASTX
NCBI GI g2344899
BLAST score 194
E value 3.0e-18



```
Match length
% identity
                   52
NCBI Description
                   (AC002388) unknown protein [Arabidopsis thaliana]
                   301977
Seq. No.
Seq. ID
                   cyk700051237.f1
Method
                   BLASTX
                 . g4406766
NCBI GI
BLAST score
                   226
E value
                   5.0e-19
Match length
                   82
                   49
% identity
NCBI Description
                   (AC006836) putative flavonol sulfotransferase [Arabidopsis
                   thaliana]
Seq. No.
                   301978
Seq. ID
                   cyk700051250.f1
Method
                   BLASTX
NCBI GI
                   q3258570
BLAST score
                   159
E value
                   4.0e-11
Match length
                   38
% identity
                   68
NCBI Description
                   (U89959) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   301979
Seq. ID
                   cyk700051256.f1
Method
                   BLASTN
NCBI GI
                   q22312
BLAST score
                   179
E value
                   3.0e-96
Match length
                   206
% identity
                   98
NCBI Description
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
                   abscisic acid)
Seq. No.
                   301980
Seq. ID
                   cyk700051271.f1
Method
                   BLASTX
NCBI GI
                   q3293031
BLAST score
                   377
E value
                   1.0e-36
Match length
                   89
% identity
                   72
                  (AJ007574) amino acid carrier [Ricinus communis]
NCBI Description
Seq. No.
                   301981
Seq. ID
                   cyk700051295.f1
Method
                  BLASTX
NCBI GI
                   q1888357
```

BLAST score 219 E value 4.0e-18 Match length 68 % identity 59

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154 emb_CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

BLAST score

Match length

% identity

E value

227

61

66

5.0e-19

```
Seq. No.
                  301982
Seq. ID
                  cyk700051321.f1
Method
                  BLASTX
NCBI GI
                  g3445397
BLAST score
                  179
E value
                  1.0e-13
Match length
                  67
% identity
                  42
NCBI Description
                  (AJ010166) S-domain receptor-like protein kinase [Zea mays]
                  301983
Seq. No.
Seq. ID
                  cyk700051334.f1
Method
                  BLASTX
NCBI GI
                  g122772
BLAST score
                  149
E value
                  6.0e-10
Match length
                  44
% identity
                  59
NCBI Description
                  TRANSCRIPTION FACTOR HBP-1B >gi 100809 pir S15347
                  transcription factor HBP-1b - wheat >gi_21635_emb_CAA40102_
                  (X56782) HBP-1b [Triticum aestivum]
Seq. No.
                  301984
Seq. ID
                  cyk700051341.f1
Method
                  BLASTX
NCBI GI
                  q2501024
BLAST score
                  196
E value
                  2.0e-15
Match length
                  42
% identity
                  81
NCBI Description
                  PROBABLE LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE)
                  (LYSRS) >gi_1086773 (U41105) coded for by C. elegans cDNA
                  yk124d11.3; coded for by C. elegans cDNA yk48a4.3; coded
                  for by C. elegans cDNA yk124d11.5; coded for by C. elegans
                  cDNA cm7h5; coded for by C. elegans cDNA cm7a10; similar
                  to class II aminoacyl-tRNA sy
Seq. No.
                  301985
Seq. ID
                  cyk700051379.f1
Method
                  BLASTX
NCBI GI
                  g3859548
BLAST score
                  225
E value
                  1.0e-18
Match length
                  49
% identity
                  84
NCBI Description
                  (AF097182) protein phosphatase 2A catalytic subunit [Oryza
                  sativa]
Seq. No.
                  301986
Seq. ID
                  cyk700051414.f1
Method
                  BLASTX
NCBI GI
                  g3335359
```



```
NCBI Description
                  (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                  301987
Seq. ID
                  cyk700051439.f1
Method
                  BLASTX
                  g3451075
NCBI GI
BLAST score
                  208
E value
                  7.0e-17
Match length
                  85
% identity
                  40
NCBI Description
                  (AL031326) putative protein [Arabidopsis thaliana]
                  301988
Seq. No.
Seq. ID
                  cyk700051460.f1
Method
                  BLASTX
                  g4587987
NCBI GI
BLAST score
                  239
                  1.0e-20
E value
Match length
                  78
% identity
                  56
NCBI Description
                  (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  301989
Seq. ID
                  cyk700051516.f1
Method
                  BLASTX
                  g461532
NCBI GI
BLAST score
                  346
                  4.0e-35
E value
Match length
                  80
% identity
                  89
                  ADP-RIBOSYLATION FACTOR >gi 1362500 pir D49993
NCBI Description
                  ADP-ribosylation factor - Ajellomyces capsulata >qi 407693
                  (L25117) ADP-ribosylation factor [Histoplasma capsulatum]
Seq. No.
                  301990
Seq. ID
                  cyk700051517.f1
Method
                  BLASTX
NCBI GI
                  q4371280
BLAST score
                  383
E value
                  3.0e-37
Match length
                  101
% identity
                  76
NCBI Description
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
```

301991 Seq. No.

cyk700051610.f1 Seq. ID

Method BLASTX NCBI GI g2582381 BLAST score 318 E value 1.0e-29 Match length 87_ % identity 72

NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana

tabacum]

Seq. No. 301992



```
Seq. ID
                  cyk700051640.f1
Method
                  BLASTN
                  g169818
NCBI GI
BLAST score
                  98
                  5.0e-48
E value
Match length
                  138
% identity
                  93
NCBI Description Rice 25S ribosomal RNA gene
                  301993
Seq. No.
                  cyk700051658.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730461
BLAST score
                  216
E value
                  1.0e-17
Match length
                  56
% identity
                  68
NCBI Description
                  40S RIBOSOMAL PROTEIN YS29A >gi 626904 pir S48503
                  ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces
                  cerevisiae) >gi 287628 dbj BAA03507 (D14676) ribosomal
                  protein YS29 [Saccharomyces cerevisiae] >gi_625108 (U19729)
                  Ylr388wp [Saccharomyces cerevisiae]
                  301994
Seq. No.
Seq. ID
                  cyk700051718.f1
Method
                  BLASTX
NCBI GI
                  q3876501
BLAST score
                  178
E value
                  3.0e-13
Match length
                  75
% identity
                  39
NCBI Description
                  (Z92784) F31C3.5 [Caenorhabditis elegans]
                  301995
Seq. No.
Seq. ID
                  cyk700051732.f1
Method
                  BLASTX
NCBI GI
                  g3334140
BLAST score
                  315
E value
                  7.0e-30
Match length
                  92
% identity
                  74
                  CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5
NCBI Description
                  (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5)
                  >gi 2737888 (U59148) nucleolar protein AnCbf5p [Emericella
                  nidulans]
Seq. No.
                  301996
Seq. ID
                  cyk700051764.f1
Method
                  BLASTX
NCBI GI
                  g1237250
BLAST score
                  141
```

3.0e-09 E value Match length 36 % identity 64

NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum]

Seq. No. 301997



```
cyk700051768.f1
Seq. ID
Method
                   BLASTX
                   g4101564
NCBI GI
                   179
BLAST score
                   2.0e-13
E value
Match length
                   77
                   52
% identity
NCBI Description
                  (AF004556) IFA-binding protein [Arabidopsis thaliana]
                   301998
Seq. No.
                   cyk700051804.fl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3236261
BLAST score
                   192
E value
                   7.0e-15
Match length
                   63
% identity
                   60
NCBI Description
                   (AC004684) putative zinc finger protein [Arabidopsis
                   thaliana]
                   301999
Seq. No.
Seq. ID
                   cyk700051808.f1
Method
                  BLASTN
NCBI GI
                   g3386564
BLAST score
                   35
E value
                   2.0e-10
Match length
                   35
                   100
% identity
NCBI Description
                  Sorghum bicolor 1-aminocyclopropane-1-carboxylate oxidase
                   (ACO1) mRNA, complete cds
Seq. No.
                   302000
Seq. ID
                   cyk700051834.f1
Method
                  BLASTX
NCBI GI
                   g3559805
BLAST score
                   295
E value
                   5.0e-27
Match length
                   69
% identity
                   70
NCBI Description
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
                   thaliana]
Seq. No.
                   302001
Seq. ID
                   cyk700051842.f1
Method
                  BLASTX
NCBI GI
                  g1402902
BLAST score
                  206
E value
                  1.0e-16
Match length
                  85
                   46
% identity
NCBI Description
                   (X98323) peroxidase [Arabidopsis thaliana]
                  >gi_1419386 emb CAA67428 (X98928) peroxidase ATP10a
```

[Arabidopsis thaliana]

Seq. No.

302002 BLASTX

Seq. ID cyk700051849.f1

Method

Match length

173



```
g2980793
NCBI GI
BLAST score
                  280
E value
                  3.0e-25
                                                                          ~ the -
Match length
                  97
                  57
% identity
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  302003
                  cyk700051863.f1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3746898
BLAST score
                  38
E value
                  4.0e-12
Match length
                  62
% identity
                  90
NCBI Description
                  Neurospora crassa clock-controlled gene-6 protein (ccg-6)
                  gene, complete cds
                  302004
Seq. No.
Seq. ID
                  cyk700051872.f1
Method
                  BLASTX
NCBI GI
                  g3451071
BLAST score
                  383
E value
                  3.0e-37
Match length
                  96
% identity
                  78
                  (AL031326) beta adaptin - like protein [Arabidopsis
NCBI Description
                  thaliana]
                  302005
Seq. No.
Seq. ID
                  cyk700051885.f1
Method
                  BLASTX
                  g3420801
NCBI GI
BLAST score
                  324
E value
                  2.0e-30
Match length
                  90
                  66
% identity
NCBI Description
                  (AF081066) IAA-amino acid hydrolase homolog ILL3
                   [Arabidopsis thaliana]
                  302006
Seq. No.
Seq. ID
                  cyk700051887.f1
Method
                  BLASTX
NCBI GI
                  g2979544
BLAST score
                  181
E value
                  6.0e-24
Match length
                  82
% identity
                  68
NCBI Description
                  (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]
Seq. No.
                  302007
Seq. ID
                  cyk700051888.f1
Method
                  BLASTN
                  g473602
NCBI GI
BLAST score
                  77
E value
                  2.0e-35
```



% identity

NCBI Description Zea mays W-22 histone H2A mRNA, complete cds

Seq. No.

302008

Seq. ID

cyk700051902.f1

Method NCBI GI BLAST score BLASTX g3355480

E value

2.0e-10

154

Match length 88 % identity 35

NCBI Description

(AC004218) Medicago nodulin N21-like protein [Arabidopsis

thaliana]

Seq. No.

302009

Seq. ID

cyk700051916.f1

Method NCBI GI BLAST score BLASTX q730464 196

E value Match length % identity

3.0e-15 55 69

NCBI Description

40S RIBOSOMAL PROTEIN RS16 HOMOLOG (RP61R HOMOLOG)

>gi_2119075_pir__S67619 ribosomal protein S16.e.B - yeast

(Saccharomyces cerevisiae) >gi 606441 emb CAA87357 (Z47071) putative ribosomal protein [Saccharomyces]

cerevisiae] >gi_1431106_emb_CAA98649 (Z74131) ORF YDL083c

[Saccharomyces cerevisiae]

Seq. No.

302010 Seq. ID

cyk700051948.f1

Method NCBI GI BLASTN g1617324

BLAST score

37 6.0e-12

E value Match length

69

% identity

88

NCBI Description

H.vulgare mRNA for myb4 transcription factor

Seq. No.

302011

Seq. ID

cyk700051969.f1

Method NCBI GI BLASTX g119136 485

BLAST score E value

3.0e-49

Match length % identity

99

NCBI Description

92 ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_84946_pir__S01193 translation elongation factor eEF-1 alpha chain (gene F2) - fruit fly (Drosophila melanogaster) >gi_7917_emb_CAA29994 (X06870) EF-1-alpha [Drosophila

melanogaster]

Seq. No.

302012

Seq. ID

cyk700051980.f1

Method NCBI GI BLASTX g4510361



```
BLAST score
                   245
E value
                   3.0e-21
Match length
                   77
% identity
                   65
NCBI Description
                  (AC007017) putative DNA-binding protein RAV2 [Arabidopsis
                   thaliana]
Seq. No.
                   302013
Seq. ID
                   cyk700052047.f1
Method
                   BLASTX
NCBI GI
                   g4388728
BLAST score
                   153
E value
                   3.0e-10
Match length
                   59
% identity
                   58
NCBI Description
                  (AC006413) putative grrl-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   302014
Seq. ID
                   cyk700052061.f1
Method
                  BLASTX
NCBI GI
                   g1617398
BLAST score
                  163
E value
                  2.0e-11
Match length
                  84
% identity
                  40
NCBI Description
                  (X96737) synaptobrevin-like protein [Mus musculus]
                  302015
Seq. No.
Seq. ID
                  cyk700052119.f1
Method
                  BLASTN
NCBI GI
                  g726477
BLAST score
                  46
E value
                  7.0e-17
Match length
                  74
% identity
                  91
NCBI Description
                  Avena fatua nondormancy-associated clone AFN3 putative ORF1
                  mRNA, partial cds
Seq. No.
                  302016
Seq. ID
                  cyk700052143.f1
Method
                  BLASTX
NCBI GI
                  g2129754
BLAST score
                  161
E value
                  3.0e-11
Match length
                  33
% identity
                  91
NCBI Description
                  translation elongation factor Tu precursor - Arabidopsis
                  thaliana >gi_1149571_emb_CAA61511_ (X89227) mitochondrial
                  elongation factor Tu [Arabidopsis thaliana]
```

200

Seq. No. 302017

Seq. ID cyk700052148.f1

Method BLASTX
NCBI GI g4454012
BLAST score 156
E value 1.0e-10



Match length 46 % identity 57

NCBI Description (AL035396) Pollen-specific protein precursor like

[Arabidopsis thaliana]

Seq. No. 302018

Seq. ID cyk700052158.f1

Method BLASTX
NCBI GI g1002796
BLAST score 228
E value 5.0e-19
Match length 49
% identity 82

NCBI Description (U33915) Cpm10 [Craterostigma plantagineum]

Seq. No.

Seq. ID cyk700052174.f1

302019

Method BLASTX
NCBI GI g543752
BLAST score 153
E value 2.0e-16
Match length 72
% identity 68

NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)

(ETHYLENE-FORMING ENZYME) (EFE) >gi_281612_pir__JQ1656 ethylene-forming enzyme - Pseudomonas syringae pv. phaseolicola plasmid pPSP1 >gi_216878 dbj_BAA02477

(D13182) 'Ethylene-forming enzyme' [Pseudomonas syringae] >gi_4323597_gb_AAD16440_ (AF101058) ethylene-forming enzyme

[Pseudomonas syringae pv. phaseolicola]

Seq. No. 302020

Seq. ID cyk700052213.f1

Method BLASTX
NCBI GI g1346735
BLAST score 273
E value 3.0e-24
Match length 73
% identity 67

NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE

(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) > gi_1076562_pir__S49647 phosphoglycerate mutase (EC 5.4.2.1) - castor bean > gi_474170_emb_CAA49995 (X70652)

phosphoglycerate mutase [Ricinus communis]

Seq. No. 302021

Seq. ID cyk700052230.f1

Method BLASTX
NCBI GI g399334
BLAST score 199
E value 5.0e-16
Match length 51
% identity 84

NCBI Description CYSTATIN I PRECURSOR (CORN KERNEL CYSTEINE PROTEINASE

INHIBITOR) >gi_322868_pir__ \$27239 cysteine proteinase
inhibitor - maize >gi_217962_dbj_BAA01472_ (D10622) corn

cystatin I [Zea mays]



```
Seq. No.
                   302022
Seq. ID
                   cyk700052253.f1
Method
                   BLASTX
NCBI GI
                   q2245039
BLAST score
                   146
E value
                   2.0e-09
Match length
                   59
% identity
                   42
NCBI Description
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   302023
Seq. ID
                   cyk700052335.f1
Method
                  BLASTX
NCBI GI
                  q4104939
BLAST score
                   206
E value
                  2.0e-16
Match length
                  98
% identity
                   41
NCBI Description
                  (AF042382) vetispiradiene synthase [Solanum tuberosum]
Seq. No.
                  302024
Seq. ID
                  cyk700052342.f1
Method
                  BLASTX
NCBI GI
                  g2809250
BLAST score
                  336
                  9.0e-32
E value
Match length
                  92
% identity
                  67
NCBI Description
                  (AC002560) F21B7.19 [Arabidopsis thaliana]
Seq. No.
                  302025
Seq. ID
                  cyk700052364.f1
Method
                  BLASTX
NCBI GI
                  g4558828
BLAST score
                  173
E value
                  1.0e-12
                                                                              18
Match length
                  76
% identity
                  45
NCBI Description
                  (AF076692) aureobasidin-resistance protein; Aur1 homolog;
                  Aur1 [Aspergillus fumigatus]
Seq. No.
                  302026
Seq. ID
                  cyk700052387.f1
Method
                  BLASTN
                  g6598431
                  36
                  7.0e-11
                  68
```

NCBI GI BLAST score E value Match length

% identity 88 Arabidopsis thaliana chromosome II BAC F7F1 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 302027

Seq. ID cyk700052459.f1

Method BLASTX NCBI GI g4321762

BLAST score

E value

197

2.0e-21



```
BLAST score
                   258
E value
                   5.0e-24
Match length
                   68
 % identity
                   85
NCBI Description
                  (AF061107) transcription factor MYC7E [Zea mays]
Seq. No.
                   302028
Seq. ID
                   cyk700052470.f1
Method
                   BLASTX
NCBI GI
                   g1546692
BLAST score
                   149
E value
                   3.0e-14
Match length
                   77
% identity
                   57
NCBI Description
                  (X98805) peroxidase ATP19a [Arabidopsis thaliana]
Seq. No.
                   302029
Seq. ID
                   cyk700052476.f1
Method
                   BLASTX
NCBI GI
                   g2493935
BLAST score
                   249
E value
                   2.0e-21
Match length
                   92
% identity
                   47
NCBI Description
                   CYTOCHROME B >gi_542522_pir__S40619 ubiquinol--cytochrome-c
                   reductase (EC 1.10.2.2) cytochrome b - migratory locust
                   mitochondrion (SGC4) >gi_1182025_emb_CAA56537_ (X80245)
                   Cytochrome B [Locusta migratoria]
Seq. No.
                   302030
Seq. ID
                   cyk700052483.f1
Method
                   BLASTX
NCBI GI
                   g2943792
BLAST score
                   330
E value
                   5.0e-31
Match length
                   98
% identity
                   56
NCBI Description
                  (AB006809) PV72 [Cucurbita sp.]
Seq. No.
                   302031
Seq. ID
                   cyk700052490.f1
Method
                   BLASTX
NCBI GI
                  g100347
BLAST score
                  170
E value
                   3.0e-12
Match length
                  47
% identity
                  70
NCBI Description
                  monosaccharide transport protein MST1 - common tobacco
                  >gi_19885_emb_CAA47324_ (X66856) monosaccharid transporter
                   [Nicotiana tabacum]
Seq. No.
                  302032
Seq. ID
                  dhd700197930.h1
Method
                  BLASTX
NCBI GI
                  g2505874
```



```
Match length
                   68
% identity
                   75
NCBI Description
                  (Y12776) putative kinase [Arabidopsis thaliana]
Seq. No.
                   302033
Seq. ID
                   dhd700197969.h1
Method
                   BLASTX
NCBI GI
                   q633110
BLAST score
                   162
E value
                   1.0e-11
Match length
                   38
% identity
                   87
NCBI Description
                  (D31843) plasma membrane H+-ATPase [Oryza sativa]
Seq. No.
                   302034
Seq. ID
                   dhd700197995.h1
Method
                   BLASTX
NCBI GI
                   q3135543
BLAST score
                   233
E value
                   6.0e-20
Match length
                   49
% identity
                   90
NCBI Description
                  (AF062393) aquaporin [Oryza sativa]
Seq. No.
                   302035
Seq. ID
                   dhd700198003.h1
Method
                   BLASTX
NCBI GI
                   g2492519
BLAST score
                  263
E value
                   1.0e-25
Match length
                   63
% identity
                  95
NCBI Description
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
                  7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase
                  subunit [Spinacia oleracea]
Seq. No.
                  302036
Seq. ID
                  dhd700198020.h1
Method
                  BLASTN
NCBI GI
                  g1498052
BLAST score
                  156
E value
                  1.0e-82
Match length
                  189
% identity
                  95
NCBI Description Zea mays ribosomal protein S8 mRNA, complete cds
Seq. No.
                  302037
Seq. ID
                  dhd700198040.h1
                  BLASTX
Method
NCBI GI
                  g1491931
                  245
```

BLAST score E value 2.0e-21 Match length 57

302038

% identity 88

NCBI Description (U52078) kinesin-like protein [Nicotiana tabacum]

Seq. No.

Seq. No.

302043



```
Seq. ID
                    dhd700198046.h1
  Method
                    BLASTN
  NCBI GI
                    g3885891
  BLAST score
                    42
  E value
                    1.0e-14
  Match length
                    54
  % identity
                    94
  NCBI Description
                    Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                    mRNA, complete cds
  Seq. No.
                    302039
  Seq. ID
                    dyk700102007.h1
  Method
                    BLASTX
  NCBI GI
                    g4514635
  BLAST score
                    191
  E value
                    1.0e-14
  Match length
                    47
  % identity
                    74
  NCBI Description
                   (AB021175) root cap protein 1 [Zea mays]
  Seq. No.
                    302040
  Seq. ID
                    dyk700102021.h1
  Method
                    BLASTX
  NCBI GI
                    g3913517
 BLAST score
                    225
 E value
                    1.0e-18
 Match length
                    51
  % identity
                    86
 NCBI Description
                    3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE
                    (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE)
                    (DPNPASE) >gi_1109672 (U33283) 3'(2'),5-diphosphonucleoside
                    3'(2') phosphohydrolase [Oryza sativa]
                    >gi_1586671_prf__2204308A diphosphonucleoside
                    phosphohydrolase [Oryza sativa]
 Seq. No.
                    302041
 Seq. ID
                    dyk700102055.h1
 Method
                    BLASTX
 NCBI GI
                    g2150000
 BLAST score
                    322
                    5.0e-30
 E value
 Match length
                    89
 % identity
                    62
 NCBI Description
                   (AF000939) aleurone ribonuclease [Hordeum vulgare]
 Seq. No.
                    302042
 Seq. ID
                    dyk700102086.h1
 Method
                    BLASTX
                    g4530126
 NCBI GI
 BLAST score
                    264
E value
                    3.0e-23
 Match length
                    96
 % identity
                    50
                    (AF078082) receptor-like protein kinase homolog RK20-1
 NCBI Description
                    [Phaseolus vulgaris]
```

% identity

90

NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

```
Seq. ID
                   dyk700102137.h1
Method
                   BLASTX
NCBI GI
                   g549063
BLAST score
                   158
E value
                   8.0e-11
Match length
                   35
% identity
                   83
NCBI Description
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                   >gi_1072464_pir A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
Seq. No.
                   302044
Seq. ID
                   dyk700102167.h1
Method
                   BLASTN
NCBI GI
                   q2668741
BLAST score
                   136
E value
                   1.0e-70
Match length
                   148
% identity
                   98
NCBI Description
                   Zea mays glycine-rich RNA binding protein (GRP) mRNA,
                   complete cds
Seq. No.
                   302045
Seq. ID
                   dyk700102170.h1
Method
                   BLASTX
NCBI GI
                   g1091678
BLAST score
                   193
E value
                   8.0e-15
Match length
                   80
% identity
                   42
NCBI Description
                   activator-like transposable element [Pennisetum glaucum]
Seq. No.
                   302046
Seq. ID
                   dyk700102178.h1
Method
                   BLASTX
NCBI GI
                   g112994
BLAST score
                   319
E value
                   1.0e-29
Match length
                   71
% identity
                   87
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                   >gi 82685 pir S04536 embryonic abundant protein,
                   glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  302047
Seq. ID
                  dyk700102188.h1
Method
                  BLASTX
NCBI GI
                  g4218535
BLAST score
                  233
E value
                  1.0e-19
Match length
                  49
```



```
Seq. No.
                   302048
Seq. ID
                   dyk700102210.h1
Method
                   BLASTX
NCBI GI
                   q729775
BLAST score
                   359
E value
                   2.0e-34
Match length
                   73
% identity
                   86
NCBI Description
                   HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION
                   FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR)
                   >gi 100264 pir S25481 heat shock transcription factor 8 -
                   Peruvian tomato >gi_19492_emb_CAA47869_ (X67600) heat shock
                   transcription factor 8 [Lycopersicon peruvianum]
Seq. No.
                   302049
Seq. ID
                   dyk700102227.h1
Method
                   BLASTX
NCBI GI
                   q3309066
BLAST score
                   406
E value
                   5.0e-40
Match length
                  78
% identity
                   94
NCBI Description
                   (AF073488) bifunctional dihydrofolate reductase-thymidylate
                   synthase [Zea mays]
Seq. No.
                  302050
Seq. ID
                  dyk700102231.h1
Method
                  BLASTX
NCBI GI
                  g3953479
BLAST score
                  414
E value
                  7.0e-41
Match length
                  98
% identity
                  81
NCBI Description
                  (AC002328) F2202.24 [Arabidopsis thaliana]
Seq. No.
                  302051
Seq. ID
                  dyk700102233.h1
Method
                  BLASTX
NCBI GI
                  g2995321
BLAST score
                  325
E value
                  1.0e-30
Match length
                  93
% identity
                  72
NCBI Description
                  (Z68759) amino acid carrier [Ricinus communis]
Seq. No.
                  302052
Seq. ID
                  dyk700102243.h1
Method
                  BLASTN
                  g433039
```

NCBI GI BLAST score 34 E value 1.0e-09 Match length 34 % identity 100

NCBI Description Zea mays W-22 clone PREM-1 retroelement PREM-1, partial

sequence

γĵ.



```
Seq. No.
                   302053
Seq. ID
                   dyk700102313.h1
Method
                   BLASTX
NCBI GI
                   g112697
BLAST score
                   204
E value
                   3.0e-16
Match length
                   48
% identity
                   79
NCBI Description
                  14 KD PROLINE-RICH PROTEIN DC2.15 PRECURSOR
                   >gi_486809_pir__S35714 proline-rich protein, 14K, embryonic
                   - carrot >gi_18316_emb_CAA33476_ (X15436) 14 kD protein (AA
                   1-137) [Daucus carota]
Seq. No.
                   302054
Seq. ID
                   dyk700102330.h1
Method
                   BLASTN
NCBI GI
                   g4115614
BLAST score
                   192
E value
                   1.0e-104
Match length
                   304
% identity
                   91
                  Zea mays mRNA for root cap-specific glycine-rich protein,
NCBI Description
                   complete cds
Seq. No.
                  302055
Seq. ID
                  dyk700102332.h1
Method
                  BLASTX
NCBI GI
                  q1402910
BLAST score
                  210
E value
                  6.0e-17
Match length
                  61
% identity
                  59
NCBI Description
                   (X98316) peroxidase [Arabidopsis thaliana]
                  >gi_1429223_emb_CAA67550_ (X99096) peroxidase [Arabidopsis
                  thaliana]
Seq. No.
                  302056
Seq. ID
                  dyk700102348.h1
Method
                  BLASTX
NCBI GI
                  g4371279
BLAST score
                  329
E value
                  6.0e-31
Match length
                  102
% identity
                  61
NCBI Description
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  302057
Seq. ID
                  dyk700102404.h1
Method
                  BLASTX
```

NCBI GI g3334661 BLAST score 222 E value 2.0e-18

Match length 96 % identity 46

NCBI Description (Y10490) putative cytochrome P450 [Glycine max]

Seq. No. 302058

NCBI Description

```
Seq. ID
                      dyk700102406.h1
   Method
                      BLASTX
   NCBI GI
                      q1353193
   BLAST score
                      315
   E value
                      3.0e-29
   Match length
                      91
   % identity
                      62
                      O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268
NCBI Description
                      O-methyltransferase (EC 2.1.1.-) - maize >gi 404070
                      (L14063) O-methyltransferase [Zea mays]
   Seq. No.
                      302059
   Seq. ID
                      dyk700102415.h1
   Method
                      BLASTX
   NCBI GI
                      q2832661
   BLAST score
                      383
                      4.0e-37
   E value
   Match length
                      106
   % identity
                      (AL021710) pherophorin - like protein [Arabidopsis
   NCBI Description
                      thaliana]
   Seq. No.
                      302060
   Seq. ID
                      dyk700102428.h1
  Method
                      BLASTX
  NCBI GI
                      g4539301
  BLAST score
                      343
  E value
                      2.0e-32
  Match length
                      99
   % identity
                      61
  NCBI Description
                      (AL049480) putative mitochondrial protein [Arabidopsis
                     thaliana]
  Seq. No.
                      302061
  Seq. ID
                     dyk700102481.h1
  Method
                     BLASTX
  NCBI GI
                     g2914700
  BLAST score
                     251
  E value
                     1.0e-21
  Match length
                     68
  % identity
                     79
  NCBI Description
                     (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
                     thaliana]
  Seq. No.
                     302062
  Seq. ID
                     dyk700102511.hl
  Method
                     BLASTX
  NCBI GI
                     g1170937
  BLAST score
                     357
  E value
                     3.0e-34
  Match length
                     75
  % identity
                     91
```

synthetase [Oryza sativa]

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine



Seq. No. 302063 Seq. ID dyk700102549.h1 Method BLASTN NCBI GI g393183

BLAST score 96
E value 5.0e-47
Match length 100
% identity 99

NCBI Description Zea mays alcohol dehydrogenase (tasselseed 2) mRNA,

complete cds

Seq. No. 302064

Seq. ID dyk700102582.h1

Method BLASTN
NCBI GI g3821780
BLAST score 38
E value 3.0e-12
Match length 38
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 302065

Seq. ID dyk700102621.h1

Method BLASTX
NCBI GI g3510249
BLAST score 312
E value 7.0e-29
Match length 73
% identity 68

NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 302066

Seq. ID dyk700102668.h1

Method BLASTX
NCBI GI g2673914
BLAST score 224
E value 2.0e-18
Match length 105
% identity 43

NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302067

Seq. ID dyk700102670.h1

Method BLASTN
NCBI GI g2668739
BLAST score 175
E value 8.0e-94
Match length 233
% identity 94

NCBI Description Zea mays translation initiation factor GOS2 (TIF) mRNA,

complete cds

Seq. No.

302068

Seq. ID dyk700102703.h1

Method BLASTN NCBI GI g6598558

BLAST score 36



E value 7.0e-11 Match length 68 % identity 88 NCBI Description Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 302069 Seq. ID dyk700102725.h1 Method BLASTX NCBI GI g3482921 BLAST score 219 E value 5.0e-18 Match length 80 % identity 55 NCBI Description (AC003970) Unknown protein [Arabidopsis thaliana] Seq. No. 302070 Seq. ID dyk700102734.h1 Method BLASTX NCBI GI g4530126 BLAST score 223 E value 1.0e-18 Match length 75 % identity 60 NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris] Seq. No. 302071 Seq. ID dyk700102740.h1 Method BLASTX NCBI GI g3355465 BLAST score 350 E value 2.0e-33 Match length 95 % identity NCBI Description (AC004218) putative Ser/Thr protein kinase [Arabidopsis thaliana] Seq. No. 302072 Seq. ID dyk700102743.h1 Method BLASTX NCBI GI g1754997 BLAST score 325 E value 2.0e-30 Match length 80 % identity 85 NCBI Description (U48690) calmodulin TaCaM2-1 [Triticum aestivum] 302073 Seq. No. Seq. ID dyk700102751.h1 Method BLASTN NCBI GI g2224845

NCBI GI g2224849
BLAST score 38
E value 5.0e-12
Match length 50

% identity 94

NCBI Description Zea mays mRNA for anionic peroxidase

Method

BLASTX

```
Seq. No.
                   302074
 Seq. ID
                   dyk700102753.h1
Method
                   BLASTX
NCBI GI
                   g2129733
                   231
BLAST score
E value
                   5.0e-21
Match length
                   75
% identity
                   72
NCBI Description
                   serine O-acetyltransferase (EC 2.3.1.30) SAT1 precursor -
                   Arabidopsis thaliana >gi_1184048 (U22964) serine
                   acetyltransferase [Arabidopsis thaliana]
Seq. No.
                   302075
Seq. ID
                   dyk700102796.h1
Method
                   BLASTX
NCBI GI
                   g2809246
BLAST score
                   222
E value
                   2.0e-18
Match length
                   68
% identity
                   60
NCBI Description
                   (AC002560) F2401.15 [Arabidopsis thaliana]
Seq. No.
                   302076
Seq. ID
                   dyk700102802.h1
Method
                   BLASTX
NCBI GI
                   g2160167
BLAST score
                   267
E value
                   2.0e-37
Match length
                   102
% identity
                   81
NCBI Description
                   (AC000132) Identical to A. thaliana Myb-like protein
                   (gb_D58424). [Arabidopsis thaliana]
Seq. No.
                   302077
Seq. ID
                   dyk700102820.h1
Method
                   BLASTX
NCBI GI
                   g1181331
BLAST score
                   223
E value
                  2.0e-18
Match length
                  74
% identity
                  59
NCBI Description (X77569) calnexin [Zea mays]
Seq. No.
                  302078
Seq. ID
                  dyk700102828.h1
Method
                  BLASTX
NCBI GI
                  g4220514
BLAST score
                  391
E value
                  3.0e-38
Match length
                  92
% identity
                  79
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  302079
Seq. ID
                  dyk700102876.h1
```

```
NCBI GI
                   g4510376
BLAST score
                   233
E value
                   1.0e-19
Match length
                   81
% identity
                   56
```

(AC007017) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 302080 Seq. ID dyk700102915.h1 Method BLASTX g417828 NCBI GI

BLAST score 205 E value 2.0e-16 Match length 69 % identity

PROTEIN TRANSLATION FACTOR SUI1 >gi_320775_pir__\$31245 NCBI Description

translation initiation factor eIF-2A - yeast (Saccharomyces cerevisiae) >gi 172787 (M77514) SUI1 protein [Saccharomyces cerevisiae] >gi_1255973_emb_CAA65499_ (X96722) ORF N0905

[Saccharomyces cerevisiae] >gi 1302282 emb CAA96150

(Z71520) ORF YNL244c [Saccharomyces cerevisiae]

Seq. No. 302081

Seq. ID dyk700102919.hl

Method BLASTN NCBI GI g557681 BLAST score 59 E value 1.0e-24 Match length 63 % identity 98

NCBI Description Z.mays mRNA for ribosomal protein S28

Seq. No. 302082

Seq. ID dyk700102931.h1

Method BLASTX NCBI GI g3043415 BLAST score 365 E value 4.0e-35 Match length 70 % identity 99

NCBI Description (Y17053) At-hsc70-3 [Arabidopsis thaliana]

302083 Seq. No.

Seq. ID dyk700102947.h1

Method BLASTX NCBI GI g4376203 BLAST score 251 E value 9.0e-22 Match length 79 % identity 59

NCBI Description (U35226) putative cytochrome P-450 [Nicotiana

plumbaginifolia]

Seq. No. 302084

Seq. ID dyk700103083.h1

Method BLASTX NCBI GI g3024500

```
BLAST score
                   310
E value
                   1.0e-28
Match length
                   68
% identity
                   90
NCBI Description
                   RAS-RELATED PROTEIN RAB11A >gi_1370142_emb_CAA98177
                   (Z73949) RAB11A [Lotus japonicus]
Seq. No.
                   302085
Seq. ID
                   dyk700103093.h1
Method
                   BLASTX
NCBI GI
                   g4584345
BLAST score
                   380
E value
                   8.0e-37
Match length
                   102
% identity
                   70
NCBI Description
                   (AC007127) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   302086
Seq. ID
                   dyk700103094.h1
Method
                  BLASTX
NCBI GI
                   q4467097
BLAST score
                   368
E value
                   2.0e-35
Match length
                  82
% identity
                  89
NCBI Description
                   (AL035538) heat shock protein 70 like protein [Arabidopsis
                  thaliana]
Seq. No.
                  302087
Seq. ID
                  dyk700103104.h1
Method
                  BLASTX
NCBI GI
                  q3695019
BLAST score
                  303
E value
                  8.0e-28
Match length
                  89
% identity
                  62
NCBI Description
                  (AF055848) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                  302088
Seq. ID
                  dyk700103145.h1
Method
                  BLASTX
NCBI GI
                  g122007
BLAST score
                  160
E value
                  4.0e-11
Match length
                  34
% identity
                  94
NCBI Description
                  HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
                  >gi_20448_emb_CAA37828 (X53831) H2A histone protein (AA 1
                  - 149) [Petroselinum crispum]
```

Seq. No. 302089

Seq. ID dyk700103188.h1 Method BLASTX

NCBI GI g3954807
BLAST score 312
E value 7.0e-29

```
Match length
                   90
% identity
                   60
NCBI Description
                   (AJ011862) flavonoid 3',5'-hydroxylase [Catharanthus
                   roseus]
                   302090
Seq. No.
Seq. ID
                   dyk700103236.h1
Method
                   BLASTX
NCBI GI
                   q2246442
BLAST score
                   224
E value
                   1.0e-18
Match length
                   93
% identity
                   44
NCBI Description
                  (U63298) farnesyltransferase alpha subunit [Pisum sativum]
Seq. No.
                   302091
Seq. ID
                   dyk700103257.h1
Method
                   BLASTX
NCBI GI
                   q3355308
BLAST score
                   236
E value
                   5.0e-20
Match length
                   91
% identity
NCBI Description
                  (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]
Seq. No.
                  302092
Seq. ID
                  dyk700103272.h1
Method
                  BLASTX
NCBI GI
                  g2459445
BLAST score
                  145
E value
                  3.0e-09
Match length
                  60
% identity
                  53
NCBI Description
                  (AC002332) putative ribonucleoprotein [Arabidopsis
                  thaliana]
Seq. No.
                  302093
Seq. ID
                  dyk700103316.h1
Method
                  BLASTX
NCBI GI
                  g2213594
BLAST score
                  211
                  5.0e-17
E value
Match length
                  53
% identity
                  70
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.
                  302094
```

Seq. ID dyk700103336.h1

Method BLASTX NCBI GI g2384675 BLAST score 236 E value 2.0e-20 Match length 82 % identity 72

NCBI Description (AF012659) putative potassium transporter AtKT4p

[Arabidopsis thaliana]

```
302095
Seq. No.
Seq. ID
                   dyk700103353.h1
Method
                   BLASTN
NCBI GI
                   q498743
BLAST score
                   55
E value
                   3.0e-22
Match length
                   245
% identity
                   46
NCBI Description
                  O.sativa (var. IR36) PIR7a and PIR7b genes
Seq. No.
                   302096
Seq. ID
                   dyk700103368.h1
Method
                   BLASTX
NCBI GI
                   g4581164
BLAST score
                   183
E value
                   1.0e-16
Match length
                   87
% identity
                   55
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   302097
Seq. ID
                   dyk700103394.h1
Method
                   BLASTX
NCBI GI
                   g2851508
BLAST score
                   245
E value
                   4.0e-21
Match length
                   64
% identity
                   69
                   60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to
NCBI Description
                   ribosomal protein L21 (gb_L38826). ESTs
                   gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis
                   thaliana] >gi_3482935 (AC003970) Putative ribosomal protein
                  L21 [Arabidopsis thaliana]
Seq. No.
                   302098
Seq. ID
                  dyk700103406.h1
Method
                  BLASTX
NCBI GI
                   g2244994
BLAST score
                  246
E value
                  2.0e-21
Match length
                  63
% identity
                  76
NCBI Description
                   (Z97341) similarity to isp4 protein - fission yeast
                   [Arabidopsis thaliana]
Seq. No.
                  302099
Seq. ID
                  dyk700103414.h1
Method
                  BLASTX
NCBI GI
                  g100907
BLAST score
                  146
E value
                  2.0e-09
Match length
                  34
% identity
                  74
NCBI Description
                  pathogenesis-related protein 1 - maize
```

[Zea mays]

>gi_228409_prf__1803521A pathogenesis-related protein 1



```
Seq. No.
                   302100
Seq. ID
                   dyk700103442.h1
Method
                   BLASTX
NCBI GI
                   g2058311
BLAST score
                   144
E value
                   3.0e-09
Match length
                   42
% identity
                   62
NCBI Description
                  (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]
Seq. No.
                   302101
Seq. ID
                   dyk700103478.h1
Method
                   BLASTX
NCBI GI
                   q3152559
BLAST score
                   256
E value
                   2.0e-22
Match length
                   54
% identity
                   80
NCBI Description
                   (AC002986) Similarity to A. thaliana gene product
                   F21M12.20, gb AC000132. EST gb_Z25651 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   302102
                                                  Ž.
Seq. ID
                   dyk700103532.h1
Method
                   BLASTX
NCBI GI
                   g2286153
BLAST score
                   193
E value
                   3.0e-17
Match length
                   56
% identity
                   93
NCBI Description
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.
                   302103
Seq. ID
                   dyk700103575.h1
Method
                   BLASTX
NCBI GI
                   g2501572
BLAST score
                   189
E value
                   1.0e-14
Match length
                   79
% identity
                   41
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545
NCBI Description
                   (L47118) EMB8 gene product [Picea glauca]
Seq. No.
                   302104
Seq. ID
                   dyk700103584.h1
Method
                   BLASTX
NCBI GI
                   g1170937
BLAST score
                   222
E value
                   2.0e-18
Match length
                   70
                   99
```

% identity NCBI Description

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 302105



dyk700103589.h1 Seq. ID Method BLASTX NCBI GI g1778145 BLAST score 299 E value 2.0e-27 Match length 82 % identity 72 NCBI Description (U66402) phosphate/phosphoenolpyruvate translocator precursor [Nicotiana tabacum] Seq. No. 302106 Seq. ID dyk700103632.h1 Method BLASTX NCBI GI q1172836 BLAST score 378 E value 1.0e-36 Match length 71 % identity 97 GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787) NCBI Description small ras-related protein [Nicotiana tabacum] Seq. No. 302107 Seq. ID dyk700103715.h1 Method BLASTN NCBI GI g3420038 BLAST score 35 E value 3.0e-10 Match length 51 92 % identity NCBI Description Zea mays gypsy/Ty3-type retrotransposon Tekay, complete sequence Seq. No. 302108 Seq. ID dyk700103723.h1 Method BLASTX NCBI GI g2827711 BLAST score 490 E value 9.0e-50 Match length 100 % identity 91 (AL021684) oxoglutarate dehydrogenase - like protein NCBI Description [Arabidopsis thaliana] Seq. No. 302109 Seq. ID dyk700103724.h1 Method BLASTX NCBI GI g2244749 BLAST score 155 E value 9.0e-11 Match length 78 % identity 48 NCBI Description

(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 302110

Seq. ID dyk700103735.h1

Method BLASTX NCBI GI q2827143



BLAST score E value 1.0e-21 Match length 74 % identity 62

NCBI Description (AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 302111

Seq. ID dyk700103772.h1

Method BLASTX NCBI GI q1657382 BLAST score 390 4.0e-38 E value Match length 87 % identity

NCBI Description (Y09101) cholinephosphate cytidylyltransferase [Pisum

sativum]

Seq. No.

302112

Seq. ID dyk700103776.h1

Method BLASTX NCBI GI g1362406 BLAST score 208 E value 8.0e-17 Match length 85 % identity 54

NCBI Description

probable membrane protein YPR011c - yeast (Saccharomyces cerevisiae) >gi_887588_emb_CAA90155_ (Z49919) unknown [Saccharomyces cerevisiae] >gi_939745 (U31900) Lpz11p [Saccharomyces cerevisiae] >gi_1314086_emb_CAA95008_

(Z71255) unknown [Saccharomyces cerevisiae]

Seq. No. 302113

Seq. ID dyk700103815.h1

Method BLASTX NCBI GI q3643611 BLAST score 199 E value 1.0e-15 Match length 58 % identity

NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No. 302114

Seq. ID dyk700103851.h1

Method BLASTX NCBI GI q4508073 BLAST score 173 E value 1.0e-12 Match length 101 % identity 39

NCBI Description (AC005882) 43220 [Arabidopsis thaliana]

Seq. No.

302115

Seq. ID dyk700103861.h1

Method BLASTX NCBI GI g3876615 BLAST score 229



E value 3.0e-19
Match length 93
% identity 49

NCBI Description (Z74031) Similarity to Yeast D-lactate dehydrogenase

(SW:DLD1_YEAST); cDNA EST EMBL:C12235 comes from this gene;

cDNA EST EMBL:C12916 comes from this gene; cDNA EST EMBL:C10532 comes from this gene; cDNA EST EMBL:C10979

comes f

Seq. No.

302116

Seq. ID

dyk700103877.h1

Method BLASTX
NCBI GI g1706260
BLAST score 362
E value 8.0e-35
Match length 90

% identity
NCBI Description

NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir___S59597

cysteine proteinase 1 precursor - maize

>gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea

mays]

79

Seq. No.

302117

Seq. ID dyk700103896.h1

Method BLASTX
NCBI GI g1330254
BLAST score 388
E value 7.0e-38
Match length 75
% identity 99

NCBI Description (D85039) calcium-dependent protein kinase [Zea mays]

Seq. No.

302118

Seq. ID dyk700103906.h1

Method BLASTN
NCBI GI g22430
BLAST score 71
E value 8.0e-32
Match length 134
% identity 89

NCBI Description Maize pseudo-Gpa2 pseudogene for glyceraldehyde-3-phosphate

dehydrogenase subunit A

Seq. No.

302119

Seq. ID

dyk700103908.h1

Method BLASTN
NCBI GI 94160401
BLAST score 157
E value 4.0e-83
Match length 172
% identity 98

NCBI Description Zea mays eIF-5 gene, exons 1-2

Seq. No.

302120

Seq. ID

dyk700103946.hl

Method NCBI GI

BLASTX

GI g4008008



```
BLAST score
                    149
E value
                    7.0e-10
Match length
                    57
% identity
                    51
NCBI Description
                    (AF084035) receptor-like protein kinase [Arabidopsis
                   thalianal
Seq. No.
                    302121
Seq. ID
                   dyk700103956.h1
Method
                   BLASTX
NCBI GI
                   q399854
BLAST score
                   161
                    4.0e-11
E value
Match length
                    57
% identity
                    63
NCBI Description
                   HISTONE H2B.2 >gi_283042 pir S28049 histone H2B - maize
                   >gi 22325_emb CAA\overline{4}0565 (X57\overline{3}\overline{1}3) H2B histone [Zea mays]
Seq. No.
                   302122
Seq. ID
                   dyk700103983.h1
Method
                   BLASTX
NCBI GI
                   q3882355
BLAST score
                   143
E value
                   5.0e-18
Match length
                   60
% identity
NCBI Description
                   (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis
                   thaliana]
Seq. No.
                   302123
Seq. ID
                   dyk700103988.h1
Method
                   BLASTX
NCBI GI
                   g4371296
BLAST score
                   389
E value
                   7.0e-38
Match length
                   100
% identity
                   75
NCBI Description
                   (AC006260) putative receptor protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   302124
Seq. ID
                   dyk700103989.h1
Method
                   BLASTX
NCBI GI
                   g1279206
BLAST score
                   310
E value
                   1.0e-28
Match length
                   64
% identity
                   98
NCBI Description
                   (X97446) alpha-tubulin [Avena sativa]
Seq. No.
                   302125
Seq. ID
                   dyk700103991.h1
Method
```

Method BLASTX
NCBI GI g2160156
BLAST score 364
E value 5.0e-35
Match length 104



```
% identity
NCBI Description
                   (AC000132) Strong similarity to S. pombe leucyl-tRNA
                   synthetase (gb_Z73100). [Arabidopsis thaliana]
Seq. No.
                   302126
Seq. ID
                   dyk700104013.h1
Method
                   BLASTX
NCBI GI
                   q4508073
BLAST score
                   201
E value
                   6.0e-16
Match length
                   97
% identity
NCBI Description
                  (AC005882) 43220 [Arabidopsis thaliana]
Seq. No.
                   302127
Seq. ID
                   dyk700104071.h1
Method
                   BLASTX
NCBI GI
                   g1172836
BLAST score
                   432
E value
                   6.0e-43
Match length
                  81
% identity
                   98
                  GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)
NCBI Description
                  small ras-related protein [Nicotiana tabacum]
Seq. No.
                  302128
Seq. ID
                  dyk700104115.h1
Method
                  BLASTX
NCBI GI
                  g4204697
BLAST score
                  238
E value
                  5.0e-21
Match length
                  93
% identity
NCBI Description
                  (AF117063) putative inositol polyphosphate 5-phosphatase
                  At5P2 [Arabidopsis thaliana]
Seq. No.
                  302129
Seq. ID
                  dyk700104327.h1
Method
                  BLASTX
NCBI GI
                  g1705585
BLAST score
                  359
E value
                  2.0e-34
Match length
                  82
% identity
                  85
                  PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE)
NCBI Description
                  >gi_82710_pir__JH0667 phosphoenolpyruvate carboxylase (EC
                  4.1.1.31) C3-form - maize >gi_429149_emb_CAA43709 (X61489)
                  phosphoenolpyruvate carboxylase [Zea mays]
Seq. No.
                  302130
Seq. ID
                  dyk700104345.h1
```

Method BLASTX NCBI GI g2738996 BLAST score 198 2.0e-17 E value Match length 86 % identity 52



NCBI Description (AF022457) CYP97B2p [Glycine max]

Seq. No. 302131

Seq. ID dyk700104350.hl

Method BLASTX NCBI GI g1706260 BLAST score 253 E value 4.0e-41 Match length 100 98 % identity

NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir \$59597

cysteine proteinase 1 precursor - maize

>gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea

mays]

Seq. No. 302132

Seq. ID dyk700104373.h1

Method BLASTX NCBI GI g122106 BLAST score 203 E value 9.0e-28 Match length 69 % identity 85

NCBI Description

HISTONE H4 >gi_70771_pir_ HSZM4 histone H4 - maize >gi_81642_pir_ S06904 histone H4 - Arabidopsis thaliana

>gi 2119028 pir S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_168742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]

 $>gi_168501$ (M13370) histone H4 [Zea mays] $>gi_168503$

(M13377) histone H4 [Zea mays] >gi 498898 (U10042) histone H4 homolog [Pisum sativum] >gi 1806285 emb CAB01914

(Z79638) histone H4 homologue [Sesbania rostrata]

>gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi 225838 prf 1314298A histone H4

[Arabidopsis thaliana]

Seq. No. 302133

Seq. ID dyk700104442.h1

Method BLASTX NCBI GI g2459446 BLAST score 234 E value 8.0e-20 Match length 89 % identity

NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis

thaliana]

Seq. No. 302134

Seq. ID dyk700104452.h1

Method BLASTX NCBI GI g2894598 BLAST score 220 E value 4.0e-18 Match length 99



% identity 42
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 302135

Seq. ID dyk700104502.h1 Method BLASTN

Method BLASTN
NCBI GI g397395
BLAST score 193
E value 1.0e-104
Match length 193
% identity 100

NCBI Description Z.mays MNB1b mRNA for DNA-binding protein

Seq. No. 302136

Seq. ID dyk700104509.h1

Method BLASTX
NCBI GI g3386600
BLAST score 453
E value 2.0e-45
Match length 102
% identity 83

NCBI Description (AC004665) putative glycoprotein [Arabidopsis thaliana]

Seq. No. 302137

Seq. ID dyk700104522.h1

Method BLASTN
NCBI GI G2226328
BLAST score 49
E value 1.0e-18
Match length 61

Match length 61 % identity 95

NCBI Description Zea mays physical impedance induced protein (IIG1) mRNA,

complete cds

Seq. No. 302138

Seq. ID dyk700104649.h1

Method BLASTX
NCBI GI g2924777
BLAST score 217
E value 2.0e-24
Match length 104
% identity 10

NCBI Description (AC002334) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 302139

Seq. ID dyk700104657.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 302140

Seq. ID dyk700104663.h1

Method BLASTX
NCBI GI g584706
BLAST score 354
E value 3.0e-37
Match length 86

NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)

>gi_2130066_pir__JC5124 aspartate transaminase (EC
2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_
(D14673) aspartate aminotransferase [Oryza sativa]

Seq. No.

% identity

Seq. ID dyk700104711.h1

80

302141

Method BLASTX
NCBI GI g3618220
BLAST score 298
E value 3.0e-27
Match length 68
% identity 81

NCBI Description (AL031579) chorismate synthase [Schizosaccharomyces pombe]

Seq. No. 302142

Seq. ID dyk700104721.h1

Method BLASTN
NCBI GI g312178
BLAST score 60
E value 4.0e-25
Match length 92
% identity 91

NCBI Description Z.mays GapC2 gene

Seq. No. 302143

Seq. ID dyk700104764.h1

Method BLASTN
NCBI GI g786131
BLAST score 78
E value 7.0e-36
Match length 137
% identity 90

NCBI Description Oryza sativa root-specific RCc3 mRNA, complete cds

Seq. No. 302144

Seq. ID dyk700104785.h1

Method BLASTX
NCBI GI g2578033
BLAST score 204
E value 3.0e-16
Match length 77
% identity 51

NCBI Description (X97016) omega-6 desaturase [Gossypium hirsutum]

Seq. No. 302145

Seq. ID dyk700104812.h1

Method BLASTX
NCBI GI g1076289
BLAST score 247
E value 6.0e-24



Match length % identity

NCBI Description amino acid permease AAP5 - Arabidopsis thaliana

>gi_608673_emb_CAA54632_ (X77501) amino acid permease

[Arabidopsis thaliana]

Seq. No.

302146

Seq. ID Method

dyk700104829.h1 BLASTX

NCBI GI BLAST score E value

201 7.0e-16 102

q4490306

Match length % identity

48

NCBI Description

(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.

302147

302148

Seq. ID Method

dyk700104836.h1

BLASTX NCBI GI q4063750 BLAST score 175 E value 1.0e-12 Match length 46

% identity 63

NCBI Description

(AC005851) putative indole-3-acetate

beta-glucosyltransferase synthetase [Arabidopsis thaliana]

Seq. No.

Seq. ID

dyk700104903.h1

Method BLASTX q2570505 NCBI GI BLAST score 430 E value 1.0e-42 Match length 95 92

% identity

NCBI Description

(AF022735) proteasome component [Oryza sativa]

Seq. No.

302149

Seq. ID

dyk700104937.h1

Method BLASTX NCBI GI q4468813 BLAST score 145 E value 2.0e-09 Match length 51 % identity 53

NCBI Description

(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.

302150

Seq. ID

dyk700104942.h1

Method BLASTN NCBI GI g1063665 BLAST score 189 E value 1.0e-102 Match length 239

% identity 95

NCBI Description Zea mays unknown protein mRNA, complete cds



```
Seq. No.
                  302151
Seq. ID
                  dyk700104960.h1
Method
                  BLASTN
NCBI GI
                  g2331140
BLAST score
                  33
E value
                  5.0e-09
Match length
                  45
% identity
                  93
NCBI Description
                  Oryza sativa water-stress inducible protein (WSI) mRNA,
                  complete cds
Seq. No.
                  302152
Seq. ID
                  dyk700104967.h1
Method
                  BLASTX
NCBI GI
                  g4559358
BLAST score
                  199
E value
                  1.0e-15
Match length
                  50
% identity
NCBI Description
                  (AC006585) putative steroid binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  302153
Seq. ID
                  dyk700104982.h1
Method
                  BLASTX
NCBI GI
                  g4263777
BLAST score
                  469
E value
                  3.0e-47
Match length
                  113
% identity
                  73
                  (AC006068) putative serine carboxypeptidase II [Arabidopsis
NCBI Description
                  thaliana] >gi 4510391_gb_AAD21479.1_ (AC007017) putative
                  serine carboxypeptidase II [Arabidopsis thaliana]
Seq. No.
                  302154
Seq. ID
                  dyk700105046.h1
Method
                  BLASTX
NCBI GI
                  g4558591
BLAST score
                  230
E value
                  3.0e-19
Match length
                  70
% identity
NCBI Description
                  (AC006555) putative beta-1,3-glucanase [Arabidopsis
                  thalianal
Seq. No.
                  302155
Seq. ID
                  dyk700105060.h1
                  BLASTX
```

Method

NCBI GI g2062169 BLAST score 188 E value 2.0e-22 Match length 75

% identity

NCBI Description (ACO01645) ABC transporter (PDR5-like) isolog [Arabidopsis

thaliana]

Seq. No.



Seq. ID dyk700105068.h1 Method BLASTX NCBI GI g2388571 BLAST score 219 E value 5.0e-18 Match length 87 % identity 54 (AC000098) Strong similarity to Arabidopsis peroxidase NCBI Description ATPEROX7A (gb X98321). [Arabidopsis thaliana] >gi 2738254 (U97684) peroxidase precursor [Arabidopsis thaliana]

Seq. No. 302157

Seq. ID dyk700105088.h1
Method BLASTX
NCBI GI g2827548
BLAST score 183
E value 9.0e-14
Match length 101
% identity 40

NCBI Description (AL021635) cytochrome P450 - like protein [Arabidopsis

thaliana]

Seq. No. 302158

Seq. ID dyk700105089.h1

Method BLASTX
NCBI GI g3810596
BLAST score 234
E value 9.0e-20
Match length 63
% identity 68

NCBI Description (AC005398) reverse-transcriptase-like protein [Arabidopsis

thaliana]

Seq. No. 302159

Seq. ID dyk700105135.h1

Method BLASTX
NCBI GI g2464915
BLAST score 266
E value 1.0e-23
Match length 87
% identity 68

NCBI Description (299708) transcription initiation factor like protein

[Arabidopsis thaliana]

Seq. No. 302160

Seq. ID dyk700105142.h1

Method BLASTX
NCBI GI 94519671
BLAST score 178
E value 3.0e-13
Match length 63
% identity 56

NCBI Description (AB017693) transfactor [Nicotiana tabacum]

Seq. No. 302161

Seq. ID dyk700105144.h1

Method BLASTX



```
NCBI GI
                    q3297818
 BLAST score
                    196
 E value
                    2.0e-15
 Match length
                    67
 % identity
                    57
                    (AL031032) putative protein [Arabidopsis thaliana]
 NCBI Description
                    302162
 Seq. No.
                    dyk700105172.h1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2618731
 BLAST score
                    344
                    9.0e-33
 E value
 Match length
                    89
 % identity
                    71
 NCBI Description
                    (U49077) IAA21 [Arabidopsis thaliana]
                    302163
 Seq. No.
                    dyk700105185.h1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3757521
 BLAST score
                    200
                    7.0e-16
 E value
 Match length
                    69
 % identity
                    52
 NCBI Description
                    (AC005167) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    302164
 Seq. ID
                    dyk700105243.h1
 Method
                    BLASTX
                    q4454026
 NCBI GI
 BLAST score
                    147
                    1.0e-09
 E value
 Match length
                    42
 % identity
                    64
 NCBI Description
                    (AL035394) phosphatase like protein [Arabidopsis thaliana]
 Seq. No.
                    302165
                    dyk700105250.h1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3434986
 BLAST score
                    296
 E value
                    4.0e-27
 Match length
                    82
 % identity
                    63
 NCBI Description
                    (AB016895) Pop3 [Schizosaccharomyces pombe]
 Seq. No.
                    302166
 Seq. ID
                    dyk700105273.h1
 Method
                    BLASTX
 NCBI GI
                    q2982452
 BLAST score
                    239
 E value
```

2.0e-20 Match length 74

22 % identity

NCBI Description (AL022223) receptor protein kinase-like protein

[Arabidopsis thaliana]

Match length

NCBI Description

% identity

76 71

```
Seq. No.
                  302167
                  dyk700105309.h1
Seq. ID
Method
                  BLASTX
                  q1710511
NCBI GI
BLAST score
                  321
                  6.0e-30
E value
Match length
                  89
                  70
% identity
                  60S RIBOSOMAL PROTEIN L1 (L4) >gi_1165139_emb_CAA57671_
NCBI Description
                  (X82180) ribosomal protein L4 [Rattus norvegicus]
Seq. No.
                  302168
                  dyk700105327.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024018
BLAST score
                  397
E value
                  7.0e-39
Match length
                  75
% identity
                  100
NCBI Description
                  INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
                  >gi 1546919 emb CAA69225 (Y07920) translation initiation
                  factor 5A [Zea mays] >gi 2668738 (AF034943) translation
                  initiation factor 5A [Zea mays]
Seq. No.
                  302169
Seq. ID
                  dyk700105423.h1
Method
                  BLASTX
NCBI GI
                  g2160692
                  203
BLAST score
                  3.0e-16
E value
Match length
                  72
% identity
                  54
                  (U73527) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                  thaliana]
                  302170
Seq. No.
                  dyk700105434.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2052094
BLAST score
                  410
                  2.0e-40
E value
Match length
                  96
% identity
                  80
                 (Z49147) phenylalanine ammonia-lyase [Hordeum vulgare]
NCBI Description
                  302171
Seq. No.
                  dyk700105453.h1
Seq. ID
Method
                  BLASTX
                  g4262148
NCBI GI
BLAST score
                  287
E value
                  5.0e-26
```

42636

[Arabidopsis thaliana]

(AC005275) predicted protein of unknown function



Seq. No. 2 302172 Seq. ID dyk700

dyk700105504.h1

Method BLASTN
NCBI GI g22292
BLAST score 80
E value 3.0e-37
Match length 180
% identity 86

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No.

302173

Seq. ID dyk700105511.h1

Method BLASTX
NCBI GI g2129581
BLAST score 325
E value 2.0e-30
Match length 92
% identity 70

NCBI Description envelope Ca2+-ATPase precursor - Arabidopsis thaliana

>gi_471089_dbj_BAA03091_ (D13984) chloroplast envelope

Ca2+-ATPase precursor [Arabidopsis thaliana]

>gi_4165448_emb_CAA49558_ (X69940) envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 302174

Seq. ID dyk700105526.h1

Method BLASTX
NCBI GI g3776579
BLAST score 239
E value 2.0e-20
Match length 96
% identity 53

NCBI Description (AC005388) Strong similarity to F22013.22 gi 3063460 myosin

homolog from A. thaliana BAC gb AC003981. [Arabidopsis

thaliana]

Seq. No. 302175

Seq. ID dyk700105605.h1

Method BLASTX
NCBI GI g3128172
BLAST score 245
E value 1.0e-31
Match length 100
% identity 65

NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302176

Seq. ID dyk700105612.h1

Method BLASTX
NCBI GI 94371280
BLAST score 197
E value 2.0e-15
Match length 42
% identity 88

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302177

....



```
dyk700105629.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3033390
                   401
BLAST score
                   2.0e-39
E value
Match length
                  98
% identity
                   64
NCBI Description
                   (AC004238) putative vacuolar sorting receptor [Arabidopsis
                  thaliana]
Seq. No.
                  302178
Seq. ID
                  dyk700105630.h1
Method
                  BLASTX
                  g1206013
NCBI GI
BLAST score
                  174
E value
                  1.0e-27
Match length
                  99
                  69
% identity
NCBI Description
                  (U44087) beta-D-glucosidase precursor [Zea mays]
                  302179
Seq. No.
Seq. ID
                  dyk700105690.h1
Method
                  BLASTX
NCBI GI
                  g1707642
BLAST score
                  266
E value
                  2.0e-23
Match length
                  91
% identity
                  55
NCBI Description
                  (Y07748) TMK [Oryza sativa]
Seq. No.
                  302180
                  dyk700105704.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                  145
E value
                  2.0e-15
Match length
                   58
                  79
% identity
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                  302181
Seq. ID
                  dyk700105720.h1
Method
                  BLASTN
NCBI GI
                  q485815
BLAST score
                  33
E value
                  4.0e-09
Match length
                  69
% identity
                  87
NCBI Description
                  Wheat mRNA for WZF1, complete cds
                  302182
Seq. No.
Seq. ID
                  dyk700105732.h1
Method
```

Method BLASTX
NCBI GI g3128228
BLAST score 386
E value 1.0e-37



Match length 82 88 NCBI Description (A

(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

L18A [Arabidopsis thaliana]

Seq. No. 302183

Seq. ID dyk700105737.h1

Method BLASTX
NCBI GI g3341697
BLAST score 326
E value 1.0e-30
Match length 96
% identity 65

NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302184

Seq. ID dyk700105802.h1

Method BLASTX
NCBI GI g4263791
BLAST score 241
E value 1.0e-20
Match length 96
% identity 50

NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 302185

Seq. ID dyk700105819.h1

Method BLASTX
NCBI GI g82696
BLAST score 249
E value 6.0e-22
Match length 60
% identity 82

NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_

(X61121) glycine-rich protein [Zea mays]

Seq. No. 302186

Seq. ID dyk700105829.h1

Method BLASTX
NCBI GI g4455301
BLAST score 162
E value 2.0e-11
Match length 45
% identity 84

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 302187

Seq. ID dyk700105933.h1

Method BLASTX
NCBI GI g3337367
BLAST score 245
E value 4.0e-21
Match length 93
% identity 51

NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
                  302188
Seq. ID
                  dyk700105937.h1
Method
                  BLASTX
NCBI GI
                  g3549626
                  153
BLAST score
                  2.0e-10
E value
                  90
Match length
                  37
% identity
NCBI Description
                  (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
                  302189
Seq. No.
                  dyk700105941.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g66009
BLAST score
                  396
                  8.0e-39
E value
Match length
                  75
% identity
                  100
NCBI Description
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,
                  cytosolic - maize >qi 22238 emb CAA30151 (X07156) GADPH
                  (AA 1-337) [Zea mays]
Seq. No.
                  302190
                  dyk700105965.h1
Seq. ID
Method
                  BLASTX
                  g1370603
NCBI GI
BLAST score
                  358
E value
                  2.0e-36
Match length
                  86
% identity
                  93
NCBI Description
                  (X98245) annexin p35 [Zea mays]
                  302191
Seq. No.
                  dyk700105968.h1
Seq. ID
Method
                  BLASTX
                  g128185
NCBI GI
BLAST score
                  141
                  8.0e-09
E value
Match length
                  44
                  64
% identity
                  NITRATE REDUCTASE (NR) >gi 66208 pir RDBHNH nitrate
NCBI Description
                  reductase (NADH) (EC 1.6.6.1) - barley (cv. Himalaya)
                  >gi 18994 emb CAA40976 (X57845) nitrate reductase [Hordeum
                  vulgare]
                  302192
Seq. No.
Seq. ID
                  dyk700105982.h1
Method
                  BLASTX
NCBI GI
                  g3810596
BLAST score
                  290
E value
                  2.0e-26
Match length
                  90
% identity
                  54
                  (AC005398) reverse-transcriptase-like protein [Arabidopsis
NCBI Description
```

thaliana]



```
Seq. No.
                  302193
                  dyk700105993.h1
Seq. ID
Method
                  BLASTX
                  g1839188
NCBI GI
BLAST score
                  297
                  4.0e-27
E value
Match length
                  82
                  68
% identity
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
NCBI Description
                  302194
Seq. No.
                  dyk700105996.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2924784
BLAST score
                  274
                  2.0e-24
E value
Match length
                  99
% identity
                  51
                  (AC002334) similar to jasmonate inducible protein
NCBI Description
                   [Arabidopsis thaliana]
                  302195
Seq. No.
                  dyk700106034.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g549063
BLAST score
                  142
E value
                  4.0e-09
Match length
                  30
% identity
                  80
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                  >gi 1072464 pir A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi 303835 dbj BAA02151 (D12626)
                  21kd polypeptide [Oryza sativa]
Seq. No.
                  302196
                  dyk700106093.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4335745
BLAST score
                  280
E value
                  4.0e-25
Match length
                  100
% identity
                  47
NCBI Description
                  (AC006284) putative hydrolase (contains an
                  esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
Seq. No.
                  302197
                  dyk700106139.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501555
```

BLAST score 171 E value 2.0e-12 Match length 51 % identity 63

NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >qi 549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]



Seq. No. 302198 dyk700106210.h1 Seq. ID Method BLASTX NCBI GI--g2959767 212 BLAST score 2.0e-20 E value 92 Match length 60 % identity (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 NCBI Description (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana] 302199 Seq. No.

dyk700106266.h1 Seq. ID

Method BLASTN g1550813 NCBI GI BLAST score 161 2.0e-85 E value 216 Match length 94 % identity

Z.mays mRNA for acidic ribosomal protein PO NCBI Description

302200 Seq. No. dyk700106293.h1 Seq. ID Method BLASTN

g4416300 NCBI GI BLAST score 129 2.0e-66 E value Match length 141 % identity 98

Zea mays chromosome 4 22 kDa zein-associated intercluster NCBI Description

region, complete sequence

302201 Seq. No.

dyk700106340.h1 Seq. ID

Method BLASTN NCBI GI · g1848280 BLAST score 44 E value 1.0e-15

Match length 44 % identity 100

Sorghum bicolor membrane intrinsic protein (Mip1) mRNA, NCBI Description

partial cds

302202 Seq. No.

dyk700106349.h1 Seq. ID

Method BLASTX NCBI GI g404690 BLAST score 233 1.0e-19 E value Match length 102 % identity 50

(L19075) cytochrome P450 [Catharanthus roseus] NCBI Description

302203 Seq. No.

Seq. ID dyk700106353.h1

Method BLASTX

NCBI GI

E value

BLAST score



```
- NCBI GI
                    q1523800
 BLAST score
                    150
 E value
                    3.0e-10
 Match length
                    39
                    69
 % identity
                    (Y07694) MAP kinase kinase alpha protein kinase
 NCBI Description
                    [Arabidopsis thaliana]
                    302204
 Seq. No.
 Seq. ID
                    dyk700106429.h1
 Method
                    BLASTX
 NCBI GI
                    g1747310
 BLAST score
                    140
                    5.0e-09
 E value
 Match length
                    25
                    100
 % identity
                    (D58424) Myb-like DNA binding protein [Arabidopsis
 NCBI Description
                    thaliana]
                    302205
 Seq. No.
                    dyk700106434.h1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3056725
 BLAST score
                    185
                    3.0e-14
 E value
 Match length
                    68
                    51
 % identity
                   (AF034774) ent-kaurene synthase [Arabidopsis thaliana]
 NCBI Description
                    302206
 Seq. No.
                    dyk700106468.h1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3292829
 BLAST score
                    145
                    4.0e-14
 E value
 Match length
                    93
  % identity
                    47
 NCBI Description
                    (AL031018) putative protein [Arabidopsis thaliana]
                    302207
  Seq. No.
                    dyk700106518.h1
  Seq. ID
 Method
                    BLASTX
                    g2665890
 NCBI GI
 BLAST score
                    309
                    2.0e-32
 E value
                    97
 Match length
  % identity
                    73
 NCBI Description
                    (AF035944) calcium-dependent protein kinase [Fragaria x
                    ananassa]
                    302208
  Seq. No.
  Seq. ID
                    dyk700106532.h1
                    BLASTN
 Method
```

1.0e-30 Match length 178

g559535



```
% identity 91
NCBI Description Z.mays mRNA for metallothionein
```

 Seq. No.
 302209

 Seq. ID
 dyk700106538.h1

 Method
 BLASTN

 NCBI GI
 g3821780

BLAST score 36
E value 7.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 302210

Seq. ID dyk700106570.h1

Method BLASTN
NCBI GI g433871
BLAST score 38
E value 4.0e-12
Match length 90
% identity 86

NCBI Description C.roseus mRNA for HMG protein

Seq. No. 302211

Seq. ID dyk700106587.h1

Method BLASTX
NCBI GI g4263048
BLAST score 185
E value 5.0e-14
Match length 46
% identity 72

NCBI Description (AC005142) putative hydrolase [Arabidopsis thaliana]

Seq. No. 302212

Seq. ID dyk700106627.h1

Method BLASTN
NCBI GI g2062705
BLAST score 36
E value 6.0e-11
Match length 36
% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 302213

Seq. ID dyk700106660.h1

Method BLASTX
NCBI GI g1352186
BLAST score 251
E value 2.0e-27
Match length 87
% identity 69

NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)

(CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide

synthase [Linum usitatissimum]

Seq. No. 302214

Seq. ID dyk700106670.h1

```
Method
                  g4581164
NCBI GI
BLAST score
                  253
                  7.0e-25
E value
Match length
                  96
                  61
% identity
NCBI Description
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
                  302215
Seq. No.
                  dyk700106681.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2257756
BLAST score
                  340
E value
                  4.0e-32
                  77
Match length
                  82
% identity
                  (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
NCBI Description
                  >gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea
                  mays]
                  302216
Seq. No.
                  dyk700106683.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3193296
BLAST score
                  142
E value
                   6.0e-09
                  51
Match length
                  49
% identity
                  (AF069298) similar to pectinesterase [Arabidopsis thaliana]
NCBI Description
                  302217
Seq. No.
                  dyk700106710.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3892051
BLAST score
                  215
                   5.0e-20
E value
Match length
                   63
                  79
% identity
                   (AC002330) predicted NADH dehydrogenase 24 kD subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   302218
Seq. ID
                  dyk700106731.hl
Method
                  BLASTX
NCBI GI
                  g3255943
BLAST score
                   153
E value
                   3.0e-10
Match length
                   28
% identity
NCBI Description
                  (AJ007333) PP2A1 protein [Catharanthus roseus]
```

Seq. ID dyk700106733.h1

MethodBLASTNNCBI GIg1129083BLAST score93E value6.0e-45

```
Match length
% identity
                   91
                  Wheat mRNA for protein H2A, complete cds, clone wcH2A-2
NCBI Description
                   302220
Seq. No.
Seq. ID
                  dyk700106842.h1
Method
                  BLASTX
NCBI GI
                  g4115388
                   263
BLAST score
                   3.0e-23
E value
Match length
                  82
% identity
                   63
                  (AC005967) putative prolylcarboxypeptidase [Arabidopsis
NCBI Description
                   thaliana]
                   302221
Seq. No.
                   dyk700106850.hl
Seq. ID
Method
                   BLASTX
                   g1161167
NCBI GI
BLAST score
                   181
                   1.0e-13
E value
Match length
                   88
                   34
% identity
                  (L42466) ethylene-forming enzyme [Picea glauca]
NCBI Description
Seq. No.
                   302222
                   dyk700106862.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3860277
BLAST score
                   256
E value
                   2.0e-22
Match length
                   73
                   63
% identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi 4314394 gb AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
                   302223
Seq. No.
Seq. ID
                   dyk700106901.h1
Method
                   BLASTN
                   g577818
NCBI GI
                   98
BLAST score
                   3.0e-48
E value
Match length
                   121
                   98
% identity
                   Z.mays gene for H2B histone (gH2B4)
NCBI Description
Seq. No.
                   302224
Seq. ID
                   dyk700106911.h1
Method
                   BLASTX
                   g347855
NCBI GI
```

Method BLASTX
NCBI GI g347855
BLAST score 156
E value 1.0e-10
Match length 78
% identity 41

NCBI Description (L21753) glucose transporter [Saccharum hybrid cultivar

H65-7052]

NCBI Description



```
302225
Seq. No.
                  dyk700106927.h1
Seq. ID
Method
                  BLASTX
                  g3176687
NCBI GI
                  392
BLAST score
E value
                  3.0e-38
Match length
                  99
                  73
% identity
                   (AC003671) Strong similarity to trehalose-6-phosphate
NCBI Description
                  synthase homolog from A. thaliana chromosome 4 contig
                  gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and
                  gb R64855 come from this gene. [Arabidopsis thaliana]
                  302226
Seq. No.
                  dyk700106945.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3176673
BLAST score
                   229
                   3.0e-19
E value
                   86
Match length
                   51
% identity
                  (AC003671) Similar to serine/threonine kinase gb Y12531
NCBI Description
                   from Brassica oleracea. [Arabidopsis thaliana]
                   302227
Seq. No.
                   dyk700106946.hl
Seq. ID
                   BLASTX
Method
                   q4056615
NCBI GI
BLAST score
                   161
                   3.0e-11
E value
                   60
Match length
                   62
% identity
                   (AF067401) Scl1 protein [Oryza sativa]
NCBI Description
                   302228
Seq. No.
                   dyk700106955.h1
Seq. ID
Method
                   BLASTX
                   q4056506
NCBI GI
BLAST score
                   319
                   1.0e-29
E value
                   100
Match length
% identity
                   61
                   (AC005896) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   302229
Seq. No.
                   fC-zmf1700337353a5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q56539
BLAST score
                   87
                   3.0e-41
E value
Match length
                   301
% identity
                   94
```

: exon v and flanks

R.norvegicus gene encoding prolactin, exon 5

>gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene



```
302230
Seq. No.
Seq. ID
                  fC-zmf1700342888g1
Method
                  BLASTX
NCBI GI
                  g4098521
                  324
BLAST score
                  2.0e-30
E value
Match length
                  76
% identity
                  76
                  (U79160) HMG-CoA synthase [Arabidopsis thaliana]
NCBI Description
                  >gi 4098523 (U79161) HMG-CoA synthase [Arabidopsis
                  thaliana]
Seq. No.
                  302231
                  fC-zmf1700344603q1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q267196
BLAST score
                  621
E value
                  9.0e-65
Match length
                  168
                  74
% identity
                  GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
NCBI Description
                  >gi_66574_pir__YUPOY ADPglucose--starch glucosyltransferase
                   (EC 2.4.1.21) precursor - potato >gi_21471_emb_CAA41359
                   (X58453) glycogen (starch) synthase [Solanum tuberosum]
Seq. No.
                  302232
Seq. ID
                  fC-zmf1700345831q1
Method
                  BLASTX
NCBI GI
                  q2879792
                  172
BLAST score
                   4.0e-12
E value
                  78
Match length
% identity
                   44
                   (AL021813) SPAC23A1.04c, possible glycosyl hydrolase,
NCBI Description
                   len:756aa, similar eg. to C. elegans Q18679, (586aa), fasta
                   scores, opt:566, E():0, (48.0% identity in 452 aa overlap),
                  also similar to YHR204W, YH04 YEAST, P38888, hypothet
Seq. No.
                   302233
Seq. ID
                   fC-zmf1700345831z1
Method
                  BLASTX
NCBI GI
                   g1504008
BLAST score
                   178
E value
                   5.0e-28
Match length
                   166
% identity
                   45
                   (D86967) Containing ATP/GTP-binding site motif A(P-loop):
NCBI Description
                   Similar to C.elegans protein(P1:CEC47E128); Similar to Mouse
                   alpha-mannosidase(P1:B54407) [Homo sapiens]
```

fC-zmf1700348376y2 Seq. ID

BLASTN Method NCBI GI g304040 BLAST score 169 2.0e-90 E value Match length 185



```
% identity
                  Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene
NCBI Description
Seq. No.
                  302235
                  fC-zmf1700349776g1
Seq. ID
                  BLASTX
Method
                  g3021270
NCBI GI
BLAST score
                  424
                  8.0e-42
E value
Match length
                  141
% identity
                  57
                  (AL022347) serine/threonine kinase -like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  302236
                   fC-zmf1700350656f5
Seq. ID
                  BLASTX
Method
                   g2104675
NCBI GI
BLAST score
                   337
                   9.0e-32
E value
Match length
                   100
% identity
                   67
                  (X97903) transcription factor [Vicia faba]
NCBI Description
                   302237
Seq. No.
Seq. ID
                   fC-zmf1700350656f6
Method
                   BLASTX
NCBI GI
                   q4587989
BLAST score
                   211
E value
                   5.0e-17
Match length
                   110
% identity
                   43
                   (AF085279) hypothetical Cys-3-His zinc finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   302238
Seq. No.
                   fC-zmf1700350815d4
Seq. ID
                   BLASTX
Method
                   q542395
NCBI GI
BLAST score
                   190
                   2.0e-14
E value
                   50
Match length
% identity
                   80
                   ubiquitin - basidiomycete (Phanerochaete chrysosporium)
NCBI Description
                   (fragment) >qi 467696 emb CAA83244 (Z31373) ubiquitin
                   [Phanerochaete chrysosporium]
                   302239
Seq. No.
                   fC-zmf1700352166b1
Seq. ID
                   BLASTX
Method
                   g4510395
NCBI GI
BLAST score
                   207
                   2.0e-16
E value
```

76 Match length 51 % identity

(AC006587) putative beta-galactosidase precursor NCBI Description

[Arabidopsis thaliana]



```
Seq. No.
                  302240
                  fC-zmf1700352582f2
Seq. ID
Method
                  BLASTX
                  g3924611
NCBI GI
                  601
BLAST score
E value
                  2.0e-62
Match length
                  128
% identity
                  89
                  (AF069442) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  302241
Seq. No.
                  fC-zmf1700354921g1
Seq. ID
Method
                  BLASTX
                  q2459435
NCBI GI
                  421
BLAST score
                  2.0e-41
E value
Match length
                  154
% identity
                  56
                  (AC002332) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                  thaliana]
                  302242
Seq. No.
                  fC-zmf1700382985h1
Seq. ID
Method
                  BLASTX
                  g4210330
NCBI GI
BLAST score
                   658
E value
                   4.0e-69
Match length
                  158
% identity
                  78
                   (AJ223802) 2-oxoglutarate dehydrogenase, El subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   302243
Seq. ID
                   fC-zmf1700464505b1
Method
                  BLASTX
NCBI GI
                   g3033400
BLAST score
                   371
E value
                   2.0e-35
Match length
                   83
% identity
NCBI Description
                   (AC004238) putative Ser/Thr protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   302244
Seq. ID
                   fC-zmf1700465148f2
Method
                   BLASTN
NCBI GI
                   g2832689
BLAST score
                   162
E value
                   5.0e-86
                   285
Match length
% identity
                   100
```

NCBI Description

Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21

(ESSAII project)

Seq. No. 302245

fC-zmf1700465406b1 Seq. ID

```
Method BLASTX
NCBI GI g1707642
BLAST score 215
E value 3.0e-17
Match length 84
% identity 54
```

NCBI Description (Y07748) TMK [Oryza sativa]

Seq. No. 302246

Seq. ID fC-zmf1700466204d4

Method BLASTX
NCBI GI g1710124
BLAST score 256
E value 3.0e-22
Match length 74
% identity 72

NCBI Description (U62279) leucine-rich repeat-containing extracellular

glycoprotein; contains six N-glycosylation sites [NX(S/T)]

[Sorghum bicolor]

Seq. No. 302247

Seq. ID fC-zmf1700467207b1

Method BLASTX
NCBI GI g3256035
BLAST score 187
E value 6.0e-14
Match length 52
% identity 62

NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum

bicolor]

Seq. No. 302248

Seq. ID fC-zmf1700467236b1

Method BLASTX
NCBI GI g3249072
BLAST score 185
E value 1.0e-13
Match length 66
% identity 53

NCBI Description (AC004473) Contains similarity to hypothetical 43.1 KD

protein in NDK-GCPE intergenic region gb_493519 from E.

coli sequence gb_U02965. [Arabidopsis thaliana]

Seq. No. 302249

Seq. ID fC-zmf1700467533b1

Method BLASTX
NCBI GI g3337361
BLAST score 387
E value 3.0e-37
Match length 105
% identity 64

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 302250

Seq. ID fC-zmf1700467714b1

Method BLASTX NCBI GI g1223926



```
BLAST score
                  2.0e-28
E value
Match length
                  64
                  92
% identity
                  (U49741) Vigna radiata carboxypeptidase II mRNA, partial
NCBI Description
                  cds [Vigna radiata]
                  302251
Seq. No.
                  fC-zmf1700467776b1
Seq. ID
                  BLASTX
Method
                  g3024362
NCBI GI
                   436
BLAST score
                   3.0e-43
E value
Match length
                   88
% identity
                   91
                  PHENYLALANINE AMMONIA-LYASE G2B >gi_2118317_pir__S60042
NCBI Description
                   phenylalanine ammonia-lyase (EC 4.3.1.5) 2b - Japanese
                  aspen x large-toothed aspen >gi_1109641_dbj_BAA07860_
                   (D43802) phenylalanine ammonia-Tyase [Populus
                   kitakamiensis]
                   302252
Seq. No.
                   fC-zmf1700467803b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1403522
                   461
BLAST score
                   5.0e-46
E value
                   96
Match length
                   85
% identity
                  (X57187) chitinase [Phaseolus vulgaris]
NCBI Description
                   302253
Seq. No.
                   fC-zmf1700468004b1
Seq. ID
Method
                   BLASTX
                   q4432830
NCBI GI
BLAST score
                   333
E value
                   5.0e-31
                   111
Match length
% identity
                   58
                   (AC006283) similar to pheromone receptor deficient mutant
NCBI Description
                   [Arabidopsis thaliana]
                   302254
Seq. No.
                   fC-zmf1700468053b1
Seq. ID
Method
                   BLASTN
                   q3769285
NCBI GI
                   63
BLAST score
                   8.0e-27
E value
Match length
                   239
                   87
% identity
                   Vigna radiata gene for 1-aminocyclopropane-1-carboxylate
NCBI Description
                   synthase, complete cds
```

Seq. No. Seq. ID 302255

fC-zmf1700468133b1

Method BLASTX NCBI GI g2493495



BLAST score 166 E value 1.0e-11 Match length 48 % identity 62

NCBI Description SERINE CARBOXYPEPTIDASE-LIKE >gi_2129878_pir__S72370

carboxypeptidase - garden pea (fragment)

>gi_1089904_emb_CAA92216_ (Z68130) carboxypeptidase [Pisum
sativum] >gi_1587217_prf__2206338A Ser carboxypeptidase

[Pisum sativum]

Seq. No. 302256

Seq. ID fC-zmf1700468226b1

Method BLASTX
NCBI GI g114947
BLAST score 201
E value 1.0e-15
Match length 104
% identity 50

NCBI Description BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR

>gi_105434_pir__B32688 beta-galactosidase-related protein -

human >gi_179421 (M27508) beta-galactosidase related

protein precursor [Homo sapiens]

Seq. No. 302257

Seq. ID fC-zmf1700468226f2

Method BLASTX
NCBI GI g2501021
BLAST score 159
E value 7.0e-11
Match length 56
% identity 59

NCBI Description LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)

>gi_1652562_dbj_BAA17483_ (D90906) lysyl-tRNA synthetase

[Synechocystis sp.]

Seq. No. 302258

Seq. ID fC-zmf1700468289b1

Method BLASTX
NCBI GI g4455369
BLAST score 178
E value 6.0e-13
Match length 46
% identity 78

NCBI Description (AL035524) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302259

Seq. ID fC-zmf1700468444f2

Method BLASTN
NCBI GI g6598508
BLAST score 81
E value 7.0e-38
Match length 153
% identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC T13P21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 302260



```
fC-zmf1700468704f2
Seq. ID
                  BLASTX
Method
                  g466190
NCBI GI
                  299
BLAST score
                  3.0e-27
E value
                  109
Match length
                  52
% identity
                  RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE B
NCBI Description
                  (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)
                  >gi 629120 pir S45555 hypothetical protein X13 - Bacillus
                  subtilis >gi_410137 (L09228) ORFX13 [Bacillus subtilis]
                  >gi_2634751_emb_CAB14248_ (Z99116) similar to hypothetical
                  proteins [Bacillus subtilis]
                  302261
Seq. No.
                  fC-zmf1700468993b1
Seq. ID
                  BLASTX
Method
                   q1935019
NCBI GI
                   719
BLAST score
                   3.0e-76
E value
Match length
                   169
                   85
% identity
                  (Z93774) sucrose transport protein [Vicia faba]
NCBI Description
                   302262
Seq. No.
                   fC-zmf1700469527b1
Seq. ID
                   BLASTX
Method
                   q2494174
NCBI GI
BLAST score
                   305
                   1.0e-27
E value
                   100
Match length
                   64
% identity
                  GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi_497979 (U10034)
NCBI Description
                   glutamate decarboxylase [Arabidopsis thaliana]
                   302263
Seq. No.
                   fC-zmf1700469527f2
Seq. ID
                   BLASTN
Method
                   q2618677
NCBI GI
                   325
BLAST score
                   0.0e + 00
E value
                   329
Match length
                   100
 % identity
                  Arabidopsis thaliana BAC F21B7 chromosome 1, complete
 NCBI Description
                   sequence [Arabidopsis thaliana]
                   302264
 Seq. No.
                   fC-zmf1700469566b1
 Seq. ID
                   BLASTX
 Method
                   q114167
 NCBI GI
                   508
 BLAST score
 E value
                   1.0e-51
```

% identity 89

NCBI Description 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE 2

104

Match length

(5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE 2) (EPSP SYNTHASE 2) >gi_100297_pir__S18354 3-phosphoshikimate

Seq. ID Method

NCBI GI

E value

BLAST score

Match length

% identity

Seq. No.

Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI BLAST score

E value

% identity

BLAST score

Match length

% identity

BLAST score

Match length

% identity

```
1-carboxyvinyltransferase (EC 2.5.1.19) - common tobacco
                  >gi 170231 (M61905) 5-enolpyruvylshikimate-3-phosphate
                  synthase [Nicotiana tabacum]
                  302265
                  fC-zmf1700469566f2
                  BLASTX
                  q1418331
                  300
                  2.0e-27
                  106
                  57
                  (X95909) receptor like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  302266
                  fC-zmf1700469777b1
                  BLASTX
                  g3367516
                  207
                  2.0e-16
                  68
                  50
                  (AC004392) Similar to beta-glucosidase BGQ60 precursor
NCBI Description
                  gb_L41869 from Hordeum vulgare. [Arabidopsis thaliana]
                  302267
                  fC-zmf1700470006b1
                  BLASTX
                  q2244867
                  246
                   6.0e-21
                  73
                   59
                  (Z97337) hydroxynitrile lyase [Arabidopsis thaliana]
NCBI Description
                   302268
                   fC-zmf1700470273f2
                   BLASTX
                   q4335736
                   219
                   7.0e-18
                   108
Match length
                   40
                   (AC006248) putative copia polyprotein [Arabidopsis
NCBI Description
                   thaliana]
```

302269 Seq. No.

fC-zmf1700470673b1 Seq. ID

BLASTX Method NCBI GI q1931655 171 BLAST score 4.0e-12 E value 44 Match length 75 % identity

(U95973) receptor-kinase isolog [Arabidopsis thaliana] NCBI Description



```
302270
Seq. No.
Seq. ID
                  fC-zmf1700471493b1
                  BLASTX
Method
                  q1706110
NCBI GI
                  325
BLAST score
                  4.0e-30
E value
                  82
Match length
                  80
% identity
                  NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR
NCBI Description
                   (CTPT) >gi_1143713 (U13632) non-green plastid
                  phosphate/triose-phosphate translocator precursor [Brassica
                   oleracea]
                   302271
Seq. No.
                   fC-zmf1700471493f2
Seq. ID
                   BLASTN
Method
                   q6598653
NCBI GI
                   228
BLAST score
                   1.0e-125
E value
                   259
Match length
                   97
% identity
                  Arabidopsis thaliana chromosome II BAC F16F14 genomic
NCBI Description
                   sequence, complete sequence
                   302272
Seq. No.
                   fC-zmf1700471593b1
Seq. ID
                   BLASTX
Method
                   g1754522
NCBI GI
                   193
BLAST score
                   1.0e-14
E value
                   60
Match length
                   65
% identity
                  (D89984) ornithine decarboxylase [Nicotiana tabacum]
NCBI Description
                   302273
Seq. No.
                   fC-zmf1700472059b1
Seq. ID
                   BLASTX
Method
                   q4538667
NCBI GI
                   193
BLAST score
                   9.0e-15
E value
                   58
Match length
                   66
 % identity
                   (AL049474) clathrin coat assembly protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   302274
 Seq. No.
                   fC-zmf1700472168b1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q3122389
                   182
 BLAST score
                   7.0e-14
 E value
                   50
 Match length
                   78
 % identity
                   WD-40 REPEAT PROTEIN MSI3 >gi 2394233 (AF016848) WD-40
 NCBI Description
```

repeat protein [Arabidopsis thaliana]



```
1
                   fC-zmf1700472661b1
Seq. ID
Method
                  BLASTN
                   a2606080
NCBI GI
                   194
BLAST score
                   1.0e-105
E value
                   277
Match length
                   100
% identity
NCBI Description Glycine max sucrose synthase (SS) mRNA, complete cds
                   302276
Seq. No.
                   fC-zmf1700472710b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2501231
                   385
BLAST score
                   3.0e-37
E value
                   88
Match length
                   76
% identity
                   HYPOTHETICAL 38.1 KD PROTEIN >gi_99505_pir__S24930
NCBI Description
                   hypothetical protein - pink corydalis >gi_18258_emb_CAA45139_ (X63595) protein of unknown
                   function [Corydalis sempervirens] >gi_444333_prf__1906382A
                   pCSC71 protein [Corydalis sempervirens]
                   302277
Seq. No.
                   fC-zmf1700472751b1
Seq. ID
Method
                   BLASTX
                   q4098129
NCBI GI
                   369
BLAST score
                   3.0e-35
E value
Match length
                   74
                   92
% identity
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
                   302278
Seq. No.
                   fC-zmf1700474549b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4115936
                   335
BLAST score
                   2.0e-31
E value
Match length
                   78
                   82
% identity
NCBI Description (AF118223) No definition line found [Arabidopsis thaliana]
                    302279
Seq. No.
                    fC-zmf1700475620b1
Seq. ID
Method
                   BLASTX
                    g1155255
NCBI GI
                    279
BLAST score
                    1.0e-24
E value
Match length
                    105
% identity
                    55
                   (U39228) beta-glucosidase [Prunus avium]
NCBI Description
```

fC-zmf1700548428f3 Seq. ID

BLASTX Method g535454 NCBI GI

```
BLAST score 377
E value 2.0e-36
Match length 109
% identity 61
```

NCBI Description (U13940) cysteine proteinase [Alnus glutinosa]

Seq. No. 302281

Seq. ID fC-zmf1700549125f3

Method BLASTX
NCBI GI g2388574
BLAST score 548
E value 3.0e-56
Match length 122
% identity 87

NCBI Description (AC000098) Strong similarity to Phalaenopsis homeobox

protein (gb U34743). [Arabidopsis thaliana]

Seq. No. 302282

Seq. ID fC-zmf1700549863r3

Method BLASTX
NCBI GI g1236949
BLAST score 257
E value 3.0e-22
Match length 68
% identity 76

NCBI Description (U50075) lipoxygenase L-5 [Glycine max]

Seq. No. 302283

Seq. ID fC-zmf1700552735f3

Method BLASTX
NCBI GI g1076531
BLAST score 481
E value 2.0e-48
Match length 123
% identity 73

NCBI Description hypothetical protein, pollen allergen homolog - garden pea

>gi_2129891_pir__S65056 pollen allergen homolog precursor (clone PPA1) - garden pea >gi_732905 emb CAA59470_ (X85187)

homology with pollen allergens [Pisum sativum]

Seq. No. 302284

Seq. ID fC-zmf1700610957h2

Method BLASTX
NCBI GI g310580
BLAST score 259
E value 3.0e-22
Match length 54
% identity 94

NCBI Description (L19360) protein kinase 2 [Glycine max]

Seq. No. 302285

Seq. ID fC-zmf1700611201a1

Method BLASTX
NCBI GI g3063691
BLAST score 534
E value 1.0e-54
Match length 156

```
% identity
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                   302286
Seq. ID
                   fC-zmf1700903880z1
Method
                   BLASTX
NCBI GI
                   q4335745
BLAST score
                   259
E value
                   2.0e-22
Match length
                   148
% identity
                   41
NCBI Description
                   (AC006284) putative hydrolase (contains an
                   esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
Seq. No.
                   302287
Seq. ID
                   fC-zmf1700903946z1
Method
                   BLASTX
NCBI GI
                   g4102600
BLAST score
                   502
E value
                   7.0e-51
Match length
                   142
% identity
                   75
NCBI Description
                  (AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.
                   302288
Seq. ID
                   fC-zmf1700904260q1
Method
                  BLASTX
                  q2809262
NCBI GI
BLAST score
                   352
E value
                   3.0e-33
Match length
                  165
% identity
                   44
NCBI Description
                  (AC002560) F21B7.31 [Arabidopsis thaliana]
Seq. No.
                  302289
Seq. ID
                  fC-zmf1700905073g1
Method
                  BLASTX
NCBI GI
                  q4510375
BLAST score
                  198
E value
                  4.0e-15
Match length
                  131
% identity
                  45
NCBI Description
                  (AC007017) putative homeotic protein BEL1 [Arabidopsis
                  thaliana]
Seq. No.
                  302290
Seq. ID
                  fC-zmf1700906621a1
Method
                  BLASTX
                  q4335763
```

47

NCBI GI BLAST score 301 E value 2.0e-27 Match length 116

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 302291

% identity



```
fC-zmle700423591r3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3639087
BLAST score
                  352
E value
                  2.0e-33
Match length
                  113
% identity
                  64
                   (AF090444) phospholipase D2 [Brassica oleracea] >gi_3924621
NCBI Description
                   (U85482) phospholipase D [Brassica oleracea var. capitata]
                  >gi_4324971_gb_AAD17209_ (AF113919) phospholipase D2
                   [Brassica oleracea var. capitata]
                  302292
Seq. No.
Seq. ID
                  fC-zmle700427538b1
Method
                  BLASTX
NCBI GI
                  g1781348
BLAST score
                  156
E value
                  1.0e-10
Match length
                  34
% identity
                  88
NCBI Description
                  (Y10380) homologous to plastidic aldolases [Solanum
                  302293
Seq. No.
Seq. ID
                  fC-zmle700428142a4
Method
                  BLASTX
NCBI GI
                  q1632822
BLAST score
                  408
E value
                  5.0e-40
Match length
                  87
% identity
                  89
NCBI Description
                  (Y08962) transmembrane protein [Oryza sativa] >gi 1667594
                   (U77297) transmembrane protein [Oryza sativa]
                  302294
Seq. No.
Seq. ID
                  fC-zmle700428946d3
Method
                  BLASTN
NCBI GI
                  g3342803
BLAST score
                  94
E value
                  2.0e-45
Match length
                  178
                  88
% identity
NCBI Description
                  Zea mays strain B73 putative 6-phosphogluconate
                  dehydrogenase mRNA, nuclear gene encoding putative plastid
                  protein, partial cds
                  302295
Seq. No.
Seq. ID
                  fC-zmle700429434f3
Method
                  BLASTN
```

NCBI GI g3342031 BLAST score 52 E value 3.0e-20 Match length 60 % identity 98

NCBI Description Oryza sativa 18S small subunit ribosomal RNA gene, complete

sequence



```
302296
Seq. No.
                  fC-zmle700431670f4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4033424
BLAST score
                  186
E value
                  2.0e-14
Match length
                  41
                  85
% identity
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                  PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
Seq. No.
                  302297
Seq. ID
                  fC-zmle700433471d3
Method
                  BLASTN
NCBI GI
                  a553071
BLAST score
                  189
E value
                  1.0e-102
                  261
Match length
% identity
                  93
NCBI Description Maize catalase (Cat2) mRNA, 3' end
                  302298
Seq. No.
Seq. ID
                  fC-zmle700434174z1
Method
                  BLASTX
                  q488571
NCBI GI
                  202
BLAST score
                  1.0e-15
E value
Match length
                   41
                   98
% identity
NCBI Description (U09462) histone H3.2 [Medicago sativa]
Seq. No.
                   302299
Seq. ID
                   fC-zmle700434272g1
Method
                  BLASTX
                   q1076755
NCBI GI
BLAST score
                   693
E value
                   4.0e-73
Match length
                   183
% identity
                  72
                  protein kinase - rice >gi_450300 (L27821) protein kinase
NCBI Description
                   [Oryza sativa]
Seq. No.
                   302300
                   fC-zmle700441222d3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1345559
BLAST score
                   170
E value
                   2.0e-12
Match length
                   46
% identity
                  72
```

NCBI Description (Z15024) hsp82 [Oryza sativa]

Seq. No.

302301

Seq. ID

fC-zmle700442391d5

Method NCBI GI BLASTX g113987



BLAST score 173 E'value 2.0e-12 Match length 45 % identity 71

NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO (DEOXYRIBONUCLEASE (APURINIC OR APYRIMIDINIC)) (APURINIC- APYRIMIDINIC)

ENDONUCLEASE) >gi_71140_pir__R5FFP0 acidic ribosomal

protein PO - fruit fly (Drosophila melanogaster) >gi_576817

(M25772) DNA repair protein [Drosophila melanogaster]

Seq. No. 302302

Seq. ID fC-zmle700443787d6

Method BLASTX
NCBI GI g731806
BLAST score 218
E value 4.0e-22
Match length 79
% identity 70

NCBI Description PROBABLE CALCIUM-TRANSPORTING ATPASE 7

>gi_626344_pir__S48431 probable membrane protein YIL048w yeast (Saccharomyces cerevisiae) >gi_557820_emb_CA86174_
(Z38060) orf, len: 1151, CAI: 0.17, similar to S30768
S30768 PROBABLE ATPASE - YEAST (SACCHAROMYCES CEREVISIAE)

3

[Saccharomyces cerevisiae]

Seq. No. 302303

Seq. ID fC-zmle700444043b1

Method BLASTX
NCBI GI g2081612
BLAST score 151
E value 9.0e-10
Match length 41
% identity 80

NCBI Description (D49714) deltal-pyrroline-5-carboxylate synthetase [Oryza

sativa]

Seq. No. 302304

Seq. ID fC-zmle700445373f5

Method BLASTX
NCBI GI g3402758
BLAST score 372
E value 9.0e-36
Match length 128
% identity 56

NCBI Description (AL031187) serine/threonine kinase - like protein

[Arabidopsis thaliana]

Seq. No. 302305

Seq. ID fC-zmle700445890d4

Method BLASTX
NCBI GI g4008006
BLAST score 151
E value 2.0e-10
Match length 59
% identity 46

NCBI Description (AF084034) receptor-like protein kinase [Arabidopsis

thaliana]



```
302306
Seq. No.
Seq. ID
                  fC-zmle700447121a1
                  BLASTX
Method
NCBI GI
                  g2842478
BLAST score
                  149
                  1.0e-09
E value
                  80
Match length
% identity
                  39
                   (AL021749) receptor protein kinase like protein
NCBI Description
                   [Arabidopsis thaliana]
                  302307
Seq. No.
Seq. ID
                  fC-zmle700447833a1
Method
                  BLASTN
NCBI GI
                  q296593
BLAST score
                  55
E value
                   4.0e-22
Match length
                  75
                  93
% identity
NCBI Description
                  H. vulgare pZE40 gene
Seq. No.
                  302308
                   fC-zmle700448273a1
Seq. ID
Method
                  BLASTX
                  q3540182
NCBI GI
BLAST score
                   360
E value
                   3.0e - 34
Match length
                   125
% identity
                  (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   302309
Seq. ID
                   fC-zmle700577059a2
Method
                  BLASTX
NCBI GI
                  q2687358
BLAST score
                   286
                   4.0e-51
E value
Match length
                  120
                   89
% identity
                  (AF033263) nonphototropic hypocotyl 1 [Zea mays]
NCBI Description
Seq. No.
                   302310
Seq. ID
                   fC-zmle700577234r1
Method
                  BLASTX
NCBI GI
                  g585421
BLAST score
                   265
                   3.0e-23
E value
Match length
                   57
```

77 % identity

LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi 541879.pir JQ2391 NCBI Description lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana

>gi 431258 (L23968) lipoxygenase [Arabidopsis thaliana]

302311 Seq. No.

Seq. ID fC-zmle700582195a2

Method BLASTX



```
NCBI GI
                   g1364161
BLAST score
                   269
                   7.0e-24
E value
Match length
                   93
% identity
                   63
NCBI Description thiolase precursor, peroxisomal - ripe mango
Seq. No.
                   302312
Seq. ID
                   fC-zmle700583812a2
Method
                   BLASTN
NCBI GI
                   q3318610
BLAST score
                   110
E value
                   3.0e-55
                   176
Match length
% identity
                   92
                  Glycine max mRNA for mitochondrial phosphate transporter,
NCBI Description
                  complete cds
                   302313
Seq. No.
                   fC-zmle700870829a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2459435
BLAST score
                   473
E value
                   1.0e-47
Match length
                   125
% identity
                   71
NCBI Description
                   (AC002332) putative serine carboxypeptidase [Arabidopsis
                   thaliana]
                   302314
Seq. No.
                   fC-zmle700870829d1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2459435
BLAST score
                   320
E value
                   2.0e-29
Match length
                   76
% identity
                   78
NCBI Description
                   (AC002332) putative serine carboxypeptidase [Arabidopsis
                   thaliana]
Seq. No.
                   302315
Seq. ID
                   fC-zmle700870883a1
Method
                   BLASTX
NCBI GI
                   g4105772
BLAST score
                   444
E value
                   4.0e-44
Match length
                  107
% identity
                   43
NCBI Description (AF049917) PGP9B [Petunia x hybrida]
Seq. No.
                   302316
Seq. ID
                   fC-zmle700871883a1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3204134
BLAST score 871
E value 4.0e-94

Match length 166

Match length

NCBI Description

% identity

81



```
% identity
NCBI Description (AJ006771) beta-galactosidase [Cicer arietinum]
Seq. No.
                  302317
Seq. ID
                  fC-zmle700871981d1
Method
                  BLASTX
NCBI GI
                  g2623300
BLAST score
                  447
E value
                  2.0e-44
Match length
                  112
% identity
                  79
NCBI Description
                  (AC002409) putative protein phosphatase 2C [Arabidopsis
                  thaliana]
                  302318
Seq. No.
Seq. ID
                  fC-zmle700889290a1
Method
                  BLASTX
NCBI GI
                  g1168493
BLAST score
                  557
E value
                  3.0e-57
Match length
                  131
% identity
                  85
NCBI Description
                  ARGINASE >gi_602422 (U15019) arginase [Arabidopsis
                  thaliana] >gi_4325373_gb_AAD17369_ (AF128396) Arabidopsis
                  thaliana arginase (SW:P46637) (Pfam: PF00491, Score=419.6,
                  E=3.7e-142 N=1) [Arabidopsis thaliana]
Seq. No.
                  302319
Seq. ID
                  fC-zmro700448758a1
Method
                  BLASTX
NCBI GI
                  g2239260
BLAST score
                  618
E value
                  2.0e-64
Match length
                  136
% identity
                  88
NCBI Description
                  (Y13734) cinnamoyl CoA reductase [Zea mays]
Seq. No.
                  302320
Seq. ID
                  fC-zmro700569244f1
Method
                  BLASTX
NCBI GI
                  g4165488
BLAST score
                  385
E value
                  3.0e-49
Match length
                  97
% identity
                  97
NCBI Description (AJ132399) alpha-tubulin 3 [Hordeum vulgare]
Seq. No.
                  302321
                  fC-zmro700570531r1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913194
BLAST score
                  171
E value
                  5.0e-12
```

42665

CINNAMYL-ALCOHOL DEHYDROGENASE 3 (CAD) >gi_548323 (L36456) cinnamyl-alcohol dehydrogenase [Stylosanthes humilis]



```
302322
Seq. No.
Seq. ID
                  fC-zmro700570954a1
Method
                  BLASTX
NCBI GI
                  g2244771
BLAST score
                  324
                  5.0e-30
E value
Match length
                  76
% identity
                  89
NCBI Description
                  (Z97335) kinesin homolog [Arabidopsis thaliana]
Seq. No.
                  302323
Seq. ID
                  fC-zmro700570954d1
                  BLASTX
Method
NCBI GI
                  g4093169
BLAST score
                  248
E value
                   4.0e-21
Match length
                  63
% identity
                  70
NCBI Description
                  (AF095933) p20-Arc [Dictyostelium discoideum]
Seq. No.
                  302324
Seq. ID
                  fC-zmro700571730a1
Method
                  BLASTX
NCBI GI
                  g3046815
BLAST score
                  190
                  2.0e-23
E value
Match length
                  72
% identity
                  76
NCBI Description
                  (AL021687) cytochrome P450 [Arabidopsis thaliana]
                  302325
Seq. No.
Seq. ID
                  fC-zmro700571850a1
Method
                  BLASTX
NCBI GI
                  g4587525
BLAST score
                  258
                  3.0e-22
E value
                  117
Match length
% identity
                  42
                   (AC007060) Contains the PF 00650 CRAL/TRIO
NCBI Description
                  phosphatidyl-inositol-transfer protein domain. ESTs
                  gb_T76582, gb N06574 and gb Z25700 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  302326
Seq. ID
                  fC-zmro700572286a1
Method
                  BLASTX
NCBI GI
                  g2739279
BLAST score
                  332
```

E value 6.0e-31 Match length 137 49 % identity

(AJ223177) short chain alcohol dehydrogenase [Nicotiana NCBI Description tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain

alcohol dehydrogenase [Nicotiana tabacum]

Seq. No. 302327



fC-zmro700572681a1 Seq. ID BLASTX Method NCBI GI g3193316 358 BLAST score 5.0e-34 E value Match length 103 % identity 68 (AF069299) contains similarity to nucleotide sugar NCBI Description epimerases [Arabidopsis thaliana] Seq. No. 302328 Seq. ID fC-zmro700573051a1 Method BLASTX NCBI GI q1352186 BLAST score 453 4.0e-45 E value Match length 140 % identity 56 ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) NCBI Description (CYTOCHROME P450 74) >gi 404866 (U00428) allene oxide synthase [Linum usitatissimum] Seq. No. 302329 Seq. ID fC-zmro700573209a1 Method BLASTX NCBI GI q2980785 BLAST score 514 E value 3.0e-52 Match length 137 % identity 64 NCBI Description (AL022198) SERINE CARBOXYPEPTIDASE II - like protein [Arabidopsis thaliana] 302330 Seq. No. Seq. ID fC-zmro700573209d1 Method BLASTX NCBI GI g2493494 BLAST score 290 5.0e-26 E value 84 Match length 69 % identity SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) NCBI Description >gi 619351 bbs 153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa] 302331 Seq. No.

Seq. ID fC-zmro700573388d1

Method BLASTN NCBI GI g2446999 BLAST score 121 E value 2.0e-61 Match length 223 % identity 95

Zea mays FAD8 gene for fatty acid desaturase, partial cds NCBI Description

Seq. No. 302332



```
Seq. ID
                  fC-zmro700573489g1
                  BLASTX
Method
NCBI GI
                  q1709000
                  612
BLAST score
                  8.0e-64
E value
Match length
                  142
% identity
                  82
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine
                  synthetase [Hordeum vulgare]
Seq. No.
                  302333
Seq. ID
                  fC-zmro700573489z1
Method
                  BLASTX
NCBI GI
                  a3024122
BLAST score
                  722
E value
                  1.0e-76
Match length
                  162
                  86
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821
                  (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
Seq. No.
                  302334
Seq. ID
                  fC-zmro700573673a1
Method
                  BLASTX
NCBI GI
                  q123620
BLAST score
                  620
E value
                  9.0e-65
Match length
                  141
% identity
                  87
NCBI Description
                  HEAT SHOCK COGNATE 70 KD PROTEIN 2 >qi 100224 pir S14950
                  heat shock cognate protein 70 - tomato
                  >gi 19258 emb CAA37971 (X54030) heat shock protein cognate
                  70 [Lycopersicon esculentum]
                  302335
Seq. No.
Seq. ID
                  fC-zmro700573673d1
Method
                  BLASTX
NCBI GI
                  g1430887
BLAST score
                  295
E value
                  1.0e-26
Match length
                  91
% identity
                  69
                  (X99197) 70 kD heatshockprotein [Medicago sativa]
NCBI Description
Seq. No.
                  302336
Seq. ID
                  fC-zmro700574787a1
```

Method BLASTX NCBI GI q4165488 BLAST score 257 E value 6.0e-33 Match length 77 86 % identity

NCBI Description (AJ132399) alpha-tubulin 3 [Hordeum vulgare]

```
Seq. No.
                   302337
Seq. ID
                   fC-zmro700574919a3
                   BLASTX
Method
                   q1236949
NCBI GI
BLAST score
                   907
E value
                   3.0e-98
Match length
                   174
                   99
% identity
NCBI Description
                  (U50075) lipoxygenase L-5 [Glycine max]
Seq. No.
Seq. ID
                   fC-zmro700575714f1
Method
                   BLASTX
NCBI GI
                   q2522210
BLAST score
                   305
E value
                   6.0e-28
Match length
                   101
% identity
                   53
                  (AF023132) choline monooxygenase [Beta vulgaris]
NCBI Description
Seq. No.
                   302339
Seq. ID
                   fC-zmro700576307a2
Method
                   BLASTX
NCBI GI
                   q3482919
BLAST score
                   141
E value
                   4.0e-09
Match length
                   33
% identity
                   73
NCBI Description
                  (AC003970) Putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   302340
Seq. ID
                   fC-zmro700807549a1
Method
                   BLASTX
NCBI GI
                   g4457221
BLAST score
                   381
E value
                   1.0e-36
Match length
                   114
                   68
% identity
                   (AF127797) putative bZIP DNA-binding protein [Capsicum
NCBI Description
                   chinense]
                   302341
Seq. No.
Seq. ID
                   fC-zmro700807584a1
Method
                  BLASTX
NCBI GI
                  g3218410
BLAST score
                   516
E value
                   1.0e-52
```

Match length 127 76 % identity

(AL023859) putative prolyl-trna synthetase NCBI Description

[Schizosaccharomyces pombe]

Seq. No. 302342

Seq. ID fC-zmro700807584r1

Method BLASTX NCBI GI g731640 BLAST score 172



```
E value 3.0e-12
Match length 78
% identity 47
NCBI Description PUTATIVE
LIGASE)
```

PUTATIVE PROLYL-TRNA SYNTHETASE YHR020W (PROLINE--TRNA LIGASE) (PRORS) >gi_626755_pir__S46774 multifunctional amino acid--tRNA ligase homolog - yeast (Saccharomyces

cerevisiae) >gi_500692 (U10399) Yhr020wp [Saccharomyces

cerevisiae]

Seq. No. 302343

Seq. ID fC-zmro700807612a1

Method BLASTX
NCBI GI g3402758
BLAST score 521
E value 4.0e-53
Match length 153
% identity 65

NCBI Description (AL031187) serine/threonine kinase - like protein

[Arabidopsis thaliana]

Seq. No. 302344

Seq. ID fC-zmro700829628a1

Method BLASTX
NCBI GI g4567246
BLAST score 362
E value 2.0e-34
Match length 112
% identity 65

NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No. 302345

Seq. ID fC-zmro700829706a1

Method BLASTX
NCBI GI g3687240
BLAST score 580
E value 5.0e-60
Match length 156
% identity 70

NCBI Description (AC005169) extensin-like protein [Arabidopsis thaliana]

Seq. No. 302346

Seq. ID fC-zmro700829731a1

Method BLASTX
NCBI GI g2492952
BLAST score 544
E value 9.0e-56
Match length 114
% identity 85

NCBI Description CHORISMATE SYNTHASE 1 PRECURSOR

(5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)
>gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1
precursor - tomato >gi 410482 emb CAA79859 (Z21796)

chorismate synthase 1 [Lycopersicon esculentum]

Seq. No. 302347

Seq. ID fC-zmro700829816d3

Method BLASTX



```
NCBI GI
                  q1730168
BLAST score
                  199
                  2.0e-15
E value
Match length
                  52
                  75
% identity
                  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 1 (GPI)
NCBI Description
                  (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
                  (PHI) >gi 1370053 emb_CAA61576_ (X89396)
                  glucose-6-phosphate isomerase [Clarkia franciscana]
Seq. No.
Seq. ID
                  fC-zmro700829944d1
Method
                  BLASTN
NCBI GI
                  q1143318
BLAST score
                  68
                  6.0e-30
E value
                  285
Match length
                  86
% identity
                  Glycine max biotin carboxyl carrier protein precursor
NCBI Description
                   (accB-1) mRNA, complete cds
                  302349
Seq. No.
Seq. ID
                  fC-zmro700830015a2
Method
                  BLASTX
                  q2507455
NCBI GI
BLAST score
                  494
                  5.0e-50
E value
Match length
                  111
% identity
                  86
                  FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE
NCBI Description
                  SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350
                  formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach
                  >gi 170145 (M83940) 10-formyltetrahydrofolate synthetase
                   [Spinacia oleracea]
                  302350
Seq. No.
Seq. ID
                  fC-zmro700830180d1
Method
                  BLASTX
NCBI GI
                  q478809
                  591
BLAST score
                  2.0e-61
E value
Match length
                  107
% identity
                  100
                  protein kinase 6 (EC 2.7.1.-) - soybean >gi_170047 (M67449)
NCBI Description
                  protein kinase [Glycine max] >gi_444789_prf__1908223A
                  protein kinase [Glycine max]
                  302351
Seq. No.
                  fC-zmro700830314d4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4249391
```

BLAST score 143 4.0e-09 E value Match length 51 % identity 53

(AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase NCBI Description from Arabidopsis thaliana BAC gb AC004473. [Arabidopsis

% identity

61



thaliana]

```
Seq. No.
                   302352
                   fC-zmro700830732d1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2980806
BLAST score
                   286
E value
                   2.0e-25
Match length
                   133
% identity
                   45
NCBI Description
                   (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   fC-zmro700830845d1
Method
                   BLASTX
NCBI GI
                   q139780
BLAST score
                   166
E value
                   2.0e-11
Match length
                   61
% identity
                   61
NCBI Description
                   WOUND-INDUCED PROTEIN 1 >gi 82293 pir JQ0398 wun1 protein
                   - potato
Seq. No.
                   302354
Seq. ID
                   fC-zmro700830845f1
Method
                   BLASTX
NCBI GI
                   q130188
BLAST score
                   465
E value
                   3.0e-47
Match length
                   113
% identity
                   PHYTOCHROME A >gi_81937_pir__S06856 phytochrome - garden
NCBI Description
                   pea >gi_169132 (M37217) phytochrome [Pisum sativum] >gi_295830 emb_CAA32242 (X14077) phytochrome apoprotein
                   [Pisum sativum] >gi 226757 prf 1604466A phytochrome [Pisum
                   sativum]
Seq. No.
                   302355
Seq. ID
                   fC-zmro700831185a2
                   BLASTX
Method
NCBI GI
                   g3402758
BLAST score
                   511
E value
                   5.0e-52
Match length
                   135
                   72
% identity
NCBI Description
                   (AL031187) serine/threonine kinase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   302356
Seq. ID
                   fC-zmro700831219d1
Method
                   BLASTX
NCBI GI
                   q4262242
BLAST score
                   147
E value
                   3.0e-09
Match length
                   61
```

NCBI Description (AC006200) NADC homolog [Arabidopsis thaliana]

% identity

```
Seq. No.
                    302357
                    fC-zmro700831372d1
 Seq. ID
 Method
                    BLASTX
                    q4490297
 NCBI GI
                    144
 BLAST score
 E value
                    6.0e-09
                    73
 Match length
 % identity
 NCBI Description
                    (AL035678) putative protein [Arabidopsis thaliana]
 Seq. No.
                    302358
                    fC-zmro700831977a2
 Seq. ID
                    BLASTX
 Method
                    g2499488
 NCBI GI
                    698
 BLAST score
                    7.0e-74
 E value
 Match length
                    150
  % identity
                    90
                    PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
 NCBI Description
                    ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                    (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                    (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849)
                    pyrophosphate-dependent phosphofructokinase alpha subunit
                    [Ricinus communis]
                    302359
  Seq. No.
                    fC-zmro700833740g1
  Seq. ID
 Method
                    BLASTX
  NCBI GI
                    g2160191
 BLAST score
                    139
 E value
                    6.0e-09
 Match length
                    32
  % identity
                    72
                    (AC000132) Identical to A. thaliana AtK-1 (gb_X79279).
  NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    302360
  Seq. ID
                    fC-zmro700833775r1
  Method
                    BLASTX
  NCBI GI
                    q4455274
  BLAST score
                    358
 E value
                    6.0e - 34
 Match length
                    164
  % identity
                    41
                    (AL035527) spliceosome associated protein-like [Arabidopsis
  NCBI Description
                    thaliana]
                    302361
  Seq. No.
  Seq. ID
                    fC-zmro700834080f1
  Method
                    BLASTX
  NCBI GI
                    q2109275
  BLAST score
                    176
                    8.0e-13
  E value
                    105
  Match length
                    40
```

NCBI Description (U97106) downy mildew resistance protein RPP5 [Arabidopsis

NCBI Description

faba]



thaliana]

```
Seq. No.
                  302362
                  fC-zmro700834281f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4490310
BLAST score
                  387
                  1.0e-37
E value
                  96
Match length
                  78
% identity
NCBI Description (AL035678) somatic embryogenesis receptor-like kinase-like
                  protein [Arabidopsis thaliana]
                  302363
Seq. No.
                  fC-zmro700834335f1
Seq. ID
                  BLASTX
Method
                  q2598579
NCBI GI
BLAST score
                  515
                  2.0e-52
E value
                  120
Match length
% identity
                  82
NCBI Description (Y15295) L-ascorbate oxidase [Medicago truncatula]
Seq. No.
                  302364
                  fC-zmro700834346f1
Seq. ID
                  BLASTX
Method
                  g1709267
NCBI GI
                  351
BLAST score
E value
                  2.0e-33
                  103
Match length
% identity
                   69
                  INDUCIBLE NITRATE REDUCTASE 1 (NR) >gi 1262166 (L23854)
NCBI Description
                  nitrate reductase [Glycine max]
Seq. No.
                   302365
Seq. ID
                   fC-zmro700834346r1
Method
                  BLASTN
NCBI GI
                   q409368
BLAST score
                   70
                   5.0e-31
E value
Match length
                   109
                   92
% identity
NCBI Description Glycine max mutant nitrate reductase mRNA, 3' end
Seq. No.
                   302366
                   fC-zmro700834406f1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2506470
BLAST score
                   389
E value
                   1.0e-37
Match length
                   150
% identity
                   61
```

ALPHA-1,4 GLUCAN PHOSPHORYLASE, L ISOFORM PRECURSOR (STARCH

alpha-1,4 Glucan Phosphorylase, L isoform precursor [Vicia

PHOSPHORYLASE L) >gi_1616637_emb_CAA85354_ (Z36880)



```
Seq. No.
                  302367
                  fC-zmro700834515a1
Seq. ID
Method
                  BLASTX
                  q2246450
NCBI GI
BLAST score
                  169
                  5.0e-12
E value
Match length
                  54
                  61
% identity
                   (U68072) 3-hydroxy-3-methylglutaryl CoA reductase 2
NCBI Description
                   [Lycopersicon esculentum]
Seq. No.
                  302368
                  fC-zmro700834515d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q322669
BLAST score
                  216
                   3.0e-34
E value
Match length
                   95
                   87
% identity
                  hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) -
NCBI Description
                   radish >gi 21102 emb CAA48610 (X68651)
                   hydroxymethylglutaryl-CoA reductase (NADPH) [Raphanus
                   sativus]
                   302369
Seq. No.
                   fC-zmro700834529f1
Seq. ID
                   BLASTX
Method
                   q1168189
NCBI GI
BLAST score
                   434
                   3.0e-43
E value
Match length
                   94
                   91
% identity
                   14-3-3-LIKE PROTEIN A (VFA-1433A) >gi_1076542_pir__S52899
NCBI Description
                   14-3-3 brain protein homolog - fava bean
                   >gi_695765_emb_CAA88415_ (Z48504) 14-3-3 brain protein
                   homolog [Vicia faba]
                   302370
Seq. No.
                   fC-zmro700834529r1
Seq. ID
                   BLASTX
Method
                   g1168196
NCBI GI
                   445
BLAST score
                   4.0e-44
E value
Match length
                   90
% identity
                   96
                   14-3-3-LIKE PROTEIN >gi 555974 (U15036) 14-3-3-like protein
NCBI Description
                   [Pisum sativum]
                   302371
Seq. No.
Seq. ID
                   fC-zmro700834608r1
                   BLASTX
Method
                   q2244899
NCBI GI
```

BLAST score 456 7.0e-50 E value Match length 119 72 % identity

NCBI Description (Z97338) similar to UFD1 protein [Arabidopsis thaliana]

```
Seq. No.
                  302372
                  fC-zmro700834677f1
Seq. ID
Method ~
                  BLASTX
NCBI GI
                  g2459435
BLAST score
                  409
E value
                  6.0e-40
Match length
                  122
% identity
NCBI Description
                  (AC002332) putative serine carboxypeptidase [Arabidopsis
                  thaliana]
Seq. No.
                  302373
Seq. ID
                  fC-zmro700834677r1
Method
                  BLASTX
NCBI GI
                  q2459435
BLAST score
                  249
E value
                  3.0e-21
Match length
                  62
                  73
% identity
                  (AC002332) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  302374
                  fC-zmro700834772f1
Seq. ID
Method
                  BLASTX
                  q4206122
NCBI GI
                  346
BLAST score
E value
                  8.0e-33
Match length
                  89
% identity
                  75
                   (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                  302375
                  fC-zmro700834861f1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1143318
BLAST score
                  52
                  3.0e-20
E value
                  52
Match length
                  100
% identity
                  Glycine max biotin carboxyl carrier protein precursor
NCBI Description
                   (accB-1) mRNA, complete cds
Seq. No.
                  302376
Seq. ID
                  fC-zmro700834891f1
Method
                  BLASTX
NCBI GI
                  g1769891
                  155
BLAST score
                  1.0e-10
E value
                  46
Match length
                   67
% identity
                   (X99747) bZIP transcription factor [Arabidopsis thaliana]
NCBI Description
                  >gi_1865679_emb_CAB04795_ (Z82043) ATB2 [Arabidopsis
```

....

thaliana]



```
302377
Seq. No.
                  fC-zmro700834955f1
Seq. ID
                  BLASTX
Method
                  g3335351
NCBI GI
BLAST score
                  311
E value
                  1.0e-28
Match length
                  116
                  53
% identity
                  (AC004512) Similar to ERECTA receptor protein kinase
NCBI Description
                  gb_D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  302378
                  fC-zmro700835422f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4490721
BLAST score
                  205
E value
                  1.0e-16
Match length
                  41
                  95
% identity
                   (AL035709) squalene epoxidase-like protein [Arabidopsis
NCBI Description
                  302379
Seq. No.
                  fC-zmro700835511f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1086263
BLAST score
                  199
E value
                   1.0e-15
Match length
                   73
                   58
% identity
                  TMV resistance protein N - tobacco (Nicotiana glutinosa)
NCBI Description
                  >gi 558887 (U15605) N [Nicotiana glutinosa]
Seq. No.
                   302380
                   fC-zmro700835640f1
Seq. ID
Method
                  BLASTX
                   g2129933
NCBI GI
                   227
BLAST score
                   5.0e-19
E value
                   43
Match length
                   93
% identity
                  myb-related transcription factor TMH27 - tomato
NCBI Description
                   >qi 1167484 emb CAA64614 (X95296) transcription factor
                   [Lycopersicon esculentum]
                   302381
Seq. No.
Seq. ID
                   fC-zmro700835753f1
                   BLASTX
Method
```

g2182029 NCBI GI 395 BLAST score 7.0e-39 E value Match length 80 89 % identity

(Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa] NCBI Description

Seq. No. 302382



```
fC-zmro700835753r1
Seq. ID
                   BLASTX
Method
                   g2129738
NCBI GI
                   283
BLAST score
                   3.0e-25
E value
Match length
                   65
% identity
                   shaggy-like kinase dzeta - Arabidopsis thaliana
NCBI Description
                   >gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta
[Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300)
                   serine/threonine kinase [Arabidopsis thaliana]
Seq. No.
                   302383
                   fC-zmro700835781a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512659
BLAST score
                   339
E value
                   1.0e-40
Match length
                   106
                   83
% identity
                   (AC006931) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >qi 4544465 gb AAD22372.1 AC006580 4 (AC006580) putative
                   protein kinase [Arabidopsis thaliana]
Seq. No.
                   fC-zmro700835853f1
Seq. ID
Method
                   BLASTX
NCBI GI
                   a3152599
BLAST score
                   509
E value
                   1.0e-51
Match length
                   151
                   32
% identity
NCBI Description
                    (AC002986) Strong similarity to lupeol synthase gb_U49919
                   and cycloartenol synthase gb_U02555 from A. thaliana (the
                   third gene with similar homology). [Arabidopsis thaliana]
                    302385
Seq. No.
                    fC-zmro700835853r1
Seq. ID
Method
                   BLASTX
                   g3688600
NCBI GI
                    271
BLAST score
                    7.0e-24
E value
                    58
Match length
% identity
                   84
                    (AB009030) beta-Amyrin Synthase [Panax ginseng]
NCBI Description
Seq. No.
                    302386
Seq. ID
                    fC-zmro700835903f1
                   BLASTX
Method
                    q322794
NCBI GI
BLAST score
                    170
                    7.0e-25
E value
```

Match length 85
% identity 74
% CDT Description HTD

NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

potato >gi_21599_emb_CAA79357_ (Z18924)

UTP--glucose-1-phosphate uridylyltransferase [Solanum

% identity

NCBI Description

thaliana]



tuberosum]

```
302387
Seq. No.
                  fC-zmro700836164f1
Seq. ID
Method
                  BLASTX
                  q4138853
NCBI GI
BLAST score
                   558
                   1.0e-57
E value
Match length
                   108
% identity
                  (AF098272) ethylene response sensor [Vigna radiata]
NCBI Description
Seq. No.
                   302388
                   fC-zmro700836189f1
Seq. ID
                   BLASTX
Method
                   q1351856
NCBI GI
                   629
BLAST score
                   7.0e-66
E value
Match length
                   139
                   83
% identity
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                   (ACONITASE) > gi_868003_dbj_BAA06108_ (D29629) \ aconitase
                   [Cucurbita sp.]
Seq. No.
                   302389
                   fC-zmse700613632y1
Seq. ID
                   BLASTX
Method
                   g1708025
NCBI GI
BLAST score
                   300
E value
                   3.0e-27
Match length
                   121
                   54
% identity
                   GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+]
NCBI Description
                   >gi 840731 emb CAA56125 (X79677) glycerol-3-phosphate
                   dehydrogenase (NAD+) [Cuphea lanceolata]
Seq. No.
                   302390
                   fC-zmse700617823a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3660471
BLAST score
                   363
                   5.0e-35
E value
                   92
Match length
                   82
% identity
                   (AJ001809) succinate dehydrogenase flavoprotein alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   302391
Seq. No.
                   fC-zmse700673147a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4585879
BLAST score
                   695
                   2.0e-73
E value
Match length
                   166
```

42679

(AC005850) Highly Simlilar to Mlo proteins [Arabidopsis



```
302392
Seq. No.
                  fC-zmse700673642a1
Seq. ID
                  BLASTX
Method
                  g1001379
NCBI GI
                  428
BLAST score
                  4.0e-42
E value
                  166
Match length
% identity
                   (D64006) aspartate beta-semialdehyde dehydrogenese
NCBI Description
                   [Synechocystis sp.]
Seq. No.
                   302393
                   fC-zmse700799143b1
Seq. ID
                   BLASTX
Method
                   g2065531
NCBI GI
                   670
BLAST score
                   2.0e-70
E value
                   178
Match length
                   73
% identity
                  (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   fC-zmse700806251b1
Seq. ID
                   BLASTX
Method
                   q2852449
NCBI GI
BLAST score
                   775
                   8.0e-83
E value
                   173
Match length
                   86
% identity
                   (D88207) protein kinase [Arabidopsis thaliana] >gi_2947061
NCBI Description
                   (AC002521) putative protein kinase [Arabidopsis thaliana]
                   302395
Seq. No.
                   fC-zmse700806251c1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2852447
                   243
                                Tata
BLAST score
                   1.0e-20
E value
Match length
                   92
% identity
                   (D88206) protein kinase [Arabidopsis thaliana]
NCBI Description
                   302396
Seq. No.
                   fC-zmse700806549b1
Seq. ID
                   BLASTX
Method
                   g2499115
NCBI GI
BLAST score
                   495
                   4.0e-50
E value
                   133
Match length
 % identity
                   73
                   VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi 1835788
NCBI Description
                    (U86662) VPS41 [Lycopersicon esculentum]
```

Seq. ID fC-zmse700836372f1

Method BLASTN



```
NCBI GI
                  g3510343
BLAST score
                  41
                  9.0e-14
E value
Match length
                  89
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  302398
Seq. ID
                  fC-zmse700836404f1
Method
                  BLASTX
NCBI GI
                  q4539944
BLAST score
                  444
E value
                  1.0e-47
                  143
Match length
                  65
% identity
NCBI Description
                  (AF133841) aldose reductase ALDRXV4 [Xerophyta viscosa]
                  302399
Seq. No.
Seq. ID
                  fC-zmse700836407f1
Method
                  BLASTX
NCBI GI
                  q4539457
BLAST score
                  358
                  4.0e-34
E value
Match length
                  78
% identity
                  82
NCBI Description
                  (AL049500) heat shock transcription factor-like protein
                   [Arabidopsis thaliana]
                  302400
Seq. No.
Seq. ID
                  fC-zmse700836661f1
Method
                  BLASTX
NCBI GI
                  g1076318
BLAST score
                  406
                  9.0e-40
E value
Match length
                  126
% identity
                  41
NCBI Description
                  dihydrolipoamide S-acetyltransferase (EC 2.3.1.12)
                  precursor - Arabidopsis thaliana (fragment)
                  >gi 559395 emb CAA86300 (Z46230) dihydrolipoamide
                  acetyltransferase (E2) subunit of PDC [Arabidopsis
                  thaliana]
                  302401
Seq. No.
                  fC-zmse700836744f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1679794
BLAST score
                  265
                  4.0e-23
E value
Match length
                  111
% identity
NCBI Description
                  (U77627) Allele: hi2 [Danio rerio]
```

Seq. ID fC-zmse700836945f1

Method BLASTX NCBI GI g4105633

```
BLAST score
E value
                   7.0e-33
Match length
                   100
% identity
                   71
                   (AF048982) putative ethylene receptor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   302403
                   fC-zmse700837239a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1906830
BLAST score
                   273
E value
                   2.0e-34
Match length
                   103
                   78
% identity
NCBI Description (Y11829) heat shock protein [Arabidopsis thaliana]
Seq. No.
                   302404
                   fC-zmse700837648f1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4522003
BLAST score
                   420
E value
                   2.0e-41
Match length
                   107
                   77
% identity
NCBI Description
                  (AC007069) putative protein kinase [Arabidopsis thaliana]
                   302405
Seq. No.
Seq. ID
                   fC-zmse700837648r1
Method
                   BLASTX
NCBI GI
                   g4220469
BLAST score
                   152
E value
                   6.0e-10
Match length
                   62
% identity
                   50
                   (AC006069) putative receptor protein kinase, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   302406
Seq. ID
                   fC-zmse700837723f1
Method
                   BLASTX
NCBI GI
                   g3641252
BLAST score
                   187
                   2.0e-14
E value
                   70
Match length
                   49
% identity
                   (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                   domestica]
```

Seq. ID fC-zmse700837891g1 Method BLASTX

Method BLASTX
NCBI GI g82211
BLAST score 331
E value 3.0e-38
Match length 117
% identity 78



```
NCBI Description rpoC protein homolog - common tobacco chloroplast
                  302408
Seq. No.
                   fC-zmse700837911f1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1170878
BLAST score
                   493
E value
                   2.0e-50
                   104
Match length
                   90
% identity
                  MALATE SYNTHASE, GLYOXYSOMAL (MS) >gi 170026 (L01629)
NCBI Description
                  malate synthase [Glycine max]
                   302409
Seq. No.
                   fC-zmse700838355f1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q576509
BLAST score
                   236
                   4.0e-25
E value
                   144
Match length
                   54
% identity
NCBI Description (L36857) GTP-binding protein [Pisum sativum]
Seq. No.
                   302410
                   fC-zmse700838355r1
Seq. ID
Method
                   BLASTX
                   q576509
NCBI GI
BLAST score
                   336
E value
                   1.0e-31
                   74
Match length
                   88
% identity
                  (L36857) GTP-binding protein [Pisum sativum]
NCBI Description
Seq. No.
                   302411
Seq. ID
                   fC-zmse700838612f1
Method
                   BLASTX
NCBI GI
                   q1362162
BLAST score
                   370
E value
                   9.0e-36
                   93
Match length
% identity
                   80
                   beta-glucosidase BGQ60 precursor - barley >gi 804656
NCBI Description
                   (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No. Seq. ID
                   302412
                   fC-zmse700838612r1
Method
                   BLASTX
NCBI GI
                   g1362162
BLAST score
                   338
                   1.0e-31
E value
                   84
Match length
                   69
% identity
                   beta-glucosidase BGQ60 precursor - barley >gi_804656
NCBI Description
                   (L41869) beta-glucosidase [Hordeum vulgare]
```

302413

fC-zmse700838722f1

Seq. No.

Seq. ID

Seq. ID

302418

fC-zmst700334018a4



```
BLASTX
Method
                  q3253165
NCBI GI
                  181
BLAST score
                  2.0e-13
E value
                  108
Match length
% identity
                  42
NCBI Description (AF015608) SR protein [Homo sapiens]
                  302414
Seq. No.
                  fC-zmse700838868f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q119745
BLAST score
                  240
                  3.0e-20
E value
Match length
                  119
% identity
                   45
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi_67242_pir__PAWTF fructose-bisphosphatase (EC 3.1.3.11)
                  precursor, chloroplast - wheat >gi_21737_emb_CAA30612_
                   (X07780) pre-FBPase [Triticum aestivum]
                   >gi_21741_emb_CAA37908_ (X53957) fructose-bisphosphatase
                   [Triticum aestivum]
                   302415
Seq. No.
                   fC-zmse700839369f1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245066
BLAST score
                   438
                   2.0e-43
E value
Match length
                   134
% identity
                   59
NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]
                   302416
Seq. No.
                   fC-zmse700839380f1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1168471
BLAST score
                   203
                   2.0e-16
E value
Match length
                   56
                   75
% identity
NCBI Description PROTEIN KINASE APK1B
                   302417
Seq. No.
                   fC-zmst1700336826d1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3169175
BLAST score
                   163
                   3.0e-11
E value
                   51
Match length
                   63
% identity
                   (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                   thaliana]
```

```
BLASTX
Method
NCBI GI
                  q4587513
BLAST score
                  147
                  7.0e-10
E value
                  36
Match length
                  78
% identity
                   (AC007060) Contains eukaryotic protein kinase domain
NCBI Description
                  PF 00069. [Arabidopsis thaliana]
                  302419
Seq. No.
Seq. ID
                  fC-zmst700336269f1
Method
                  BLASTN
NCBI GI
                  q6598495
                   98
BLAST score
                   3.0e-48
E value
                   106
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T10J7 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   302420
Seq. No.
                   fC-zmst700336816f1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g16473
BLAST score
                   271
                   1.0e-151
E value
Match length
                   331
                   95
% identity
NCBI Description Arabidopsis thaliana 25S-18S ribosomal DNA spacer
                   302421
Seq. No.
                   fC-zmst700457222a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3687654
BLAST score
                   310
                   2.0e-28
E value
Match length
                   107
                   62
% identity
                   (AF047975) putative ethylene receptor; ETR2 [Arabidopsis
NCBI Description
                   thaliana]
                   302422
Seq. No.
                   fC-zmst700619814a1
Seq. ID
Method
                   BLASTX
                   g553076
NCBI GI
BLAST score
                   312
E value
                   8.0e-29
Match length
                   97
% identity
                   65
                   (L08589) alcohol dehydrogenase 1 [Zea mays]
NCBI Description
```

fC-zmst700620908d1 Seq. ID

BLASTN Method g4098966 NCBI GI BLAST score 63

8.0e-27 E value



```
Match length
                  92
% identity
NCBI Description Glycine max putative reistance gene analog genomic sequence
                  302424~
Seq. No.
Seq. ID
                  fC-zmst700620948a1
                  BLASTX
Method
                  g4510402
NCBI GI
BLAST score
                  464
                  1.0e-46
E value
                  127
Match length
                  72
% identity
NCBI Description (AC006587) putative AP2 domain [Arabidopsis thaliana]
                  302425
Seq. No.
Seq. ID
                  fC-zmst700621688a1
                  BLASTX
Method
                  g4210330
NCBI GI
                  547
BLAST score
                  2.0e-58
E value
                  129
Match length
% identity
                  86
                   (ÅJ223802) 2-oxoglutarate dehydrogenase, El subunit
NCBI Description
                   [Arabidopsis thaliana]
                  302426
Seq. No.
                  fC-zmst700621764d1
Seq. ID
Method
                  BLASTX
                  g1052973
NCBI GI
                  362
BLAST score
E value
                  2.0e-34
Match length
                  87
% identity
                  80
NCBI Description (U37838) fructokinase [Beta vulgaris]
                  302427
Seq. No.
Seq. ID
                  fC-zmst700621904z1
Method
                  BLASTX
                  g1076723
NCBI GI
BLAST score
                  165
E value
                   1.0e-11
Match length
                   43
                   67
% identity
                  Ids2 protein - barley >gi 285634 dbj_BAA03647_ (D15051)
NCBI Description
                   ids2 [Hordeum vulgare]
                   302428
Seq. No.
Seq. ID
                   fC-zmst700621982d1
                  BLASTN
Method
NCBI GI
                   q791097
BLAST score
                   148
E value
                   1.0e-77
                   336
Match length
```

% identity

87

NCBI Description P.vulgaris plsB mRNA

```
fC-zmst700622384a1
Seq. ID
                  BLASTX
Method
                  g4100433
NCBI GI
                  290
BLAST score
E value
                  4.0e-26
Match length
                  113
% identity
                  (AF000378) beta-glucosidase [Glycine max]
NCBI Description
                  302430
Seq. No.
                  fC-zmst700622484a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4467158
                  258
BLAST score
                  2.0e-22
E value
                  102
Match length
% identity
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                  302431
Seq. No.
                  fC-zmst700623156a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352186
BLAST score
                  394
                  2.0e-38
E value
Match length
                  126
% identity
                  ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)
NCBI Description
                   (CYTOCHROME P450 74) >gi 404866 (U00428) allene oxide
                  synthase [Linum usitatissimum]
                  302432
Seq. No.
Seq. ID
                  fC-zmst700623179a1
Method
                  BLASTX
NCBI GI
                  g4098129
                  623
BLAST score
                  5.0e-65
E value
                  164
Match length
% identity
                  71
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
                   302433
Seq. No.
                   fC-zmst700623908a1
Seq. ID
Method
                  BLASTX
                  g1351945
NCBI GI
BLAST score
                  590
                   3.0e-61
E value
                   134
Match length
                   79
% identity
                  FLORAL HOMEOTIC PROTEIN APETALA2 >gi 533709 (U12546)
NCBI Description
                  APETALA2 protein [Arabidopsis thaliana]
                   >gi 2464888_emb_CAB16765.1_ (Z99707) APETALA2 protein
```

Seq. ID fC-zmst700624459a3 Method BLASTX

Seq. No.

302434

42687

[Arabidopsis thaliana]

```
NCBI GI
                  q3641252
BLAST score
                  140
                  5.0e-09
E value
                  35
Match length
                  77
% identity
                  (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                  domestica]
                  302435
Seq. No.
                  fC-zmst700808401a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2498887
BLAST score
                  159
                  7.0e-11
E value
                  74
Match length
                   43
% identity
                  3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID
NCBI Description
                   5-ALPHA-REDUCTASE 1) (SR TYPE 1) >gi_999036_bbs_164548
                   (S77162) steroid 5 alpha-reductase type 1 isoenzyme, SR
                   type 1 [Cynomolgus monkeys, prostate, Peptide, 263 aa]
                   [Macaca fascicularis]
Seq. No.
                   302436
Seq. ID
                   fC-zmst700808407a1
                   BLASTX
Method
                   q4206110
NCBI GI
                   185
BLAST score
                   1.0e-13
E value
Match length
                   125
                   49
% identity
NCBI Description (AF097661) cytochrome [Mesembryanthemum crystallinum]
Seq. No.
                   302437
                   fC-zmst700888153a1
Seq. ID
Method
                   BLASTX
                   g2648032
NCBI GI
BLAST score
                   751
E value
                   5.0e-80
Match length
                   164
                   77
% identity
                  (AJ001374) alpha-glucosidase [Solanum tuberosum]
NCBI Description
                   302438
Seq. No.
                   fC-zmst700888545d1
Seq. ID
                   BLASTX
Method
                   g633678
NCBI GI
BLAST score
                   227
E value
                   9.0e-19
                   47
Match length
% identity
                   98
NCBI Description (X83500) ADP-glucose pyrophosphorylase [Spinacia oleracea]
                   302439
Seq. No.
                   fC-zmst700889690a1
Seq. ID
                   BLASTX
Method
```

g2388985

295

NCBI GI BLAST score

BLAST score

% identity

E value Match length 147 8.0e-10

30 87

```
1.0e-26
E value
                  109
Match length
% identity
                  52
                 (Z98980) transcription factor [Schizosaccharomyces pombe]
NCBI Description
                  302440
Seq. No.
                  fC-zmst700892444a1
Seq. ID
                  BLASTX
Method
                  g4006829
NCBI GI
                  614
BLAST score
                  6.0e-64
E value
                  164
Match length
% identity
                  (AC005970) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  302441
Seq. No.
                  fC-zmst700894694a1
Seq. ID
                  BLASTX
Method
                  g4204303
NCBI GI
BLAST score
                   482
                   2.0e-48
E value
                  109
Match length
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   302442
Seq. No.
                   fC-zmst700894873d1
Seq. ID
                   BLASTX
Method
                   g2501353
NCBI GI
                   188
BLAST score
                   3.0e-14
E value
                   41
Match length
                   93
% identity
                  TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir__S54300
NCBI Description
                   transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum
                   (fragment) >gi_664901_emb_CAA86607_ (Z46646) transketolase
                   [Craterostigma plantagineum]
                   302443
Seq. No.
                   fdz701158323.h1
Seq. ID
                   BLASTN
Method
                   g312178
NCBI GI
                   46
BLAST score
                   6.0e-17
E value
Match length
                   108
                   85
% identity
                   Z.mays GapC2 gene
NCBI Description
                   302444
 Seq. No.
                   fdz701158370.hl
 Seq. ID
                   BLASTX
Method
                   q4512694
NCBI GI
```

```
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]
                  302445
Seq. No.
```

fdz701158383.h1 Seq. ID Method BLASTX g2129742 NCBI GI BLAST score 242 6.0e-21 E value 63 Match length % identity

stress-induced protein OZI1 precursor - Arabidopsis NCBI Description

thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related

protein [Arabidopsis thaliana] >gi 2252869 (AF013294) No

definition line found [Arabidopsis thaliana]

Seq. No. 302446

fdz701158385.h1 Seq. ID

BLASTX Method q2982295 NCBI GI 254 BLAST score E value 2.0e-22 Match length 55 % identity

(AF051232) probable 60S ribosomal protein L31 [Picea NCBI Description

mariana]

Seq. No. 302447

fdz701158405.h1 Seq. ID

BLASTX Method g2897595 NCBI GI 184 BLAST score E value 4.0e-14 52 Match length % identity 60

(AJ224162) lipoic acid synthetase [Homo sapiens] NCBI Description

Seq. No. 302448

fdz701158413.hl Seq. ID

BLASTN Method g453669 NCBI GI BLAST score 50 E value 1.0e-19 58 Match length 97 % identity

NCBI Description Maize heat shock protein 26 (HSP26) mRNA, complete cds

302449 Seq. No.

fdz701158474.h1 Seq. ID

BLASTX Method g1362067 NCBI GI BLAST score 363 4.0e-35 E value 78 Match length 94 % identity

NCBI Description small GTP-binding protein - garden pea



>gi_871508_emb_CAA90082_ (Z49902) small GTP-binding protein [Pisum sativum]

Seq. No. 302450 Seq. ID fdz701158519.hl Method BLASTX

g2500347 NCBI GI 152 BLAST score 3.0e-10 E value 56 Match length % identity 59

NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG NCBI Description

>gi 3878691_emb CAA90127 (Z49911) similar to ribosomal protein (L7AE family); cDNA EST EMBL:D73957 comes from this gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST EMBL: D74077 comes from this gene; cDNA EST EMBL: D71393

comes from this gene; cD

Seq. No. 302451

fdz701158569.hl Seq. ID

BLASTX Method q2244994 NCBI GI BLAST score 145 E value 1.0e-09 76 Match length 37 % identity

(Z97341) similarity to isp4 protein - fission yeast NCBI Description

[Arabidopsis thaliana]

302452 Seq. No.

fdz701158611.h1 Seq. ID

Method BLASTX NCBI GI g3360289 BLAST score 256 E value 1.0e-22 76 Match length % identity 67

(AF023164) leucine-rich repeat transmembrane protein kinase NCBI Description

1 [Zea mays]

Seq. No. 302453

fdz701158613.hl Seq. ID

Method BLASTX NCBI GI g2500378 BLAST score 326 9.0e-31E value Match length 69 % identity 86

NCBI Description 60S RIBOSOMAL PROTEIN L37

Seq. No. Seq. ID 302454

fdz701158659.hl

BLASTX Method NCBI GI g3668086 206 BLAST score 7.0e-17 E value 72 Match length



% identity 64
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 302455

Seq. ID fdz701158796.hl

Method BLASTX
NCBI GI 94006892
BLAST score 221
E value 2.0e-18
Match length 70
% identity 56

NCBI Description (Z99708) glucosyltransferase-like protein [Arabidopsis

thaliana]

302456

Seq. No.

Seq. ID fdz701158805.h1

Method BLASTX
NCBI GI g4006831
BLAST score 143
E value 3.0e-09
Match length 80
% identity 39

NCBI Description (AC005970) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 302457

Seq. ID fdz701158835.h1

Method BLASTX
NCBI GI g4506183
BLAST score 332
E value 2.0e-31
Match length 70
% identity 90

NCBI Description proteasome (prosome, macropain) subunit, alpha type, 3

>gi 130859 sp P25788 PRC8 HUMAN PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi 67730 pir SNHUC8 multicatalytic endopeptidase complex (EC 3.4.99.46) chain C8 - human >gi 220028 dbj BAA00659 (D00762) proteasome subunit C8

[Homo sapiens]

Seq. No. 302458

Seq. ID fdz701158873.h1

Method BLASTX
NCBI GI g417216
BLAST score 380
E value 5.0e-37
Match length 83
% identity 90

NCBI Description KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)

>gi 476345 pir A41919 kinesin heavy chain - human

>gi 34083 emb CAA46703 (X65873) kinesin heavy chain [Homo

sapiens]

Seq. No. 302459

Seq. ID fdz701158918.h2

Method BLASTX



```
NCBI GI
                  q729366
                  228
BLAST score
                  3.0e-19
E value
Match length
                  59
                  73
% identity
                  PHOSPHATIDYLSERINE DECARBOXYLASE PROENZYME 1 PRECURSOR
NCBI Description
                  >gi_542338_pir__A48053 phosphatidylserine decarboxylase (EC
                  4.1.1.65) - yeast (Saccharomyces cerevisiae) >gi_414845
                  (L20973) phosphatidylserine decarboxylase [Saccharomyces
                  cerevisiae] >gi 1302147 emb CAA96063 (Z71448) ORF YNL169c
                  [Saccharomyces cerevisiae]
Seq. No.
                  302460
                  fdz701158929.h2
Seq. ID
                  BLASTX
Method
                  q423988
NCBI GI
                  192
BLAST score
E value
                  6.0e-15
                  71
Match length
                  56
% identity
                  serine/threonine kinase homolog PRO25 - Arabidopsis
NCBI Description
                  thaliana >gi 166813 (L04999) serine threonine kinase
                   [Arabidopsis thaliana]
                  302461
Seq. No.
                   fdz701158984.h2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3228517
BLAST score
                  243
                   6.0e-21
E value
Match length
                  85
                   58
% identity
NCBI Description (AF007788) ETTIN [Arabidopsis thaliana]
Seq. No.
                   302462
                   fdz701158985.h2
Seq. ID
Method
                  BLASTN
                   q533251
NCBI GI
                   129
BLAST score
                   2.0e-66
E value
                   129
Match length
                   100
% identity
                   Zea mays (clone pSM8) sucrose synthase 2 (Sus1) gene,
NCBI Description
                   complete cds
                   302463
Seq. No.
                   fdz701158995.h2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22223
                   70
BLAST score
                   3.0e-31
E value
                   117
Match length
```

92 % identity

Maize cab-1 gene for chlorophyll a/b-binding protein NCBI Description

302464 Seq. No.

fdz701159002.h1 Seq. ID

```
BLASTX
Method
                  g4490330
NCBI GI
                  172
BLAST score
                  1.0e-12
E value
                  40
Match length
                  78
% identity
                   (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  302465
Seq. No.
                  fdz701159041.h1
Seq. ID
Method
                  BLASTN
                  q439712
NCBI GI
                  120
BLAST score
                  2.0e-61
E value
                  128
Match length
                   98
% identity
                  Human mRNA for precursor of P100 serine protease of
NCBI Description
                  Ra-reactive factor, complete cds
                   302466
Seq. No.
Seq. ID
                   fdz701159048.h1
Method
                  BLASTN
                   g4185305
NCBI GI
                   105
BLAST score
                   3.0e-52
E value
                   213
Match length
                   96
% identity
                   Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                   protein, polyprotein, and copia protein genes, complete
                   cds; and unknown genes
                   302467
Seq. No.
                   fdz701159080.hl
Seq. ID
                   BLASTN
Method
                   g516248
NCBI GI
                   53
BLAST score
                   4.0e-21
E value
                   126
Match length
                   88
% identity
                   A.thaliana gene for porphobilinogen deaminase
NCBI Description
                   302468
Seq. No.
                   fdz701159089.h1
Seq. ID
                   BLASTN
Method
                   g4505256
NCBI GI
BLAST score
                   68
                   4.0e-30
E value
                   76
Match length
```

97 % identity

Homo sapiens moesin (MSN) mRNA NCBI Description

>gi_188625_gb_M69066_HUMMOESIN Human moesin mRNA, complete

cds

302469 Seq. No.

fdz701159095.hl Seq. ID

```
Method
                  BLASTX
NCBI GI
                  g3928095
BLAST score
                  372
E value
                  4.0e-36
Match length
                  85
% identity
                  80
                  (AC005770) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  302470
Seq. No.
                  fdz701159541.h1
Seq. ID
Method
                  BLASTN
                  g4557596
NCBI GI
BLAST score
                  159
E value
                  2.0e-84
Match length
                  239
                  92
% identity
                  Homo sapiens gamma filamin (FLNC) mRNA
NCBI Description
                  >gi 4218954 gb AF089841 AF089841 Homo sapiens gamma-filamin
                   (ABPL) mRNA, complete cds
Seq. No.
                  302471
                  fdz701159557.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g598826
BLAST score
                  128
E value
                  8.0e-66
Match length
                  151
                  96
% identity
                  Human HepG2 3' region MboI cDNA, clone hmd4f06m3
NCBI Description
                   302472
Seq. No.
Seq. ID
                  fdz701159606.h1
Method
                  BLASTX
NCBI GI
                  g1082356
                  279
BLAST score
                  3.0e-25
E value
Match length
                  78
                  74
% identity
                  epidermal autoantigen 450K (clone pE450-C/D) - human
NCBI Description
                   (fragment)
Seq. No.
                   302473
Seq. ID
                   fdz701159648.hl
Method
                  BLASTN
NCBI GI
                  q3873185
BLAST score
                  44
                  1.0e-15
E value
Match length
                  68
                  91
% identity
                  Homo sapiens chromosome 17, clone hRPC.906 A 24, complete
NCBI Description
                  sequence [Homo sapiens]
                  302474
Seq. No.
                  fdz701159654.hl
Seq. ID
```

Method BLASTX

NCBI GI g3036802 BLAST score 151



```
3.0e-10
E value
Match length
                  39
% identity
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                  >qi 3805864 emb CAA21484_ (AL031986) putative protein
                   [Arabidopsis thaliana]
                   302475
Seq. No.
                   fdz701159655.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3746127
BLAST score
                   245
E value
                   4.0e-21
                   59
Match length
% identity
                   (U76253) E25B protein [Mus musculus]
NCBI Description
                   302476
Seq. No.
                   fdz701159660.h1
Seq. ID
                   BLASTX
Method
                   q3176686
NCBI GI
                   208
BLAST score
E value
                   7.0e-29
Match length
% identity
                   71
                   (AC003671) Similar to high affinity potassium transporter,
NCBI Description
                   HAK1 protein gb_U22945 from Schwanniomyces occidentalis.
                   [Arabidopsis thaliana]
                   302477
Seq. No.
                   fdz701159674.h1
Seq. ID
Method
                   BLASTX
                   g695411
NCBI GI
BLAST score
                   311
                   6.0e-29
E value
Match length
                   62
% identity
                   100
                   (D49475) glutamate dehydrogenase [Zea mays]
NCBI Description
                   302478
Seq. No.
                   fdz701159693.h1
Seq. ID
                   BLASTX
Method
                   g1841546
NCBI GI
                   266
BLAST score
                   1.0e-23
E value
                   63
Match length
% identity
                   28
                   (U89337) tenascin X [Homo sapiens]
NCBI Description
                   302479
Seq. No.
                   fdz701159701.h2
Seq. ID
                   BLASTN
Method
```

Method BLASIN
NCBI GI g2822137
BLAST score 66
E value 5.0e-29
Match length 144
% identity 88



NCBI Description Human Chromosome X, complete sequence [Homo sapiens] 302480 Seq. No. fdz701159702.h2 Seq. ID BLASTX Method q2827631 NCBI GI BLAST score 259 9.0e-23 E value 67 Match length 73 % identity NCBI Description (AL021636) putative protein [Arabidopsis thaliana] Seq. No. 302481 fdz701159740.h2 Seq. ID BLASTN Method g2995989 NCBI GI BLAST score 44 1.0e-15 E value Match length 68 91 % identity NCBI Description Arabidopsis thaliana dormancy-associated protein (DRM1) mRNA, complete cds Seq. No. 302482 fdz701159769.h2 Seq. ID Method BLASTX NCBI GI g202719 183 BLAST score 3.0e-19 E value Match length 60 87 % identity NCBI Description (M96160) adenylyl cyclase type VI [Rattus norvegicus] Seq. No. 302483 fdz701159825.h1 Seq. ID Method BLASTN NCBI GI q3043553 85 BLAST score 3.0e-40 E value Match length 201 % identity NCBI Description Homo sapiens mRNA for KIAA0515 protein, partial cds 302484 Seq. No. Seq. ID fdz701159840.hl BLASTN Method q598826 NCBI GI BLAST score 60 E value 3.0e-25 80 Match length % identity 94 NCBI Description Human HepG2 3' region MboI cDNA, clone hmd4f06m3 302485 Seq. No. fdz701159865.h1 Seq. ID

42697

BLASTN

g2133864

Method

NCBI GI



```
BLAST score
                  2.0e-63
E value
                  180
Match length
                  92
% identity
                  Genomic sequence from Human 13, complete sequence [Homo
NCBI Description
                  302486
Seq. No.
                  fdz701159877.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2494132
BLAST score
                  183
E value
                   7.0e-14
                   74
Match length
                   42
% identity
                   (AC002376) Contains similarity to human dimethylaniline
NCBI Description
                  monooxygenase (gb_M64082). [Arabidopsis thaliana]
                   302487
Seq. No.
                   fdz701160317.hl
Seq. ID
Method
                   BLASTX
                   q2924779
NCBI GI
BLAST score
                   167
E value
                   7.0e-12
                   87
Match length
% identity
                   47
                   (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
NCBI Description
                   thaliana] >gi_2981616_dbj_BAA25248_ (AB008854)
                   3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                   >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA
                   thiolase [Arabidopsis thaliana]
                   302488
Seq. No.
                   fdz701160329.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3395439
BLAST score
                   181
                   1.0e-13
E value
                   47
Match length
% identity
                   77
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   302489
Seq. No.
                   fdz701160335.h1
Seq. ID
Method
                   BLASTN
                   g435458
NCBI GI
BLAST score
                   79
                   1.0e-36
E value
Match length
                   183
                   87
% identity
NCBI Description
```

Proso millet gene for aspartate aminotransferase, complete

302490 Seq. No.

fdz701160361.hl Seq. ID

BLASTX Method g3785989 NCBI GI

```
BLAST score
                  1.0e-27
E value
                   92
Match length
% identity
                   62
                   (AC005560) unknown protein [Arabidopsis thaliana]
NCBI Description
                   302491
Seq. No.
                   fdz701160362.h1
Seq. ID
                   BLASTN
Method
                   q1418758
NCBI GI
BLAST score
                   77
```

E value 2.0e-35
Match length 224
% identity 84

NCBI Description H.sapiens mRNA for AFX protein

 Seq. No.
 302492

 Seq. ID
 fdz701160396.h1

 Method
 BLASTX

NCBI GI g4508041
BLAST score 237
E value 3.0e-20
Match length 73
% identity 62

NCBI Description zinc finger protein 91 (HPF7, HTF10)

>gi_549839_sp_Q05481_ZN91_HUMAN ZINC FINGER PROTEIN 91
(ZINC FINGER PROTEIN HTF10) (HPF7) >gi_479766_pir__S35305
finger protein ZNF91 - human >gi_186774 (L11672) zinc

finger protein [Homo sapiens]

Seq. No. 302493

Seq. ID fdz701160405.h1

Method BLASTX
NCBI GI g1911550
BLAST score 317
E value 1.0e-29
Match length 79
% identity 80

NCBI Description (S80867) smooth muscle myosin light chain kinase, smMLCK

{C-terminal} [sheep, myometrial tissue, day 127 of gestation, Peptide Partial, 438 aa] [Ovis aries]

Seq. No. 302494

Seq. ID fdz701160489.h1

Method BLASTX
NCBI GI g3928091
BLAST score 219
E value 3.0e-18
Match length 72
% identity 56

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 302495

Seq. ID fdz701160496.hl

Method BLASTX
NCBI GI g631502
BLAST score 147

Match length

% identity

77



```
E value
                  6.0e-10
Match length
                  54
% identity
                  finger protein HZF9, Krueppel-related - human (fragment)
NCBI Description
                  >gi 498736_emb_CAA55532_ (X78932) zinc finger protein [Homo
                  sapiens]
                   302496
Seq. No.
                   fdz701160503.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                   q479413
BLAST score
                   352
E value
                   1.0e-33
                   97
Match length
                   72
% identity
                  myosin-like protein - Arabidopsis thaliana
NCBI Description
                   302497
Seq. No.
                   fdz701160593.hl
Seq. ID
                   BLASTX
Method
                   g3885515
NCBI GI
                   330
BLAST score
                   4.0e-31
E value
Match length
                   64
% identity
                   (AF084202) similar to ribosomal protein S26 [Medicago
NCBI Description
                   sativa]
                   302498
Seq. No.
                   fdz701160651.hl
Seq. ID
Method
                   BLASTX
                   q4455293
NCBI GI
                   161
BLAST score
E value
                   3.0e-11
                   69
Match length
% identity
                   51
                   (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                   302499
Seq. No.
                   fdz701160659.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3873182
BLAST score
                   143
E value
                   9.0e-75
                   273
Match length
                   89
% identity
                   Homo sapiens chromosome 17, clone hRPK.235_I_10, complete
NCBI Description
                   sequence [Homo sapiens]
                   302500
 Seq. No.
                   fdz701160738.h1
 Seq. ID
                   BLASTX
Method
                   g132819
 NCBI GI
                   260
BLAST score
                   6.0e-23
 E value
                   64
```



```
50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24)
NCBI Description
                  >gi 71307_pir__R5PM24 ribosomal protein L24 precursor,
                  chloroplast - garden pea >gi_20873_emb_CAA32185_ (X14020)
                  CL24 ribosomal preprotein (AA -39 to 155) [Pisum sativum]
                  302501
Seq. No.
                  fdz701160780.h1
Seq. ID
Method
                  BLASTN
                  g2921303
NCBI GI
                  176
BLAST score
E value
                  2.0e-94
Match length
                  240
% identity
                  Zea mays herbicide safener binding protein (SBP1) mRNA,
NCBI Description
                  complete cds
                  302502
Seq. No.
Seq. ID
                  fdz701160796.h1
                  BLASTX
Method
                  q2130022
NCBI GI
                   250
BLAST score
                   7.0e-22
E value
Match length
                   58
% identity
                   76
                  aldose reductase homolog - wild oat >gi 1155213 (U21747)
NCBI Description
                   aldose reductase-related protein [Avena fatua]
                   >qi 1587923 prf 2207360A aldose reductase [Avena fatua]
Seq. No.
                   302503
                   fdz701160819.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2058282
BLAST score
                   218
E value
                   5.0e-18
Match length
                   49
% identity
                   84
                  (X97377) atranbpla [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   302504
                   fdz701160826.h1
Seq. ID
Method
                   BLASTX
                   g4337175
NCBI GI
BLAST score
                   215
E value
                   1.0e-17
Match length
                   67
% identity
                   63
                   (AC006416) ESTs gb_T20589, gb T04648, gb AA597906,
NCBI Description
                   gb T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                   gb R90004, gb T45020, gb T42457, gb T20921, gb AA042762 and
                   gb_AA720210 come from this gene. [Arabidopsis thaliana]
                   302505
Seq. No.
                   fdz701160833.h1
Seq. ID
                   BLASTX
```

Method BLASTX
NCBI GI g134194
BLAST score 340
E value 2.0e-32



51

Match length

NCBI Description

% identity

```
Match length
                   89
% identity
                  STRESS-INDUCED PROTEIN SAM22 >gi_99918_pir__S20518
NCBI Description
                  hypothetical protein - soybean >gi_18744_emb_CAA42646_
                   (X60043) ORF [Glycine max]
                   302506
Seq. No.
                   fdz701160857.h1
Seq. ID
Method
                   BLASTX
                   q3063459
NCBI GI
BLAST score
                   142
E value
                   3.0e-09
Match length
                   60
                   48
% identity
                   (AC003981) F22013.21 [Arabidopsis thaliana]
NCBI Description
                   302507
Seq. No.
                   fdz701160861.h1
Seq. ID
Method
                   BLASTX
                   g3242729
NCBI GI
BLAST score
                   166
                   2.0e-15
E value
Match length
                   55
% identity
                   80
                   (AC003040) curly leaf protein (polycomb-group) [Arabidopsis
NCBI Description
                   thaliana]
                   302508
Seq. No.
                   fdz701160914.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539662
BLAST score
                   318
E value
                   1.0e-29
Match length
                   88
                   69
% identity
                   (AF061282) polyprotein [Sorghum bicolor]
NCBI Description
                   302509
Seq. No.
                   fdz701160915.h1
Seq. ID
                   BLASTN
Method
                   g22504
NCBI GI
                   94
BLAST score
                   1.0e-45
E value
                   94
Match length
                   100
% identity
                   Maize DNA for U6 small nuclear RNA (snRNA)
NCBI Description
                   302510
Seq. No.
                   fdz701160925.h1
Seq. ID
                   BLASTX
Method
                   g2431769
NCBI GI
                   164
BLAST score
                   1.0e-11
E value
```

42702

(U62752) acidic ribosomal protein Pla [Zea mays]

```
Seq. No.
Seq. ID
                  fdz701160926.hl
                  BLASTX
Method
                  g2828293
NCBI GI
                  179
BLAST score
                  3.0e-13
E value
                  50
Match length
                  72
% identity
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]
                  302512
Seq. No.
                   fdz701160956.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q452593
                   311
BLAST score
                   6.0e-29
E value
                   84
Match length
                   69
% identity
                  (D21814) ORF [Lilium longiflorum]
NCBI Description
                   302513
Seq. No.
                   fdz701161033.h1
Seq. ID
Method
                   BLASTX
                   g4249409
NCBI GI
BLAST score
                   169
                   2.0e-12
E value
                   60
Match length
                   47
% identity
                   (AC006072) putative sugar transporter [Arabidopsis
NCBI Description
                   thaliana]
                   302514
Seq. No.
                   fdz701161040.h1
Seq. ID
Method
                   BLASTX
                   q4432861
NCBI GI
BLAST score
                   150
E value
                   5.0e-10
                   40
Match length
                   62
% identity
                   (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   302515
Seq. No.
                   fdz701161050.h1
Seq. ID
Method
                   BLASTX
                   g2723473
NCBI GI
                   220
BLAST score
                   3.0e-18
E value
                   48
Match length
% identity
                   96
                   (D89726) defender against apoptotic death 1 protein [Oryza
NCBI Description
                   sativa] >gi_2723883_dbj_BAA24104_ (D89727) defender against
                   apoptotic death 1 protein [Oryza sativa]
                   302516
Seq. No.
                   fdz701161080.hl
Seq. ID
                   BLASTN
Method
```

g2921303

NCBI GI



BLAST score 4.0e-64 E value 221 Match length 89 % identity Zea mays herbicide safener binding protein (SBP1) mRNA, NCBI Description complete cds

Seq. No. fdz701161090.hl Seq. ID BLASTX Method NCBI GI q730536 BLAST score 421 E value 8.0e-42 85 Match length 95

% identity 60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal NCBI Description

protein subunit L17 [Nicotiana tabacum]

302518 Seq. No.

fdz701161091.hl Seq. ID

BLASTX Method q2498078 NCBI GI BLAST score 345 E value 6.0e-33 70 Match length 94 % identity

NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) NCBI Description

>gi_1236951 (U50150) nucleoside diphosphate kinase [Glycine

max]

302519 Seq. No.

fdz701161177.hl Seq. ID

BLASTX Method NCBI GI q3287696 316 BLAST score 2.0e-29 E value Match length 86 71 % identity

(AC003979) Strong similarity to phosphoribosylanthranilate NCBI Description transferase gb_D86180 from Pisum sativum. This ORF may be

part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

302520 Seq. No.

fdz701161239.h1 Seq. ID

BLASTX Method NCBI GI g730456 BLAST score 249 1.0e-21 E value Match length 62 74 % identity

40S RIBOSOMAL PROTEIN S19 NCBI Description

302521 Seq. No.

fdz701161251.h1 Seq. ID

BLASTX Method NCBI GI g4102839



```
BLAST score
                  4.0e-22
E value
                  84
Match length
                  57
% identity
                  (AF016713) LeOPT1 [Lycopersicon esculentum]
NCBI Description
                  302522
Seq. No.
                  fdz701161301.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4204268
BLAST score
                  253
                   4.0e-22
E value
                  87
Match length
                   61
% identity
                  (AC005223) 62134 [Arabidopsis thaliana]
NCBI Description
                   302523
Seq. No.
                   fdz701161303.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g66615
BLAST score
                   297
                   3.0e-27
E value
Match length
                   57
                   98
% identity
NCBI Description glutathione transferase (EC 2.5.1.18) I - maize
                   302524
Seq. No.
                   fdz701161321.hl
Seq. ID
Method
                   BLASTX
                   g4006878
NCBI GI
                   207
BLAST score
                   9.0e-17
E value
Match length
                   53
% identity
                   64
                  (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
NCBI Description
                   302525
Seq. No.
                   fdz701161385.h1
Seq. ID
                   BLASTN
Method
                   g857572
NCBI GI
                   77
BLAST score
                   2.0e-35
E value
                   121
Match length
                   91
% identity
                   Oryza sativa U2 small nuclear RNA (U2snRNA) gene, complete
NCBI Description
                   sequence
                   302526
Seq. No.
                   fdz701161389.hl
Seq. ID
                   BLASTX
Method
                   g3645898
NCBI GI
                   424
BLAST score
                   3.0e-42
E value
                   82
Match length
                   99
 % identity
                   (U68408) in-frame stop codon; possibly a post-transposition
 NCBI Description
```

mutation [Zea mays]

```
302527
Seq. No.
                  fdz701161395.h1
Seq. ID
                  BLASTX
Method
                  g70774
NCBI GI
BLAST score
                  145
                  2.0e-09
E value
Match length
                  55
% identity
                  histone H4 (TH091) - wheat >gi_170747 (M12277) histone H4
NCBI Description
                   [Triticum aestivum]
Seq. No.
                  302528
                  fdz701161413.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q102457
BLAST score
                  404
                  7.0e-40
E value
                  79
Match length
                   96
% identity
                  actin 1 and actin 3 - Caenorhabditis elegans (fragment)
NCBI Description
                   >gi_552061 (J01042) actin [Caenorhabditis elegans]
                   >gi_552063 (J01044) actin [Caenorhabditis elegans]
                   302529
Seq. No.
                   fdz701161418.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1173055
BLAST score
                   230
                   7.0e-22
E value
                   72
Match length
                   75
% identity
                   60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497
NCBI Description
                   ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819
                   RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090
                   (X78284) RL5 ribosomal protein [Medicago sativa]
                   302530
Seq. No.
                   fdz701161419.h1
Seq. ID
                   BLASTN
Method
                   g433706
NCBI GI
                   146
BLAST score
                   1.0e-76
E value
                   265
Match length
                   89
% identity
NCBI Description
                  Z.mays PRP gene
                   302531
Seq. No.
Seq. ID
                   fdz701161428.h1
                   BLASTN
Method
                   g18743
NCBI GI
BLAST score
                   86
                   6.0e-41
E value
```

NCBI Description G.max mRNA from stress-induced gene (SAM22)

166

89

Match length

% identity



```
302532
Seq. No.
                  fdz701161446.h1
Seq. ID
                  BLASTX
Method
                  g3212852
NCBI GI
                  250
BLAST score
                  8.0e-22
E value
                  80
Match length
                  59
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                  302533
Seq. No.
                  fdz701161549.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3851004
BLAST score
                   45
                  2.0e-16
E value
                   69
Match length
                   93
% identity
                  Zea mays pyruvate dehydrogenase E1 alpha subunit RNA,
NCBI Description
                   nuclear gene encoding mitochondrial protein, complete cds
                   302534
Seq. No.
Seq. ID
                   fdz701161562.h1
Method
                   BLASTN
                   q347843
NCBI GI
                   78
BLAST score
                   5.0e-36
E value
                   229
Match length
% identity
                   84
NCBI Description Zea mays globulin-1 gene, promoter region
                   302535
Seq. No.
                   fdz701161573.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539334
                   195
BLAST score
                   2.0e-15
E value
                   83
Match length
% identity
                   48
                   (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   302536
Seq. No.
                   fdz701161635.h1
Seq. ID
Method
                   BLASTN
                   g1815627
NCBI GI
                   47
BLAST score
                   2.0e-17
E value
                   111
Match length
% identity
                   Oryza sativa metallothionein-like type 2 (OsMT-2) mRNA,
NCBI Description
                   complete cds
                   302537
Seq. No.
Seq. ID
                   fdz701161649.h1
                   BLASTN
Method
```

g3646023

181

NCBI GI BLAST score



```
2.0e-97
E value
                  241
Match length
% identity
                  Human DNA sequence from clone 1033B10 on chromosome
NCBI Description
                  6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of
                  the BING4 gene, the gene for GalT3
                   (beta3-Galactosyltransferase), the RPS18 (40S ribosomal
                  protein S18) gene,
                  302538
Seq. No.
                  fdz701161651.hl
Seq. ID
                  BLASTN
Method
                  g168654
NCBI GI
                  45
BLAST score
                  2.0e-16
E value
                  169
Match length
                  87
% identity
                  Zea mays ADP glucose pyrophosphorylase (shrunken-2) gene,
NCBI Description
                   complete cds
                   302539
Seq. No.
                   fdz701161691.h1
Seq. ID
                   BLASTN
Method
                   g236729
NCBI GI
                   82
BLAST score
                   2.0e-38
E value
                   206
Match length
                   85
% identity
NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
                   302540
Seq. No.
                   fdz701161720.hl
Seq. ID
                   BLASTX
Method
                   g2500497
NCBI GI
BLAST score
                   214
                   7.0e-26
E value
                   67
Match length
                   78
% identity
                   40S RIBOSOMAL PROTEIN S21 >gi_1419372_emb_CAA67225_
NCBI Description
                   (X98656) ribosomal protein S21 [Zea mays]
                   302541
Seq. No.
                   fdz701161725.h1
 Seq. ID
                   BLASTN
Method
```

q1089800 NCBI GI 154 BLAST score E value 2.0e-81 174 Match length % identity

Rice mitochondrial atp9 gene for ATPase subunt 9, partial NCBI Description

sequence

Seq. No. 302542

fdz701161757.h1 Seq. ID

BLASTX Method NCBI GI g4191786 BLAST score 201

Match length

NCBI Description

% identity

75

59

sapiens]



```
5.0e-16
E value
Match length
                  86
% identity
                  53
NCBI Description
                  (AC005917) unknown protein [Arabidopsis thaliana]
                  302543
Seq. No.
                  fdz701161780.h1
Seq. ID
                  BLASTN
Method
                  g3435156
NCBI GI
                  198
BLAST score
                  1.0e-107
E value
Match length
                  248
% identity
                  96
NCBI Description
                  Homo sapiens TACC1 (TACC1) mRNA, complete cds
                  302544
Seq. No.
                  fdz701161787.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2780183
BLAST score
                  121
E value
                  9.0e-62
Match length
                  205
% identity
                  93
NCBI Description
                  Human DNA sequence from PAC 509L4 on chromosome
                  6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS
Seq. No.
                  302545
Seq. ID
                  fdz701161796.h1
                  BLASTX
Method
NCBI GI
                  g2245394
BLAST score
                  297
E value
                  4.0e-27
Match length
                  88
                  64
% identity
NCBI Description
                  (U89771) ARF1-binding protein [Arabidopsis thaliana]
Seq. No.
                  302546
                  fdz701161849.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4240280
BLAST score
                  67
E value
                  2.0e-29
Match length
                  118
% identity
                  91
NCBI Description Homo sapiens mRNA for KIAA0896 protein, partial cds
                  302547
Seq. No.
                  fdz701161875.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2352947
BLAST score
                  187
E value
                  2.0e-14
```

42709

(AF020091) smooth muscle myosin heavy chain SM1 [Homo



```
302548
Seq. No.
                  fdz701161890.h1
Seq. ID
                  BLASTX
Method
                  g1168968
NCBI GI
                  223
BLAST score
                  1.0e-18
E value
                  52
Match length
% identity
                  85
                  SPLICING FACTOR, ARGININE/SERINE-RICH 5 (PRE-MRNA SPLICING
NCBI Description
                  FACTOR SRP40) (INSULIN-INDUCED GROWTH RESPONSE PROTEIN
                  CL-4) (DELAYED-EARLY PROTEIN HRS) >gi 539957 pir B47112
                  growth response protein HRS, insulin-induced - rat
                  >gi 349079 (L13635) growth response protein [Rattus rattus]
                   302549
Seq. No.
                   fdz701161896.h1
Seq. ID
Method
                  BLASTX
                   g1203969
NCBI GI
BLAST score
                   281
                   2.0e-25
E value
Match length
                   81
                   72
% identity
NCBI Description (L44140) filamin [Homo sapiens]
                   302550
Seq. No.
                   fdz701162792.h1
Seq. ID
                   BLASTN
Method
                   g4406685
NCBI GI
                   206
BLAST score
                   1.0e-112
E value
                   254
Match length
                   95
% identity
NCBI Description Homo sapiens clone 25015 mRNA sequence
                   302551
Seq. No.
                   fdz701162849.h1
Seq. ID
                   BLASTN
Method
                   g3522919
NCBI GI
                   38 -
BLAST score
                   3.0e-12
E value
                   98
Match length
                   85
% identity
                   Homo sapiens chromosome 16, P1 clone 109-9G (LANL),
NCBI Description
                   complete sequence [Homo sapiens]
                   302552
Seq. No.
                   fdz701162915.h1
Seq. ID
                   BLASTX
Method
                   q321246
NCBI GI
                   277
BLAST score
                   5.0e-25
E value
                   64
Match length
 % identity
```

Seq. No. 302553

NCBI Description

Seq. ID fdz701162937.h1

smooth muscle protein SM22 homolog - mouse

```
BLASTN
Method
NCBI GI
                  q1572626
                  38
BLAST score
                  4.0e-12
E value
                  50
Match length
                  94
% identity
                  Triticum aestivum Cu/Zn superoxide dismutase (SOD1.2) mRNA,
NCBI Description
                  nuclear gene encoding chloroplast protein, complete cds
                  302554
Seq. No.
                  fdz701162994.hl
Seq. ID
Method
                  BLASTN
                  g3789715
NCBI GI
                  71
BLAST score
                  5.0e-32
E value
                  131
Match length
% identity
                  Homo sapiens chromosome 17, clone hRPK.62_F_10, complete
NCBI Description
                  sequence [Homo sapiens]
                   302555
Seq. No.
                   fdz701163001.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4503482
                   214
BLAST score
                   1.0e-117
E value
                   265
Match length
                   95
% identity
                   Homo sapiens eukaryotic translation elongation factor 2
NCBI Description
                   (EEF2) mRNA >gi 31105 emb X51466_HSEF2 Human mRNA for
                   elongation factor
                   302556
Seq. No.
                   fdz701163061.h1
Seq. ID
Method
                   BLASTX
                   g168489
NCBI GI
                   308
BLAST score
                   1.0e-28
E value
Match length
                   60
                   97
% identity
                   (M16902) glutathione S-transferase I [Zea mays] >gi_168491
NCBI Description
                   (M16901) glutathione S-transferase I [Zea mays]
                   >gi_225458_prf__1303351A transferase,glutathione S [Zea
                   mays]
                   302557
Seq. No.
                   fdz701163075.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4503163
                   374
BLAST score
                   3.0e-36
E value
                   87
Match length
                   86
% identity
```

NCBI Description

(CUL-2) >gi 1923243 (U83410) CUL-2 [Homo sapiens]

cullin 2 >gi 2493907 sp Q13617 CUL2 HUMAN CULLIN HOMOLOG 2

BLAST score

E value

146 8.0e-10



```
fdz701163096.h1
Seq. ID
                  BLASTN
Method
                  q178996
NCBI GI
                  118
BLAST score
                   5.0e-60
E value
                  193
Match length
% identity
                   91
NCBI Description Human arginine-rich nuclear protein mRNA, complete cds
                   302559
Seq. No.
                   fdz701163101.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                   q3033550
BLAST score
                   172
                   4.0e-92
E value
                   196
Match length
                   97
% identity
                  Homo sapiens secreted frizzled related protein mRNA,
NCBI Description
                   complete cds
                   302560
Seq. No.
Seq. ID
                   fdz701163146.h1
Method
                   BLASTX
NCBI GI
                   q3367568
BLAST score
                   226
                   3.0e-19
E value
                   51
Match length
                   78
% identity
                   (AL031135) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   302561
Seq. No.
                   fdz701163190.h1
Seq. ID
                   BLASTX
Method
                   q3256066
NCBI GI
                   309
BLAST score
                   6.0e-29
E value
                   78
Match length
% identity
                   85
                   (Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]
NCBI Description
                   302562
Seq. No.
                   fdz701163196.hl
Seq. ID
Method
                   BLASTX
                   g3169719
NCBI GI
BLAST score
                   221
                   2.0e-18
E value
                   76
Match length
                   61
% identity
                  (AF007109) similar to yeast dcpl [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   302563
Seq. ID
                   fdz701163288.h1
                   BLASTX
Method
NCBI GI
                   g2739383
```



```
Match length
% identity
                  (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  fdz701163289.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q386158
BLAST score
                  222
                  1.0e-122
E value
Match length
                  254
% identity
                  97
                  TLS/CHOP=hybrid gene {translocation breakpoint} [human,
NCBI Description
                  myxoid liposarcomas cells, mRNA Mutant, 1682 nt]
                   302565
Seq. No.
                   fdz701163303.h1
Seq. ID
Method
                  BLASTN
                   g4416300
NCBI GI
BLAST score
                   41
                   7.0e-14
E value
                   45
Match length
% identity
                   Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
                   302566
Seq. No.
                   fdz701163417.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2829889
                   165
BLAST score
                   7.0e-12
E value
Match length
                   42
% identity
                   86
                   (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   302567
Seq. No.
                   fdz701163433.h1
Seq. ID
Method
                   BLASTX
                   g4337198
NCBI GI
BLAST score
                   153
                   2.0e-10
E value
                   59
Match length
% identity
                   54
                   (AC006403) putative auxin-induced protein [Arabidopsis
NCBI Description
                   thaliana]
                   302568
Seq. No.
                   fdz701163462.hl
Seq. ID
                   BLASTX
Method
                   g4559358
NCBI GI
```

140 BLAST score 8.0e-09 E value 57 Match length 47 % identity

(AC006585) putative steroid binding protein [Arabidopsis NCBI Description

thaliana]

```
302569
Seq. No.
                  fdz701163475.h1
Seq. ID
                  BLASTN
Method
                  g998429
NCBI GI
                  97
BLAST score
                  2.0e-47
E value
                  221
Match length
% identity
                  49
                  GRF1=general regulatory factor [Zea mays, XL80, Genomic,
NCBI Description
                  5348 nt]
                  302570
Seq. No.
                  fdz701163478.h1
Seq. ID
Method
                  BLASTX
                  g4587595
NCBI GI
                   161
BLAST score
                   3.0e-11
E value
                   37
Match length
                   78
% identity
                  (AC006951) putative proline-rich protein APG [Arabidopsis
NCBI Description
                   thaliana]
                   302571
Seq. No.
                   fdz701163510.hl
Seq. ID
                   BLASTX
Method
                   g3850576
NCBI GI
BLAST score
                   365
                   2.0e-35
E value
Match length
                   80
                   82
% identity
                   (AC005278) Strong similarity to gb_U04968 nucleotide
NCBI Description
                   excision repair protein (ERCC2) from Cricetulus grisseus.
                   [Arabidopsis thaliana]
                   302572
Seq. No.
                   fdz701163552.h1
Seq. ID
                   BLASTX
Method
                   q4160532
NCBI GI
BLAST score
                   142
                   4.0e-09
E value
                   42
Match length
                   60
% identity
                   (AJ011304) sphingosine-1-phosphate lyase [Homo sapiens]
NCBI Description
                   302573
Seq. No.
                   fdz701163594.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2244951
                   304
BLAST score
E value
                   4.0e-28
                   63
Match length
% identity
                   (Z97340) strong similarity to dynein light chain
NCBI Description
                   [Arabidopsis thaliana]
```

302574

Seq. No.

NCBI Description

maize



```
fdz701163950.hl
Seq. ID
                  BLASTX
Method
                  q4406808
NCBI GI
                  142
BLAST score
                  2.0e-09
E value
                  43
Match length
% identity
                  72
                  (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
                  302575
Seq. No.
                   fdz701164037.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1929412
                   210
BLAST score
E value
                   3.0e-17
                   58
Match length
% identity
                   (Z93772) protein phosphatase type 2A [Nicotiana tabacum]
NCBI Description
                   302576
Seq. No.
                   fdz701164040.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2129550
BLAST score
                   154
                   2.0e-10
E value
Match length
                   64
% identity
                   calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -
NCBI Description
                   Arabidopsis thaliana >gi 2129554 pir__S71901
                   calcium-dependent protein kinase 6 - Arabidopsis thaliana
                   >gi_836940 (U20623) calcium-dependent protein kinase
                   [Arabidopsis thaliana] >gi_836944 (U20625)
                   calcium-dependent protein \overline{k}inase [Arabidopsis thaliana]
                   >gi_4454034 emb CAA23031.1 (AL035394) calcium-dependent
                   protein kinase (CDPK6) [Arabidopsis thaliana]
                   302577
Seq. No.
                   fdz701164107.hl
Seq. ID
Method
                   BLASTX
                   g3192929
NCBI GI
                   265
BLAST score
                   9.0e-24
E value
                   67
Match length
                   85
% identity
                   (AF068688) malate dehydrogenase [Glycine max]
NCBI Description
                   302578
Seq. No.
                   fdz701164108.hl
Seq. ID
                   BLASTX
Method
                   g131772
NCBI GI
                   164
BLAST score
                   6.0e-12
E value
                   44
Match length
                   80
 % identity
```

42715

>gi 82723_pir__A30097 ribosomal protein S14 (clone MCH1) -

40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)

```
Seq. No.
                  302579
                  fdz701164124.h1
Seq. ID
Method
                  BLASTN
                  g1710211
NCBI GI
                  169
BLAST score
E value
                  2.0e-90
                  204
Match length
% identity
NCBI Description Human clone 23732 mRNA, partial cds
                  302580
Seq. No.
Seq. ID
                   fdz701164182.hl
                  BLASTN
Method
                   q1245964
NCBI GI
                   99
BLAST score
                   1.0e-48
E value
Match length
                   155
% identity
NCBI Description basic calponin [human, aorta, mRNA, 1496 nt]
                   302581
Seq. No.
                   fdz701164185.h1
Seq. ID
Method
                   BLASTX
                   q4538993
NCBI GI
                   384
BLAST score
                   2.0e-37
E value
                   97
Match length
                   70
% identity
                   (ALO49481) putative host response protein [Arabidopsis
NCBI Description
                   thaliana]
                   302582
Seq. No.
                   fdz701164196.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1841870
BLAST score
                   209
                   4.0e-17
E value
                   68
Match length
% identity
                   63
                   (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
NCBI Description
                   302583
Seq. No.
Seq. ID
                   fdz701164221.h1
Method
                   BLASTN
NCBI GI
                   g21892
BLAST score
                   95
E value
                   4.0e-46
                   147
Match length
                   91
% identity
NCBI Description T.aestivum (clone pTAU1.3) U1 snRNA
                   302584
Seq. No.
                   fdz701164237.h1
Seq. ID
Method
                   BLASTX
                   g4530611
NCBI GI
```

BLAST score



```
2.0e-32
E value
Match length
                   75
% identity
                   (AF134552) serine/threonine protein phosphatase PP2A-2
NCBI Description
                   catalytic subunit [Oryza sativa subsp. indica]
Seq. No.
                   302585
                   fdz701164258.hl
Seq. ID
                   BLASTX
Method
                   g2494164
NCBI GI
BLAST score
                   163
E value
                   8.0e-12
Match length
                   51
                   55
% identity
                   PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE
NCBI Description
                   (ATP)) >gi_3874600 emb_CAA98242_ (Z73970) predicted using Genefinder; Similarity to Mouse DNA ligase I
                   (SW:DNL1 MOUSE); cDNA EST yk320h11.3 comes from this gene;
                   cDNA EST yk320h11.5 comes from this gene; cDNA EST
                   yk398a11.3 comes from this gene; cDNA EST yk398
                   302586
Seq. No.
Seq. ID
                   fdz701164322.h1
Method
                   BLASTN
                   g168402
NCBI GI
                   39
BLAST score
                   1.0e-12
E value
                   47
Match length
                   96
% identity
                   Maize transposable element Activator (Ac9) from the waxy
NCBI Description
                   locus
                   302587
Seq. No.
                   fdz701164339.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3122673
BLAST score
                   286
                   3.0e-26
E value
Match length
                   56
                   93
% identity
                   60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447
NCBI Description
                    (Z97341) ribosomal protein [Arabidopsis thaliana]
                    302588
Seq. No.
                    fdz701164348.hl
Seq. ID
Method
                   BLASTX
                    g1209703
NCBI GI
```

Method BLASTX
NCBI GI g1209703
BLAST score 196
E value 2.0e-15
Match length 71
% identity 49

NCBI Description (U40489) maize gll homolog [Arabidopsis thaliana]

Seq. No. 302589

Seq. ID fdz701164538.hl

Method BLASTN NCBI GI g4062933

```
BLAST score
                  4.0e-49
E value
Match length
                  156
                  91
% identity
                  Hordeum vulgare mRNA for formate dehydrogenase, complete
NCBI Description
                  302590
Seq. No.
Seq. ID
Method
                  BLASTN
```

fdz701164553.h1

NCBI GI q1518673 BLAST score 44 E value 1.0e-15 80 Match length 89 % identity

Zea mays beta-D-glucosidase (glu1) gene, intron 4 NCBI Description

transposon 1, complete sequence

Seq. No. 302591 fdz701164566.h1 Seq. ID Method BLASTX

g2832300 NCBI GI BLAST score 235 E value 7.0e-20 Match length 82 60 % identity

(AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus NCBI Description

roseus]

302592 Seq. No.

fdz701164639.h1 Seq. ID

Method BLASTX NCBI GI q3688186 BLAST score 321 E value 4.0e-30 Match length 66 % identity

(AL031804) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 302593

Seq. ID fdz701164739.h1

Method BLASTX NCBI GI g1709358 BLAST score 160 E value 1.0e-18 Match length 70 % identity

NCBI Description NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE

PHOSPHOHYDROLASE) (NTPASE) >gi 629638_pir__S48859

nucleoside triphosphatase - garden pea

>gi 2129890 pir S65147 nucleoside triphosphatase

precursor, chromatin-associated - garden pea

>gi 563612 emb CAA83655 (Z32743) nucleoside triphosphatase

[Pisum sativum] >gi_4519173_dbj_BAA75506.1_ (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

Seq. No. 302594



```
fdz701164745.hl
Seq. ID
                  BLASTN
Method
                  q1906603
NCBI GI
                  137
BLAST score
                  4.0e-71
E value
                  272
Match length
% identity
                  Zea mays ACCase gene, intron containing colonist1 and
NCBI Description
                  colonist2 retrotransposons and reverse transcriptase
                  pseudogene, complete sequence
                  302595
Seq. No.
Seq. ID
                  fdz701164771.h1
                  BLASTX
Method
                  q1351359
NCBI GI
                  218
BLAST score
                   6.0e-18
E value
                   54
Match length
% identity
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN
NCBI Description
                   (MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi_1071788_pir__S48690
                   ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein
                   - potato >gi_488712_emb_CAA55860_ (X79273)
                   ubiquinol--cytochrome c reductase [Solanum tuberosum]
                   302596
Seq. No.
                   fdz701164791.hl
Seq. ID
                   BLASTX
Method
                   g1280208
NCBI GI
                   344
BLAST score
                   1.0e-32
E value
                   82
Match length
                   87
% identity
                   (L76937) Homo sapiens Werner syndrome gene, complete cds
NCBI Description
                   [Homo sapiens] >gi_3719421 (AF091214) WRN [Homo sapiens]
                   302597
Seq. No.
                   fdz701164834.hl
Seq. ID
                   BLASTN
Method
NCBI GI
                   q798835
                   97
BLAST score
E value
                   3.0e-47
                   145
Match length
                   92
 % identity
                   H.sapiens mRNA for purinergic receptor
NCBI Description
                   >gi 1408419_gb_G28604_G28604 human STS SHGC-35403
                   302598
 Seq. No.
 Seq. ID
                   fdz701164854.hl
                   BLASTX
 Method
 NCBI GI
                   q4098331
                   207
 BLAST score
```

(U76896) beta-tubulin 5 [Triticum aestivum]

8.0e-17

51

76

E value

Match length

NCBI Description

% identity



```
302599
Seq. No.
                  fdz701164857.h1
Seg. ID
                  BLASTN
Method
                  g598826
NCBI GI
                  120
BLAST score
                  5.0e-61
E value
                  150
Match length
                  95
% identity
                  Human HepG2 3' region MboI cDNA, clone hmd4f06m3
NCBI Description
                  302600
Seq. No.
Seq. ID
                   fdz701164866.h1
Method
                  BLASTN
NCBI GI
                  g2738815
BLAST score
                   151
                   1.0e-79
E value
Match length
                   222
                   92
% identity
NCBI Description Homo sapiens P2Y1 receptor (P2YR1) mRNA, partial cds
Seq. No.
                   302601
Seq. ID
                   fdz701164869.h1
Method
                   BLASTX
NCBI GI
                   g2398829
BLAST score
                   156
                   9.0e-11
E value
                   61
Match length
                   59
% identity
                   (Y11220) mitochondrial uncoupling protein [Solanum
NCBI Description
                   tuberosum]
                   302602
Seq. No.
                   fdz701164923.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3822035
BLAST score
                   166
                   2.0e-88
E value
                   220
Match length
                   95
% identity
                   Zea mays endo-1,3-1,4-beta-D-glucanase mRNA, complete cds
NCBI Description
                   302603
Seq. No.
                   fdz701165002.h1
Seq. ID
Method
                   BLASTN
                   g3659506
NCBI GI
                   121
BLAST score
E value
                   1.0e-61
Match length
                   189
                   91
% identity
                   Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1,
NCBI Description
                   complete sequence [Homo sapiens]
                   302604
Seq. No.
Seq. ID
                   fdz701165005.h1
```

Method BLASTN NCBI GI g902200

BLAST score 50

```
E value
                    1.0e-19
  Match length
                    82
                    90
  % identity
  NCBI Description Z.mays complete chloroplast genome
                    302605
  Seq. No.
                    fdz701165011.h1
  Seq. ID
  Method
                    BLASTN
                    q1321660
  NCBI GI
                    45
  BLAST score
  E value
                    2.0e-16
  Match length
                    69
  % identity
                    91
  NCBI Description Rice mRNA for ascorbate peroxidase, complete cds
                    302606
  Seq. No.
                    fdz701165026.h1
  Seq. ID
  Method
                    BLASTN
                    g2895780
  NCBI GI
  BLAST score
                    50
                    3.0e-19
  E value
                    117
  Match length
                     86
  % identity
  NCBI Description Zea mays nitrate-induced NOI protein mRNA, complete cds
                     302607
  Seq. No.
                     fdz701165060.h1
  Seq. ID
  Method
                    BLASTX
                     g1708462
  NCBI GI
  BLAST score
                     142
                     5.0e-09
  E value
  Match length
                     85
                     39
  % identity
                    IAA-AMINO ACID HYDROLASE HOMOLOG 2 PRECURSOR >gi_902791
  NCBI Description
                     (U23796) ILL2 [Arabidopsis thaliana]
  Seq. No.
                     302608
Seq. ID
                     fdz701165181.h1
                     BLASTN
  Method
  NCBI GI
                     q168508
                     33
  BLAST score
                     4.0e-09
  E value
                     49
  Match length
                     92
  % identity
  NCBI Description Maize oleosin KD18 (KD18; L2) gene, complete cds
                     302609
  Seq. No.
                     fdz701165182.hl
  Seq. ID
  Method
                     BLASTX
                     q4567302
  NCBI GI
  BLAST score
                     176
  E value
                     3.0e-17
  Match length
                     72
                     72
  % identity
```

NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

302610

Seq. No.



```
fdz701165201.h1
Seq. ID
                  BLASTX
Method
                  q2182029
NCBI GI
                  228
BLAST score
                  2.0e-19
E value
Match length
                  52
% identity
                  (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]
NCBI Description
Seq. No.
                  302611
                  fdz701165256.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2865623
BLAST score
                  221
                  2.0e-18
E value
Match length
% identity
                  61
NCBI Description
                  (AF045286)
                  GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                   [Arabidopsis thaliana]
                  302612
Seq. No.
Seq. ID
                  fdz701165281.h1
Method
                  BLASTX
NCBI GI
                  q4502507
BLAST score
                  318
                  7.0e-30
E value
Match length
% identity
                  complement component 5 > gi 116607 sp_P01031_CO5_HUMAN
NCBI Description
                  COMPLEMENT C5 PRECURSOR (CONTAINS: C5A ANAPHYLATOXIN)
                  >gi_68769_pir__C5HU complement C5 precursor - human
                  >gi 179983 (M57729) complement component C5 [Homo sapiens]
Seq. No.
                   302613
Seq. ID
                   fdz701165296.h1
Method
                  BLASTN
NCBI GI
                  g3419837
BLAST score
                   60
                   1.0e-25
E value
Match length
                  104
% identity
                   89
                  Homo sapiens chromosome 17, clone hRPK.214_O_1, complete
NCBI Description
                   sequence [Homo sapiens]
Seq. No.
                   302614
                   fdz701165330.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2183249
                   148
BLAST score
                  1.0e-13
E value
                   49
Match length
                   84
% identity
                   (AF002211) glutathione-S-transferase [Triticum aestivum]
NCBI Description
                   >gi 4185800 (AF109714) glutathione S-transferase [Triticum
```

aestivum]



```
302615
Seq. No.
                  fdz701165342.h1
Seq. ID
                  BLASTN
Method
                  g22459
NCBI GI
                  201
BLAST score
                  1.0e-109
E value
                  217
Match length
                   98
% identity
NCBI Description Z.mays rab28 gene
                  302616
Seq. No.
                   fdz701165356.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1495251
BLAST score
                   186
                   2.0e-14
E value
Match length
                   53
% identity
                   64
NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]
                   302617
Seq. No.
Seq. ID
                   fdz701165359.h1
Method
                   BLASTN
NCBI GI
                   g3763941
BLAST score
                   76
E value
                   8.0e-35
Match length
                   127
                   91
% identity
                  Homo sapiens clone UWGC:rg041a03 from 7p14-15, complete
NCBI Description
                   sequence [Homo sapiens]
                   302618
Seq. No.
                   fdz701165447.h1
Seq. ID
                   BLASTX
Method
                   q3096922
NCBI GI
                   205
BLAST score
                   1.0e-16
E value
                   50
Match length
                   80
% identity
                  (AL023094) putative protein [Arabidopsis thaliana]
NCBI Description
                   302619
Seq. No.
                   fdz701165459.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4506468
                   157
BLAST score
                   3.0e-83
E value
Match length
                   185
                   96
% identity
                   Homo sapiens RecQ protein-like (DNA helicase Q1-like)
NCBI Description
                   (RECQL) mRNA >gi 619862 gb L36140_HUMRECQ Homo sapiens
                   (clone 1311) DNA helicase (RECQL) mRNA, complete cds
                   302620
Seq. No.
Seq. ID
                   fdz701165461.h1
```

, e...

42723

BLASTN

g22314

Method

NCBI GI

```
BLAST score
                  1.0e-37
E value
Match length
                  120
                  92
% identity
NCBI Description Maize mRNA for GSH gluthathione S-transferase I (GST; EC
                  2.5.1.18)
                  302621
Seq. No.
                  fdz701165465.h1
Seq. ID
                  BLASTX
Method
                  g461665
NCBI GI
                  142
BLAST score
                  3.0e-09
E value
                  69
Match length
% identity
                  38
NCBI Description C4B-BINDING PROTEIN PRECURSOR (C4BP)
                  302622
Seq. No.
                  fdz701165490.h1
Seq. ID
                  BLASTX
Method
                  g3661618
NCBI GI
                  172
BLAST score
                   8.0e-13
E value
                   43
Match length
% identity
NCBI Description (AF093141) fruit-ripening protein [Lycopersicon esculentum]
                   302623
Seq. No.
                   fdz701165532.h1
Seq. ID
Method
                   BLASTX
                   g4502047
NCBI GI
                   142
BLAST score
                   1.0e-16
E value
                   56
Match length
% identity
                   aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde
NCBI Description
                   dehydrogenase, E3 isozyme) >gi_1706390_sp_P49189_DHAG_HUMAN
                   ALDEHYDE DEHYDROGENASE, E3 ISOZYME
                   (GAMMA-AMINOBUTYRALDEHYDE DEHYDROGENASE)
                   (R-AMINOBUTYRALDEHYDE DEHYDROGENASE) >gi_1049219 (U34252)
                   gamma-aminobutyraldehyde dehydrogenase [Homo sapiens]
                   302624
Seq. No.
                   fdz701165608.h1
 Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g115204
BLAST score 252

E value 4.0e-35 Match length 91 % identity 84

NCBI Description COMPLEMENT C1R COMPONENT PRECURSOR >gi_67614_pir__C1HURB complement subcomponent C1r (EC 3.4.21.41) precursor -

human >gi_179644 (M14058) human complement Clr [Homo

sapiens]

Seq. No. 302625

Seq. ID fdz701165609.h1

```
BLASTX
Method
                  q4220481
NCBI GI
                  190
BLAST score
                   1.0e-14
E value
Match length
                   100
% identity
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   302626
Seq. No.
Seq. ID
                   fdz701165656.hl
Method
                  BLASTX
NCBI GI
                   g2738248
BLAST score
                   283
                   2.0e-25
E value
                   91
Match length
                   70
% identity
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                   302627
Seq. No.
                   fdz701165681.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1262344
BLAST score
                   44
                   9.0e-16
E value
                   48
Match length
                   98
% identity
NCBI Description H.sapiens mRNA for myosin light chain kinase
                   302628
Seq. No.
                   fdz701165728.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2623679
BLAST score
                   70
E value
                   2.0e-31
                   93
Match length
                   95
% identity
                   Zea mays calmodulin (Zmrcalm) mRNA, complete cds
NCBI Description
                   302629
Seq. No.
                   fdz701165742.h1
Seq. ID
                   BLASTX
Method
                   g3980035
NCBI GI
                   168
BLAST score
                   4.0e-12
E value
                   89
Match length
% identity
                   39
                   (AL033514) predicted using Genefinder; cDNA EST yk465c10.5
NCBI Description
                   comes from this gene [Caenorhabditis elegans]
                   302630
Seq. No.
Seq. ID
                   fdz701165760.hl
                   BLASTX
Method
                   g3461822
NCBI GI
                   293
BLAST score
```

9.0e-27

78

E value

Match length

NCBI Description

thaliana]



```
% identity
NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]
                   302631
Seq. No.
                   fdz701165781.hl
Seq. ID
Method
                   BLASTX
                   g3608481
NCBI GI
                   152
BLAST score
                   3.0e-10
E value
Match length
                   67
                   55
% identity
NCBI Description (AF088913) ribosomal protein L27a [Petunia x hybrida]
Seq. No.
                   302632
                   fdz701165787.h1
Seq. ID
Method
                   BLASTX
                   g3549669
NCBI GI
                   184
BLAST score
                   5.0e-14
E value
Match length
                   89
                   44
% identity
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
Seq. No.
                   302633
                   fdz701165795.h1
Seq. ID
Method
                   BLASTX
                   g2653879
NCBI GI
                   176
BLAST score
                    5.0e-13
E value
Match length
                    50
% identity
                    64
NCBI Description (AF026389) adenyl cyclase [Nicotiana tabacum]
                    302634
Seq. No.
                    fdz701165812.hl
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1169013
BLAST score
                    211
                    4.0e-17
E value
Match length
                    93
% identity
                    48
                    COP9 PROTEIN (FUSCA PROTEIN FUS7) >gi 625971 pir A54842
NCBI Description
                    COP9 protein - Arabidopsis thaliana >gi_530870 (\overline{L3}2874) COP9 [Arabidopsis thaliana] >gi_2244767 emb_CAB10190_
                    (Z97335) COP9 protein [Arabidopsis thaliana]
                    302635
Seq. No.
                    fdz701165904.h1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4455223
BLAST score
                    244
E value
                    4.0e-21
Match length
                    73
                    63
% identity
```

(AL035440) putative DNA binding protein [Arabidopsis

E value Match length

% identity

NCBI Description

```
302636
Seq. No.
Seq. ID
                    fdz701166026.hl
Method
                   BLASTX
                    g2832672
NCBI GI
                    160
BLAST score
                    3.0e-11
E value
Match length
                    37
% identity
                    (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
                    302637
Seq. No.
                    fdz701166094.h1
Seq. ID
Method
                    BLASTX
                    q283391
NCBI GI
BLAST score
                    249
                    9.0e-22
E value
                    62
Match length
                    87
% identity
                    ADP-ribosylation factor - yeast (Candida albicans)
NCBI Description
                    >gi 254344_bbs_111914 (S43354) ADP-ribosylation factor, Arf
                    [Candida albicans, Peptide, 179 aa] [Candida albicans]
Seq. No.
                    302638
Seq. ID
                    fdz701166145.hl
Method
                    BLASTX
                    g1710077
NCBI GI
                    321
BLAST score
                    2.0e-30
E value
                    68
Match length
% identity
                    93
                    PEROXIREDOXIN (REHYDRIN HOMOLOG) (B15C)
NCBI Description
                    >gi_2130029_pir__S60285 B15C protein - barley
                    >gi_471321_emb_CAA54066_ (X76605) HvB15C [Hordeum vulgare]
>gi_1694833_emb_CAA65387_ (X96551) peroxiredoxin [Hordeum
                    vulgare]
                    302639
Seq. No.
                    fdz701166160.h1
Seq. ID
                    BLASTN
Method
NCBI GI
                    q169818
                    85
BLAST score
E value
                    3.0e-40
                    89
Match length
                    99
% identity
NCBI Description Rice 25S ribosomal RNA gene
                    302640
Seq. No.
                    fdz701166248.hl
Seq. ID
Method
                    BLASTN
                    q3511235
NCBI GI
BLAST score
                    109
```

42727

Zea mays starch branching enzyme IIb (ae) gene, complete

2.0e-54

185 90



```
Seq. No.
                  302641
                  fdz701166390.hl
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2052354
BLAST score
                  157
E value
                  3.0e-83
Match length
                  165
                  99
% identity
NCBI Description Human uncoupling protein homolog (UCPH) mRNA, complete cds
Seq. No.
Seq. ID
                  fdz701166482.hl
Method
                  BLASTX
NCBI GI
                  q1351364
BLAST score
                  149
                  6.0e-10
E value
                  78
Match length
% identity
                  45
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING
NCBI Description
                  PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 11
                  KD PROTEIN) (COMPLEX III SUBUNIT VIII) >gi 687739 (U20790)
                  ubiquinol-cytochrome c oxidoreductase subunit VIII
                   [Neurospora crassa]
                   302643
Seq. No.
                   fdz701166587.h1
Seq. ID
                  BLASTX
Method
                  a3334441
NCBI GI
BLAST score
                   143
                   2.0e-09
E value
                   48
Match length
% identity
                  HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II
NCBI Description
                   >gi_2642161 (AC003000) hypothetical protein [Arabidopsis
                   thaliana]
Seq. No.
                   302644
                   fdz701166621.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2494111
BLAST score
                   171
                   2.0e-14
E value
Match length
                   56
% identity
                   79
                   (AC002376) Contains similarity to Glycine protein kinase 6
NCBI Description
                   (gb M67449). [Arabidopsis thaliana]
Seq. No.
                   302645
                   fdz701166637.h1
Seq. ID
```

Method BLASTX
NCBI GI g312179
BLAST score 214
E value 1.0e-17
Match length 84
% identity 64

NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic



glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

302646 Seq. No. fdz701166651.h1 Seq. ID BLASTN Method g1063665 NCBI GI BLAST score 169 E value 2.0e-90 200 Match length % identity 42 Zea mays unknown protein mRNA, complete cds NCBI Description 302647 Seq. No. fdz701166715.h1 Seq. ID

Method BLASTX
NCBI GI g3063447
BLAST score 231
E value 2.0e-19
Match length 94
% identity 50

NCBI Description (AC003981) F22013.9 [Arabidopsis thaliana]

 Seq. No.
 302648

 Seq. ID
 fdz701166737.h1

 Method
 BLASTX

 NCBI GI
 g2832661

 BLAST score
 286

BLAST score 286 E value 7.0e-26 Match length 95 % identity 60

NCBI Description (AL021710) pherophorin - like protein [Arabidopsis

thaliana]

Seq. No. 302649

Seq. ID fdz701166786.h1

Method BLASTX
NCBI GI g2435517
BLAST score 193
E value 5.0e-15
Match length 89
% identity 48

NCBI Description (AF024504) contains similarity to peptidase family Al

[Arabidopsis thaliana]

Seq. No. 302650

Seq. ID fdz701166808.h1

Method BLASTX
NCBI GI g2129832
BLAST score 267
E value 1.0e-23
Match length 54
% identity 89

NCBI Description heat shock transcription factor 5 - soybean

>gi_671868_emb_CAA87080_ (Z46956) heat shock transcription

factor 5 [Glycine max]

42729



```
Seq. No.
                  302651
                  fdz701166811.hl
Seq. ID
Method
                  BLASTX
                  g3176673
NCBI GI
                  275
BLAST score
                  6.0e-25
E value
                  66
Match length
                  76
% identity
                  (AC003671) Similar to serine/threonine kinase gb_Y12531
NCBI Description
                  from Brassica oleracea. [Arabidopsis thaliana]
Seq. No.
                  302652
                  fdz701166871.h1
Seq. ID
                  BLASTN
Method
                  g1049254
NCBI GI
                  43
BLAST score
                  3.0e-15
E value
                  92
Match length
                  87
% identity
NCBI Description Zea mays H+-pyrophosphatase mRNA, partial cds
                  302653
Seq. No.
Seq. ID
                  fdz701166872.h1
                  BLASTX
Method
                  g3738288
NCBI GI
                  167
BLAST score
                   5.0e-12
E value
Match length
                   55
                   55
% identity
                   (AC005309) auxin-responsive GH3-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   302654
                   fdz701166880.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2181190
BLAST score
                   203
                   3.0e-16
E value
Match length
                   59
                   73
% identity
                  (Y12531) serine/threonine kinase [Brassica oleracea]
NCBI Description
Seq. No.
                   302655
                   fdz701166881.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3236249
                   250
BLAST score
                   1.0e-21
E value
                   57
Match length
                   75
% identity
                   (AC004684) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   302656
Seq. No.
                   fdz701167024.h1
Seq. ID
```

BLASTX

g2924515

Method

NCBI GI

```
BLAST score
E value
                   9.0e-13
                   68
Match length
% identity
                  (AL022023) putative protein [Arabidopsis thaliana]
NCBI Description
                   302657
Seq. No.
                   fwa700097068.h1
Seq. ID
                  BLASTX
Method
                   g4581164
NCBI GI
BLAST score
                   233
                   1.0e-19
E value
Match length
                   107
% identity
                   43
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   302658
                   fwa700097105.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2500980
BLAST score
                   407
                   5.0e-40
E value
                   89
Match length
                   82
% identity
                   GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS)
NCBI Description
                   >gi_1076718_pir__S51684 glutamate--tRNA ligase (EC
                   6.1.1.17) precursor - barley >gi_603849_emb_CAA58505_
                   (X83523) glutamate--tRNA ligase [Hordeum vulgare]
                   302659
Seq. No.
                   fwa700097118.h1
Seq. ID
                   BLASTX
Method
                   q1184776
NCBI GI
BLAST score
                   470
E value
                   2.0e-47
Match length
                   102
% identity
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC4 [Zea mays]
                   302660
Seq. No.
                   fwa700097141.h1
Seq. ID
Method.
                   BLASTX
NCBI GI
                   g1673456
BLAST score
                   356
E value
                   4.0e-34
                   70
Match length
                   100
% identity
NCBI Description
                   (Y09214) rubisco small subunit [Zea mays]
```

Seq. No. 302661

Seq. ID fwa700097147.h1

Method BLASTX
NCBI GI g2160144
BLAST score 183
E value 9.0e-14
Match length 83



```
% identity
                   (AC000375) Strong similarity to Arabidopsis oligopeptide
NCBI Description
                  transporter (gb X77503). [Arabidopsis thaliana]
                  302662
Seq. No.
                  fwa700097162.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3201633
                  193
BLAST score
                  5.0e-15
E value
                  86
Match length
% identity
                  57
                   (AC004669) putative cell division protein [Arabidopsis
NCBI Description
                  thalianal
                  302663
Seq. No.
                  fwa700097166.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g169133
BLAST score
                  65
                  1.0e-28
E value
Match length
                  105
% identity
                   90
                  Zea mays precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein mRNA, complete cds
                   302664
Seq. No.
                   fwa700097170.h1
Seq. ID
                  BLASTX
Method
                  q2979543
NCBI GI
BLAST score
                  174
E value
                  9.0e-13
Match length
                   47
                   77
% identity
                  (AC003680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   302665
Seq. No.
                   fwa700097217.h1
Seq. ID
                  BLASTX
Method
                   g1617274
NCBI GI
BLAST score
                   289
E value
                   4.0e-26
                   79
Match length
                   67
                                                                   2
% identity
                  (Z72152) AMP-binding protein [Brassica napus]
NCBI Description
Seq. No.
                   302666
Seq. ID
                   fwa700097238.h1
Method
                  BLASTX
                  g82080
NCBI GI
BLAST score
                   267
                   2.0e-28
E value
Match length
                  85
% identity
                   79
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
```

[Lycopersicon esculentum]

>gi 226872 prf 1609235A chlorophyll a/b binding protein



```
302667
Seq. No.
Seq. ID
                   fwa700097272.h1
                   BLASTX
Method
                   g82080
NCBI GI
                   253
BLAST score
                   6.0e-22
E value
Match length
                   69
                   72
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   302668
Seq. No.
                   fwa700097276.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4581164
BLAST score
                   206
                   2.0e-16
E value
Match length
                   100
 % identity
                   39
NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]
Seq. No.
                   302669
                   fwa700097286.h1
Seq. ID
Method
                   BLASTX
                   g1871187
NCBI GI
BLAST score
                   174
                   1.0e-12
E value
                   41
Match length
                   80
 % identity
NCBI Description (U90439) unknown protein [Arabidopsis thaliana]
                   302670
 Seq. No.
                   fwa700097309.hl
 Seq. ID
                   BLASTX
Method
                   q132147
NCBI GI
BLAST score
                   450
                   4.0e-45
E value
                   87
Match length
                   100
 % identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi 68089 pir RKZMS
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - maize >gi 22474 emb CAA29784 (X06535)
                   ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor
                   [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose
                   1,5-bisphosphate carboxylase small subunit [Zea mays]
                   >gi 359512 prf 1312317A ribulosebisphosphate carboxylase
                   [Zea mays]
 Seq. No.
                   302671
                   fwa700097323.h1
```

 Seq. ID
 fwa700097323.h1

 Method
 BLASTN

 NCBI GI
 g2286120

 BLAST score
 45

 E value
 3.0e-16



Match length 105 % identity 86

NCBI Description Oryza sativa sec14 like protein mRNA, complete cds

Seq. No. 302672

Seq. ID fwa700097325.h1

Method BLASTN
NCBI GI g21843
BLAST score 134
E value 2.0e-69
Match length 253
% identity 89

NCBI Description Wheat PsbO mRNA for 33kDa oxygen evolving protein of

photosystem II

Seq. No. 302673

Seq. ID fwa700097329.h1

Method BLASTX
NCBI GI 94336606
BLAST score 455
E value 1.0e-45
Match length 100
% identity 90

NCBI Description (AF099110) sigma factor; Sig1 [Zea mays]

Seq. No. 302674

Seq. ID fwa700097332.h1

Method BLASTX
NCBI GI g1086900
BLAST score 143
E value 4.0e-09
Match length 44
% identity 52

NCBI Description (U41278) contains similarity to G beta repeats

(PROSITE: PS00670) of the beta-transducin family

[Caenorhabditis elegans]

Seq. No. 302675

Seq. ID fwa700097352.h1

Method BLASTX
NCBI GI g82080
BLAST score 267
E value 1.0e-23
Match length 73
% identity 71

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 302676

Seq. ID fwa700097360.hl

Method BLASTN
NCBI GI g22294
BLAST score 291
E value 1.0e-163
Match length 295
% identity 100



Maize Gpa1 gene for glyceraldehyde-3-phosphate NCBI Description dehydrogenase subunit A >qi 168478 gb M18976 MZEG3PD Zea mays chloroplast glyceraldehyde-3-phosphate dehydrogenase gene, complete cds, clone lambda-gapA1 Seq. No. 302677 fwa700097424.h1 Seq. ID Method BLASTX g1935912 NCBI GI BLAST score 216 1.0e-17 E value Match length 102 % identity NCBI Description (U77346) LLS1 [Zea mays] 302678 Seq. No. Seq. ID fwa700097425.h1 Method BLASTX NCBI GI g4586022 BLAST score 166 E value 9.0e-12 Match length 82 % identity (AC007170) hypothetical protein [Arabidopsis thaliana] NCBI Description 302679 Seq. No. fwa700097436.h1 Seq. ID Method BLASTN NCBI GI q22356 BLAST score 103 7.0e-51 E value 266 Match length % identity 85 Maize mRNA for light-harvesting chlorophyll a/b binding NCBI Description protein LHCP Seq. No. 302680 fwa700097440.h1 Seq. ID Method BLASTX q3176674 NCBI GI BLAST score 455 1.0e-45 E value Match length 102

% identity 83

(AC003671) Contains similarity to Ste20-like kinase homolog NCBI Description

from A. thaliana chromosome 4 contig gb Z97336.

[Arabidopsis thaliana]

Seq. No. 302681

fwa700097457.hl Seq. ID

BLASTX Method g2500055 NCBI GI BLAST score 294 9.0e-27 E value 100 Match length 58 % identity

NCBI Description DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS



HOMOLOG) >gi_1653575_dbj_BAA18488_ (D90914) sms protein
[Synechocystis sp.]

Seq. No. 302682

Seq. ID fwa700097522.h1

Method BLASTX
NCBI GI g2655031
BLAST score 548
E value 1.0e-56
Match length 100
% identity 100

NCBI Description (AF019297) starch synthase isoform zSTSII-2 [Zea mays]

Seq. No. 302683

Seq. ID fwa700097524.h1

Method BLASTX
NCBI GI g4406764
BLAST score 179
E value 2.0e-13
Match length 48
% identity 71

NCBI Description (AC006836) putative uridylyl transferase [Arabidopsis

thaliana]

Seq. No. 302684

Seq. ID fwa700097536.h1

Method BLASTX
NCBI GI g2765821
BLAST score 199
E value 1.0e-15
Match length 98
% identity 51

NCBI Description (Z95496) Mlo-hl protein [Hordeum vulgare]

Seq. No.

Seq. ID fwa700097553.h1

302685

Method BLASTN
NCBI GI g452340
BLAST score 80
E value 2.0e-37
Match length 92
% identity 97

NCBI Description Z.mays mRNA for type II light-harvesting chlorophyll

a/b-binding protein

Seq. No. 302686

Seq. ID fwa700097595.h1

Method BLASTX
NCBI GI g4101707
BLAST score 212
E value 2.0e-17
Match length 54
% identity 67

NCBI Description (AF006080) glucose acyltransferase [Solanum berthaultii]

Seq. No. 302687

Seq. ID fwa700097613.h1

42736

NCBI GI

BLAST score

g643596 204



```
BLASTX
Method
                  q3928084
NCBI GI
                  313
BLAST score
                   6.0e-29
E value
                  101 .
Match length
% identity
                   56
                   (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   302688
Seq. No.
                   fwa700097688.h1
Seq. ID
                  BLASTN
Method
                  g260552
NCBI GI
                   38
BLAST score
                   5.0e-12
E value
                   90
Match length
% identity
                   86
                  Wx (wx-B2) {transposable element Tourist-Zm1} [Zea
NCBI Description
                  mays=corn, Transposon Mutant, 150 nt]
                   302689
Seq. No.
Seq. ID
                   fwa700097720.h1
Method
                   BLASTX
NCBI GI
                   g2306981
BLAST score
                   250
                   1.0e-21
E value
Match length
                   66
% identity
                   80
                  (AF010321) photosystem I antenna protein [Oryza sativa]
NCBI Description
                   302690
Seq. No.
                   fwa700097811.h1
Seq. ID
Method
                   BLASTX
                   g67155
NCBI GI
BLAST score
                   179
                   1.0e-13
E value
                   41
Match length
                   88
% identity
                   pyruvate, orthophosphate dikinase (EC 2.7.9.1) precursor -
NCBI Description
                   maize
                   302691
Seq. No.
                   fwa700097824.h1
Seq. ID
                   BLASTX
Method
                   g3789954
NCBI GI
                   291
BLAST score
                   2.0e-26
E value
                   81
Match length
                   77
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   302692
                   fwa700097841.h1
Seq. ID
                   BLASTN
Method
```



```
1.0e-111
E value
                  278
Match length
% identity
NCBI Description Corn mRNA for cysteine proteinase, clone CCP, complete cds
                   302693
Seq. No.
                   fwa700097866.hl
Seq. ID
                  BLASTN
Method
NCBI GI
                   g733455
BLAST score
                   64
E value
                   1.0e-27
Match length
                   64
% identity
                   100
                   Zea mays chlorophyll a/b-binding apoprotein CP26 (Lhcb5-2)
NCBI Description
                  mRNA, complete cds
                   302694
Seq. No.
Seq. ID
                   fwa700097873.hl
Method
                   BLASTX
NCBI GI
                   g4507455
                   155
BLAST score
                   1.0e-10
E value
Match length
                   69
% identity
                   45
                  transferrin receptor 2 >gi 3135312 (AF053356)
NCBI Description
                   transferrin-receptor2 [Homo sapiens]
                   302695
Seq. No.
                   fwa700097892.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4585882
                   257
BLAST score
E value
                   5.0e-32
Match length
                   82
                   76
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   302696
                   fwa700097931.h1
Seq. ID
Method
                   BLASTX
                   g479413
NCBI GI
                   298
BLAST score
E value
                   3.0e-27
Match length
                   103
% identity
                   56
NCBI Description myosin-like protein - Arabidopsis thaliana
                   302697
Seq. No.
                   fwa700097971.h1
Seq. ID
                   BLASTX
Method
                   q4502599
NCBI GI
                   163
BLAST score
                   2.0e-11
E value
Match length
                   61
                   62
% identity
```

NCBI Description carbonyl reductase 1 >gi_118519_sp_P16152_DHCA_HUMAN



CARBONYL REDUCTASE (NADPH) (NADPH-DEPENDENT CARBONYL REDUCTASE) (PROSTAGLANDIN-E2 9-REDUCTASE) (PROSTAGLANDIN 9-KETOREDUCTASE) (15-HYDROXYPROSTAGLANDIN DEHYDROGENASE (NADP+)) >gi_476534_pir__ RDHUCB carbonyl reductase (NADPH) (EC 1.1.1.184) - human >gi_179978 (M62420) carbonyl reductase [Homo sapiens] >gi_181037 (J04056) carbonyl reductase [Homo sapiens] >gi_3702679_dbj_BAA33498_ (AB003151) carbonyl reductase [Homo sapiens] >gi_226828_prf__1608111A carbonyl reductase [Homo sapiens]

Seq. ID fwa700098023.h1
Method BLASTX
NCBI GI g283038
BLAST score 231
E value 2.0e-19
Match length 43

Match length 43 % identity 95

Seq. No.

NCBI Description chlorophyll a/b-binding protein (cab-m7) precursor - maize

>gi 22230 emb CAA37474 (X53398) light harvesting

chlorophyll a /b binding protein [Zea mays]

Seq. No. 302699

Seq. ID fwa700098043.h1

Method BLASTX
NCBI GI g3025189
BLAST score 157
E value 9.0e-11
Match length 45
% identity 67

NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770

>gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis

sp.]

Seq. No. 302700

Seq. ID fwa700098049.h1

Method BLASTX
NCBI GI g4455338
BLAST score 350
E value 2.0e-33
Match length 79
% identity 76

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 302701

Seq. ID fwa700098050.h1

Method BLASTX
NCBI GI g2244996
BLAST score 316
E value 3.0e-29
Match length 97
% identity 59

NCBI Description (Z97341) similarity to a membrane-associated salt-inducible

protein [Arabidopsis thaliana]

Seq. No. 302702

Seq. ID fwa700098085.hl



```
Method
                  BLASTX
                  g282994
NCBI GI
                  213
BLAST score
                  9.0e-21
E value
                  88
Match length
                  67
% identity
                  Sip1 protein - barley >gi 167100 (M77475) seed imbibition
NCBI Description
                  protein [Hordeum vulgare]
Seq. No.
                  302703
                   fwa700098107.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3036807
                   167
BLAST score
                   8.0e-12
E value
                   77
Match length
                   49
% identity
                  (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                   302704
Seq. No.
                   fwa700098124.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3785980
BLAST score
                   312
                   7.0e-29
E value
                   105
Match length
% identity
                   55
                  (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   302705
Seq. No.
                   fwa700098167.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22447
BLAST score
                   50
E value
                   3.0e-19
Match length
                   58
                   97
% identity
                  Zea mays ZMPMS2 gene for 19 kDa zein protein
NCBI Description
Seq. No.
                   302706
                   fwa700098178.h1
Seq. ID
                   BLASTX
Method
                   g4558683
NCBI GI
BLAST score
                   151
                   5.0e-10
E value
Match length
                   81
% identity
                   37
                   (AC006586) putative retrotransposon Ttol ORF1 protein
NCBI Description
                   [Nicotiana tabacum] [Arabidopsis thaliana]
                   302707
Seq. No.
                   fwa700098202.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g70639
```

246

82

3.0e-35

BLAST score

Match length

E value



```
% identity
                  ubiquitin precursor - Neurospora crassa
NCBI Description
                  >qi 295930 emb CAA31530 (X13140) ubiquitin [Neurospora
                  302708
Seq. No.
                  fwa700098235.h1
Seq. ID
Method
                  BLASTX
                  g132147 ·
NCBI GI
                  463
BLAST score
E value
                  1.0e-46
Match length
                  89
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 68089 pir RKZMS
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - maize >gi_22474_emb CAA29784 (X06535)
                  ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor
                  [Zea mays] >gi 217964_dbj_BAA00120_ (D00170) ribulose
                  1,5-bisphosphate carboxylase small subunit [Zea mays]
                  >gi_359512_prf__1312317A ribulosebisphosphate carboxylase
                  [Zea mays]
Seq. No.
                  302709
                  fwa700098309.hl
Seq. ID
Method
                  BLASTN
                  g19010
NCBI GI
                  63
BLAST score
E value
                  6.0e-27
                  160
Match length
% identity
NCBI Description H.vulgare mRNA for jasmonate-induced protein
Seq. No.
                  302710
                  fwa700098357.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170242
                  150
BLAST score
E value
                  3.0e-10
Match length
                  36
                  83
% identity
                  FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
NCBI Description
                  SYNTHETASE) >gi_474966_dbj_BAA05101 (D26105)
                   ferrochelatase [Hordeum vulgare]
                  302711
Seq. No.
                   fwa700098421.hl
Seq. ID
Method
                  BLASTX
                  q1052960
NCBI GI
                  289
```

Method BLASTX
NCBI GI g1052960
BLAST score 289
E value 5.0e-37
Match length 85
% identity 92

NCBI Description (U37437) PNIL34 [Ipomoea nil]

Seq. No. 302712

Seq. ID fwa700098518.h1



```
BLASTX
Method
                   q2245104
NCBI GI
                   146
BLAST score
                   6.0e-11
E value
                   76
Match length
                   46
% identity
                   (Z97343) LTR retrotransposon [Arabidopsis thaliana]
NCBI Description
                   302713
Seq. No.
                   fwa700098538.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3694807
BLAST score
                   172
                   8.0e-13
E value
                   33
Match length
                   97
% identity
                   (AF055898) alanine aminotransferase [Zea mays]
NCBI Description
                   302714
Seq. No.
                   fwa700098556.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3063446
BLAST score
                   249
E value
                   2.0e-21
                   107
Match length
                   39
% identity
                   (AC003981) F22013.8 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   302715
                   fwa700098568.h1
Seq. ID
Method
                   BLASTX
                   g2829911
NCBI GI
BLAST score
                   381
                   6.0e-37
E value
Match length
                   101
                   74
% identity
                   (AC002291) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   302716
Seq. No.
                   fwa700098569.hl
Seq. ID
                   BLASTX
Method
                   g82080
NCBI GI
BLAST score
                   278
                   6.0e-25
E value
                   72
Match length
                   75
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi_226872_prf _1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   302717
Seq. No.
Seq. ID
                   fwa700098608.h1
                   BLASTX
Method
NCBI GI
                   g4056493
BLAST score
                   156
```

1.0e-10

61

E value Match length



% identity NCBI Description (AC005896) unknown protein [Arabidopsis thaliana] 302718 Seq. No. fwa700098719.hl Seq. ID Method BLASTN NCBI GI q507844 44 BLAST score 1.0e-15 E value 120 Match length % identity NCBI Description Zea mays A188 retrotransposon gag gene, complete cds 302719 Seq. No. Seq. ID fwa700098754.h1 BLASTX Method q2626753 NCBI GI BLAST score 400 4.0e-39 E value Match length 111 % identity 71 NCBI Description (AB008782) sulfate transporter [Arabidopsis thaliana] Seq. No. 302720 fwa700098826.h1 Seq. ID BLASTX Method q126888 NCBI GI 225 BLAST score E value 8.0e-19 55 Match length 84 % identity MALATE DEHYDROGENASE (NADP), CHLOROPLAST PRECURSOR NCBI Description (NADP-MDH) >gi_319840_pir DEMZMC malate dehydrogenase (NADP+) (EC 1.1.1.82) precursor, chloroplast - maize >gi_22368_emb_CAA34213_ (X16084) precursor protein (AA -57 to 375) [Zea mays] >gi_226766_prf__1604473A NADP malate dehydrogenase [Zea mays] Seq. No. 302721 fwa700098827.hl Seq. ID Method BLASTX NCBI GI g3341687 157 BLAST score E value 1.0e-10 Match length 46 % identity 63 NCBI Description (AC003672) putative ras protein [Arabidopsis thaliana] 302722 Seq. No. fwa700098837.h1 Seq. ID BLASTX Method q3334349 NCBI GI BLAST score 212 E value 4.0e-17

% identity 66
NCBI Description GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)

58

Match length



>gi_2564215_emb_CAA05162_(AJ002062) glycyl-tRNA synthetase
[Arabidopsis thaliana]

Seq. No. 302723

Seg. ID fwa700098910.h1

Method BLASTX
NCBI GI g3298538
BLAST score 154
E value 2.0e-10
Match length 96
% identity 39

NCBI Description (AC004681) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302724

Seq. ID fwa700098927.h1

Method BLASTN
NCBI GI g3550435
BLAST score 66
E value 9.0e-29
Match length 138
% identity 87

NCBI Description Hordeum vulgare Hotrl gene

Seq. No. 302725

Seq. ID fwa700098935.hl

Method BLASTX
NCBI GI g1731475
BLAST score 241
E value 1.0e-20
Match length 73
% identity 63

NCBI Description (U35619) ribulose-1,5 bisphosphate carboxylase/oxygenase

large subunit N-methyltransferas [Nicotiana tabacum]

>gi 1731477 (U35620) ribulose-1,5 bisphosphate

carboxylase/oxygenase large subunit N-methyltransferase

[Nicotiana tabacum]

Seq. No. 302726

Seq. ID fwa700099002.h1

Method BLASTN
NCBI GI g596077
BLAST score 136
E value 1.0e-70
Match length 204
% identity 92

NCBI Description Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA,

complete cds

Seq. No. 302727

Seq. ID fwa700099003.h1

Method BLASTX
NCBI GI g1946355
BLAST score 291
E value 2.0e-26
Match length 96
% identity 58

NCBI Description (U93215) maize transposon MuDR mudrA protein isolog

E value

Match length % identity

6.0e-17 79

58



[Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

302728 Seq. No. fwa700099018.hl Seq. ID Method BLASTX NCBI GI g131772 282 BLAST score 2.0e-25 E value Match length 59 95 % identity 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) NCBI Description >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) -302729 Seq. No. fwa700099057.h1 Seq. ID Method BLASTX NCBI GI q4185740 278 BLAST score 7.0e-25 E value 97 Match length 59 % identity (AF079999) putative glutamate receptor [Arabidopsis NCBI Description thaliana] 302730 Seq. No. fwa700099069.hl Seq. ID Method BLASTX q4587556 NCBI GI 442 BLAST score E value 4.0e-44 109 Match length % identity 79 (AC006577) Similar to gi 1653162 (p)ppGpp NCBI Description 3-pyrophosphohydrolase from Synechocystis sp genome gb D90911. EST gb W43807 comes from this gene. [Arabidopsis thaliana] Seq. No. 302731 fwa700099123.hl Seq. ID Method BLASTN NCBI GI g22272 BLAST score 122 E value 3.0e-62 217 Match length % identity Maize mRNA for enolase (2-phospho-D-glycerate hydrolase) NCBI Description 302732 Seq. No. fwa700099215.h1 Seq. ID Method BLASTX g3935183 NCBI GI 210 BLAST score

42745

NCBI Description

Seq. No.

302738



```
NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]
                  302733
Seq. No.
                  fwa700099243.h1
Seq. ID
                  BLASTX
Method
                  q2494266
NCBI GI
BLAST score
                   338
                   6.0e-32
E value
                   97
Match length
                   66
% identity
                  GTP-BINDING PROTEIN LEPA >gi_1653961_dbj_BAA18871 (D90917)
NCBI Description
                  LepA [Synechocystis sp.]
                   302734
Seq. No.
                   fwa700099261.hl
Seq. ID
                  BLASTX
Method
                   q3928095
NCBI GI
BLAST score
                   247
                   3.0e-21
E value
                   58
Match length
                   72
% identity
                   (AC005770) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   302735
                   fwa700099285.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4325368
                   342
BLAST score
                   2.0e-32
E value
Match length
                   87
                   72
% identity
                   (AF128396) Arabidopsis thaliana flavin-type blue-light
NCBI Description
                   photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2,
                   E=2.6e-226, N=1) [Arabidopsis thaliana]
Seq. No.
                   302736
                   fwa700099319.h1
Seq. ID
                   BLASTX
Method
                   g2982452
NCBI GI
BLAST score
                   153
                   3.0e-10
E value
Match length
                   88
                   41
% identity
                   (AL022223) receptor protein kinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   302737
Seq. ID
                   fwa700099336.hl
Method
                   BLASTX
NCBI GI
                   q4580990
                   208
BLAST score
                   1.0e-16
E value
                   84
Match length
                   44
% identity
                   (AF120335) putative transposase [Arabidopsis thaliana]
```

42746

```
fwa700099424.h1
Seq. ID
Method
                  BLASTX
                   q4581109
NCBI GI
                   185
BLAST score
                   5.0e-14
E value
Match length
                   87
                   46
% identity
                   (AC005825) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   302739
                   fwa700099426.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2654226
BLAST score
                   241
                   1.0e-20
E value
Match length
                   82
                   54
% identity
                   (AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   302740
Seq. No.
                   fwa700099532.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455371
BLAST score
                   164
                   7.0e-12
E value
Match length
                   88
                   44
% identity
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   302741
Seq. No.
                   fwa700099568.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4335761
BLAST score
                   173
E value
                   1.0e-12
Match length
                   102
                   38
% identity
                  (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   302742
                   fwa700099574.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3831457
BLAST score
                   229
E value
                   9.0e-27
Match length
                   98
                   57
% identity
                   (AC005700) putative ion channel protein [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 302743

Seq. ID fwa700099576.h1

Method BLASTX
NCBI GI g82080
BLAST score 260
E value 8.0e-23



Match length 69 % identity 72

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 302744

Seq. ID fwa700099609.h1

Method BLASTX
NCBI GI g1350821
BLAST score 155
E value 2.0e-10
Match length 42
% identity 69

NCBI Description CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR

>gi 280403 pir__S26204 RNA-binding protein 31 -

curled-leaved tobacco >gi_19710_emb_CAA46233_ (X65117) RNA

binding protein 31 [Nicotiana plumbaginifolia]

Seq. No. 302745

Seq. ID fwa700099622.h1

Method BLASTX
NCBI GI g82080
BLAST score 267
E value 1.0e-23
Match length 70
% identity 74

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 302746

Seq. ID fwa700099647.h1

Method BLASTN
NCBI GI g3821780
BLAST score 34
E value 1.0e-09
Match length 34
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 302747

Seq. ID fwa700099690.h1

Method BLASTX
NCBI GI g1076626
BLAST score 261
E value 7.0e-23
Match length 48
% identity 100

NCBI Description glycine rich protein - common tobacco

>gi 790473 emb CAA58702 (X83731) soluble, glycine rich

protein [Nicotiana tabacum]

Seq. No. 302748

Seq. ID fwa700099723.hl

Method BLASTX NCBI GI g2058273



```
BLAST score
                  6.0e-40
E value
                  89
Match length
                  90
% identity
                  (D83527) YK426 [Oryza sativa]
NCBI Description
                  302749
Seq. No.
                  fwa700099758.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4539654
BLAST score
                  44
E value
                  5.0e-16
Match length
                  76
% identity
                  89
                  Sorghum bicolor 22 kDa kafirin cluster
NCBI Description
                   302750
Seq. No.
                   fwa700099761.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q168652
BLAST score
                   43
                   5.0e-15
E value
Match length
                   43
% identity
                   100
                  Maize amyloplast-specific transit protein (waxy; wx+
NCBI Description
                   locus), complete cds
                   302751
Seq. No.
                   fwa700099794.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115385
BLAST score
                   279
E value
                   5.0e-25
Match length
                   58
                   86
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
                   302752
Seq. No.
                   fwa700099851.hl
Seq. ID
                   BLASTX
Method
                   g3122858
NCBI GI
BLAST score
                   362
                   9.0e-35
E value
Match length
                   105
% identity
                   71
                   D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR
NCBI Description
                   >qi 2189964 dbj BAA20405 (AB003280) Phosphoglycerate
                   dehydrogenase [Arabidopsis thaliana]
                   >qi 2804258 dbj BAA24440 (AB010407) phosphoglycerate
```

dehydrogenase [Arabidopsis thaliana]

Seq. No. 302753

Seq. ID fwa700099925.h1

Method BLASTX NCBI GI g132147



```
BLAST score
E value
                  1.0e-46
Match length
                  89
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 68089_pir__RKZMS
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - maize >gi 22474 emb CAA29784_ (X06535)
                  ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor
                  [Zea mays] >gi 217964_dbj_BAA00120_ (D00170) ribulose
                  1,5-bisphosphate carboxylase small subunit [Zea mays]
                  >gi 359512_prf__1312317A ribulosebisphosphate carboxylase
                  [Zea mays]
                  302754
Seq. No.
                  fwa700099935.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q456567
BLAST score
                  41
                  7.0e-14
E value
Match length
% identity
                  Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                  302755
Seq. No.
                  fwa700099991.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4314400
                  173
BLAST score
E value
                  1.0e-12
Match length
                  100
% identity
                  (AC006232) putative selenium-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  302756
                  fwa700100010.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914368
BLAST score
                   468
E value
                  3.0e-47
Match length
                  101
                  82
% identity
                  GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
NCBI Description
                  >gi_167519 (M80571) glycerol-3-phosphate acyltransferase
                   [Cucumis sativus] >gi 444331 prf 1906380A glycerol
                  phosphate acyltransferase [Cucumis sativus]
                   302757
Seq. No.
                   fwa700100209.h1
Seq. ID
                  BLASTX
Method
```

Method BLASTX
NCBI GI g1769898
BLAST score 314
E value 4.0e-29
Match length 103
% identity 54





NCBI Description (Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq. No. 302758

Seq. ID fwa700100214.h1

Method BLASTX
NCBI GI g2127768
BLAST score 177
E value 5.0e-13
Match length 96
% identity 36

NCBI Description arsenical pump-driving ATPase homolog - Methanococcus jannaschii >gi 1591774 (U67556) arsenical pump-driving

ATPase (arsA) [Methanococcus jannaschii]

Seq. No. 302759

Seq. ID fwa700100242.h1

Method BLASTX
NCBI GI g82080
BLAST score 263
E value 4.0e-23
Match length 63
% identity 78

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi 226872 prf__1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 302760

Seq. ID fwa700100255.hl

Method BLASTX
NCBI GI 94580456
BLAST score 216
E value 1.0e-17
Match length 78
% identity 56

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 302761

Seq. ID fwa700100310.h1

Method BLASTX
NCBI GI g1705463
BLAST score 176
E value 6.0e-13
Match length 74
% identity 50

NCBI Description BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir__S71201

biotin sythase - Arabidopsis thaliana >gi_1045316 (U24147) biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806) BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413)

biotin synthase [Arabidopsis thaliana] >gi_2288983

(AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >gi 1589016 prf 2209438A biotin synthase [Arabidopsis

thaliana]

Seq. No. 302762

Seq. ID fwa700100314.h1

Method BLASTX NCBI GI g82080



```
261
BLAST score
E value
                  7.0e-23
Match length
                  70
                  73
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872_prf __1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  302763
Seq. No.
                  fwa700100316.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3874155
BLAST score
                  181
E value
                  1.0e-16
                  98
Match length
                  49
% identity
                  (Z73103) Similarity to Yeast ATP-dependent RNA helicase
NCBI Description
                   (SW:SUV3_YEAST); cDNA EST EMBL:T01340 comes from this gene;
                  cDNA EST yk244e10.3 comes from this gene; cDNA EST
                  yk213b9.3 comes from this gene; cDNA EST yk244e10.5 comes
                  302764
Seq. No.
                  fwa700100320.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4646223
                   230
BLAST score
                  3.0e-19
E value
                  102
Match length
% identity
                   48
                  (AC007295) hypothetical protein, 5' partial [Arabidopsis
NCBI Description
                   thaliana]
                   302765
Seq. No.
                   fwa700100338.hl
Seq. ID
Method
                   BLASTX
                   g115786
NCBI GI
BLAST score
                   408
                   4.0e-40
E value
                   77
Match length
                   97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding
                   protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
                   mays]
                   302766
Seq. No.
                   fwa700100373.hl
Seq. ID
Method
                   BLASTX
                   q1001355
NCBI GI
BLAST score
                   208
                   1.0e-16
E value
                   96
Match length
                   47
% identity
                   (D64006) auxin-induced protein [Synechocystis sp.]
```

Seq. No. 302767

NCBI Description



```
fwa700100385.hl
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
                  36
BLAST score
                  7.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  302768
Seq. No.
                  fwa700100438.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82080
                  249
BLAST score
                  2.0e-21
E value
                  67
Match length
                  73
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   302769
Seq. ID
                   fwa700100465.hl
Method
                  BLASTX
                   g2795806
NCBI GI
BLAST score
                   161
E value
                   3.0e-11
Match length
                   50
% identity
                   52
                  (AC003674) unknown protein [Arabidopsis thaliana]
NCBI Description
                   302770
Seq. No.
Seq. ID
                   fwa700100473.hl
Method
                   BLASTX
NCBI GI
                   g295855
BLAST score
                   320
                   7.0e-30
E value
                   61
Match length
                   100
% identity
                   (X15642) P-pyruvate carboxylase [Zea mays]
NCBI Description
                   302771
Seq. No.
                   fwa700100478.h1
Seq. ID
                   BLASTX
Method
                   g3059131
NCBI GI
                   147
BLAST score
                   1.0e-09
E value
Match length
                   97
                   38
% identity
                  (AJ000478) cytochrome P450 [Helianthus tuberosus]
NCBI Description
                   302772
Seq. No.
                   fwa700100552.h1
Seq. ID
                   BLASTX
Method
                   g3080420
NCBI GI
```

1.0e-40

BLAST score E value

NCBI Description



```
Match length
% identity
                  77
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  302773
Seq. No.
                  fwa700100554.h1
Seq. ID
Method
                  BLASTN
                  q500854
NCBI GI
                  53
BLAST score
E value
                  5.0e-21
Match length
                  105
% identity
NCBI Description Maize dissociation element DNA
                  302774
Seq. No.
                  fwa700100570.hl
Seq. ID
Method
                  BLASTN
                  g3821780
NCBI GI
                   36
BLAST score
                   7.0e-11
E value
Match length
                   48
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   302775
Seq. No.
                   fwa700100579.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4056507
                   152
BLAST score
                   4.0e-10
E value
                   77
Match length
                   42
% identity
                   (AC005896) putative RNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   302776
                   fwa700100679.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3452304
BLAST score
                   72
E value
                   1.0e-32
Match length
                   116
% identity
                   99
NCBI Description Zea mays retrotransposon Opie-1 5' LTR, partial sequence
Seq. No.
                   302777
                   fwa700100682.h1
Seq. ID
Method
                   BLASTX
                   q3170230
NCBI GI
                   374
BLAST score
                   4.0e-36
E value
                   107
Match length
% identity
                   66
```

/fructose-2,6-bisphosphatase [Spinacia oleracea]

(AF041848) fructose-6-phosphate 2-kinase

```
302778
Seq. No.
                  fwa700100686.MM
Seq. ID
                  BLASTX
Method
                  g4454467
NCBI GI
                  370
BLAST score
                  1.0e-35
E value
                  101
Match length
                  71
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                  302779
Seq. No.
                  fwa700100701.hl
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  34
                  1.0e-09
E value
                  34
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   302780
Seq. No.
                   fwa700100796.h1
Seq. ID
                   BLASTN
Method
                   g312178
NCBI GI
BLAST score
                   72
                   2.0e-32
E value
                   139
Match length
% identity
                   45
NCBI Description Z.mays GapC2 gene
                   302781
Seq. No.
                   fwa700100806.h1
Seq. ID
                   BLASTX
Method
                   g4558549
NCBI GI
BLAST score
                   265
                   2.0e-23
E value
                   73
Match length
                   73
% identity
                  (AC007138) putative SecA-type chloroplast protein transport
NCBI Description
                   factor [Arabidopsis thaliana]
                   302782
Seq. No.
                   fwa700100810.hl
Seq. ID
                   BLASTN
Method
                   g169133
NCBI GI
                   44
BLAST score
                   4.0e-16
E value
                   48
Match length
                   98
 % identity
                   Zea mays precursor of the oxygen evolving complex 17 kDa
NCBI Description
                   protein mRNA, complete cds
                   302783
Seq. No.
                   fwa700100832.h1
 Seq. ID
```

BLASTX

189

g2459448

Method

NCBI GI

BLAST score

E value

Match length

3.0e-26 101



```
1.0e-14
E value
                  80
Match length
% identity
                  (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
                  302784
Seq. No.
                  fwa700100839.h1
Seq. ID
                  BLASTX
Method
                  g1495802
NCBI GI
                  295
BLAST score
                   5.0e-27
E value
                   67
Match length
% identity
                   82
NCBI Description (X96405) 13-lipoxygenase [Solanum tuberosum]
                   302785
Seq. No.
                   fwa700100847.h1
Seq. ID
                   BLASTN
Method
                   g21843
NCBI GI
                   34
BLAST score
                   9.0e-10
E value
                   60
Match length
                   90
% identity
                   Wheat PsbO mRNA for 33kDa oxygen evolving protein of
NCBI Description
                   photosystem II
                   302786
Seq. No.
                   fwa700100850.h1
Seq. ID
                   BLASTX
Method
                   g130269
NCBI GI
                   217
BLAST score
                   8.0e-18
E value
                   98
Match length
                   46
% identity
                   PLASTOCYANIN PRECURSOR >gi_82414_pir__S00206 plastocyanin
NCBI Description
                   precursor - barley
                   302787
Seq. No.
                   fwa700100920.hl
 Seq. ID
                   BLASTX
Method
                   q2500959
NCBI GI
                   283
BLAST score
                   2.0e-25
E value
                   75
Match length
                   69
 % identity
                   ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS)
 NCBI Description
                   >gi_1653611_dbj_BAA18523_ (D90915) alanyl-tRNA synthetase
                   [Synechocystis sp.]
 Seq. No.
                   302788
                   fwa700100932.h1
 Seq. ID
 Method
                   BLASTX
                   g3004555
 NCBI GI
                   289
 BLAST score
```

42756

NCBI Description

thaliana]



```
% identity
                  (AC003673) similar to salt inducible protein [Arabidopsis
NCBI Description
                  thaliana]
                  302789
Seq. No.
                  fwa700100940.h1
Seq. ID
                  BLASTX
Method
                  g3345477
NCBI GI
                  285
BLAST score
                  9.0e-26
E value
                  77
Match length
                  74
% identity
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
                   302790
Seq. No.
                   fwa700100961.hl
Seq. ID
                   BLASTX
Method
                   g553073
NCBI GI
                   324
BLAST score
                   2.0e-30
E value
Match length
                   90
                   72
% identity
NCBI Description (M94481) reverse transcriptase [Zea mays]
                   302791
Seq. No.
                   fwa700100967.h1
Seq. ID
Method
                   BLASTN
                   g21834
NCBI GI
BLAST score
                   85
                   4.0e-40
E value
                   105
Match length
                   95
% identity
NCBI Description Wheat mRNA for cytosolic phosphoglycerate kinase (EC
                   2.7.2.3)
                   302792
Seq. No.
                   fwa700100978.h1
Seq. ID
                   BLASTX
Method
                   g3800853
NCBI GI
                   261
BLAST score
                   7.0e-23
E value
                   52
Match length
                   100
% identity
                   (AFO%4478) ribulose-1,5-bisphosphate carboxylase/oxygenase
NCBI Description
                   activase precursor [Zea mays]
                   302793
Seq. No.
                   fwa700101018.hl
Seq. ID
                   BLASTX
Method
                   g4455323
NCBI GI
BLAST score
                   220
                   4.0e-18
E value
                   79
Match length
                   53
% identity
                   (AL035525) aminopeptidase-like protein [Arabidopsis
```

42757



```
302794
Seq. No.
                  fwa700101079.h1
Seq. ID
Method
                  BLASTX
                  g115771
NCBI GI
                  505
BLAST score
E value
                  1.0e-51
Match length
                  96
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding
                  preprotein (AA 1 - 262) [Zea mays]
                  302795
Seq. No.
                  fwa700101091.hl
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3821780
                  36
BLAST score
                  6.0e-11
E value
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   302796
Seq. No.
                   fwa700101106.hl
Seq. ID
                  BLASTX
Method
                   a4567273
NCBI GI
BLAST score
                   202
                   5.0e-16
E value
Match length
                   62
% identity
                   (AC006841) putative vacuolar proton ATPase subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   302797
                   fwa700101113.h1
Seq. ID
Method
                   BLASTX
                   q4416302
NCBI GI
BLAST score
                   166
                   9.0e-12
E value
Match length
                   46
% identity
NCBI Description (AF105716) copia-type pol polyprotein [Zea mays]
                   302798
Seq. No.
                   fwa700101147.h1
 Seq. ID
Method
                   BLASTX
                   g3894186
NCBI GI
BLAST score
                   232
                   1.0e-19
E value
```

65 Match length 65 % identity

(AC005662) putative embryo-abundant protein [Arabidopsis NCBI Description

thaliana]

302799 Seq. No.

Seq. No.

Seq. ID



```
fwa700101261.h1
 Seq. ID
Method
                    BLASTX
 NCBI GI
                    q82166
                    373
 BLAST score
                    5.0e-36
 E value
                    82
 Match length
 % identity
                    glyceraldehyde-3-phosphate dehydrogenase (NADP+)
 NCBI Description
                    (phosphorylating) (EC 1.2.1.13) B, chloroplast - common
                    tobacco (fragment)
                    302800
 Seq. No.
                    fwa700101265.h1
 Seq. ID
                    BLASTX
 Method
                    q4586246
 NCBI GI
                    177
 BLAST score
                    4.0e-13
 E value
                    42
 Match length
 % identity
                    (AL049640) putative protein [Arabidopsis thaliana]
 NCBI Description
                    302801
 Seq. No.
                    fwa700101317.hl
 Seq. ID
                    BLASTN
 Method
                    g4140643
 NCBI GI
                    146
 BLAST score
                    2.0e-76
 E value
                    282
 Match length
                    45
  % identity
                    Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
 NCBI Description
                    complete sequence
                    302802
  Seq. No.
                    fwa700101340.h1
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    q115786
  BLAST score
                    240
                    1.0e-20
  E value
                    57
  Match length
  % identity
                    86
                    CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
  NCBI Description
                     (CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding
                     protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
                    mays]
                     302803
  Seq. No.
                     fwa700101364.h1
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     q168586
                     237
  BLAST score
                     4.0e-20
  E value
                     69
  Match length
                     71
  % identity
                     (M58656) pyruvate, orthophosphate dikinase [Zea mays]
  NCBI Description
                     302804
```

fwa700101418.h1



```
Method
                  q115808
NCBI GI '
                  505
BLAST score
                  1.0e-51
E value
                  96
Match length
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-91R) (LHCP) >gi_72732_pir CDPJ91 chlorophyll
                  a/b-binding protein 91R precursor - petunia
                  >gi_20487_emb_CAA26209_ (X02356) cab 91R precursor
                  polypeptide (aa -34 to 233) [Petunia sp.]
                  302805
Seq. No.
                  fwa700101440.h1
Seq. ID
                  BLASTN
Method
                  q3789951
NCBI GI
                   35
BLAST score
                   3.0e-10
E value
                  124
Match length
                   89
% identity
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
Seq. No.
                   302806
                   fwa700101449.h1
Seq. ID
                   BLASTX
Method
                   g115786
NCBI GI
                   295
BLAST score
                   7.0e-27
E value
                   68
Match length
                   82
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB) (LHCP) >gi 82680 pir_A29119 chlorophyll a/b-binding
                   protein - maize >gi 22357 emb CAA68451 (Y00379) LHCP [Zea
                   mays]
                   302807
Seq. No.
                   fwa700101530.h1
 Seq. ID
 Method
                   BLASTN
                   q435678
 NCBI GI
                   47
 BLAST score
                   2.0e-17
 E value
                   87
Match length
 % identity
                   L.esculentum Mill (cv. Rutgers) mRNA for ribosomal protein
 NCBI Description
                   302808
 Seq. No.
                   fwa700101582.h1
 Seq. ID
 Method
                   BLASTX
                   q1076781
 NCBI GI
 BLAST score
                   176
```

9.0e-22 E value Match length 64 % identity 80

NCBI Description transcription factor HBP-la(c14) - wheat



>gi 497895 dbj BAA02304 (D12920) transcription factor HBP-la(c14) [Triticum aestivum]

302809 Seq. No.

fwa700101607.hl Seq. ID

Method BLASTX NCBI GI g543938 457 BLAST score 7.0e-46 E value 98 Match length

% identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB48) (LHCP) >gi_82681_pir__S22497 chlorophyll a/b-binding protein precursor (cab-48) - maize

>gi 22228_emb_CAA44888_ (X63205) chlorophyll a /b binding

protein [Zea mays]

302810 Seq. No.

fwa700101622.hl Seq. ID

Method BLASTX g126737 NCBI GI 390 BLAST score 5.0e-38 E value Match length 74 % identity 99

MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME) NCBI Description

(ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi 65939 pir__DEZMMX malate dehydrogenase

(oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) precursor, chloroplast - maize >gi_168528 (J05130) NADP-dependent malic enzyme (EC $1.\overline{1}.1.40$) [Zea mays]

302811 Seq. No.

fwa700101634.h1 Seq. ID

BLASTX Method NCBI GI q3650039 BLAST score 245 5.0e-21 E value 92 Match length 51 % identity

(AC005396) putative En/Spm transposon protein, 5' partial NCBI Description

[Arabidopsis thaliana]

302812 Seq. No.

fwa700101636.hl Seq. ID

BLASTN Method g168527 NCBI GI BLAST score 201 1.0e-109 E value Match length 223 % identity 98

Maize NADP-dependent malic enzyme (Me1) mRNA, complete cds NCBI Description

302813 Seq. No.

fwa700101638.hl Seq. ID

BLASTX Method g1076402 NCBI GI

```
BLAST score
E value
                  3.0e-11
                  62
Match length
% identity
                  45
                  S-like ribonuclease RNS2 - Arabidopsis thaliana
NCBI Description
                  302814
Seq. No.
                  fwa700101657.hl
Seq. ID
                  BLASTX
Method
                  g3970652
NCBI GI
BLAST score
                  318
                  1.0e-29
E value
Match length
                  97
% identity
                   64
                  (X77499) amino acid permease [Arabidopsis thaliana]
NCBI Description
                   302815
Seq. No.
Seq. ID
                   fwa700101728.hl
Method
                  BLASTN
NCBI GI
                   g21843
BLAST score
                   36
                   5.0e-11
E value
                   62
Match length
                   90
% identity
                  Wheat PsbO mRNA for 33kDa oxygen evolving protein of
NCBI Description
                   photosystem II
                   302816
Seq. No.
                   fwa700101731.hl
Seq. ID
                   BLASTX
Method
                   g115786
NCBI GI
                   241
BLAST score
                   4.0e-32
E value
Match length
                   85
% identity
                   86
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB) (LHCP) >gi 82680 pir A29119 chlorophyll a/b-binding
                   protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
                   mays]
                   302817
Seq. No.
                   fwa700101744.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4406759
BLAST score
                   260
                   8.0e-23
E value
                   101
Match length
% identity
                   (AC006836) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 302818

Seq. ID fwa700101777.h1

Method BLASTX
NCBI GI g3800878
BLAST score 270
E value 2.0e-28
Match length 101



```
% identity
                   (AF096281) threonine dehydratase/deaminase [Arabidopsis
NCBI Description
                  thaliana]
                   302819
Seq. No.
                   fwa700101791.h1
Seq. ID
Method
                  BLASTX
                  q1706260
NCBI GI
                   358
BLAST score
                  2.0e-34
E value
Match length
                   90
                   78
% identity
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
NCBI Description
                   cysteine proteinase 1 precursor - maize
                   >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                   mays]
                   302820
Seq. No.
                   fwa700101807.h1
Seq. ID
Method
                   BLASTN
                   g3511235
NCBI GI
BLAST score
                   41
                   7.0e-14
E value
Match length
                   61
% identity
                   92
                   Zea mays starch branching enzyme IIb (ae) gene, complete
NCBI Description
                   302821
Seq. No.
                   fwa700101811.h1
Seq. ID
                   BLASTX
Method
                   q1402883
NCBI GI
                   141
BLAST score
E value
                   3.0e-09
                   55
Match length
% identity
                   49
                   (X98130) unknown [Arabidopsis thaliana]
NCBI Description
                   >gi_1495263_emb_CAA66119_ (X97487) orf09 [Arabidopsis
                   thaliana]
                   302822
Seq. No.
                   fwa700101868.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1707007
BLAST score
                   212
                   4.0e-17
E value
Match length
                   101
                   10
% identity
                  (U78721) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   302823
Seq. No.
                   fwa700101881.hl
Seq. ID
                   BLASTX
Method
                   g100226
NCBI GI
```

189

90

2.0e-14

BLAST score

Match length

E value



```
% identity
NCBI Description hypothetical protein - tomato >gi_19275_emb_CAA78112_
                  (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi_445619_prf__1909366A Leu zipper protein
                  [Lycopersicon esculentum]
                  302824
Seq. No.
Seq. ID
                  fwa700101891.h1
Method
                  BLASTX
NCBI GI
                  g3935148
BLAST score
                  194
E value
                  9.0e-24
Match length
                  93
% identity
                  65
NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]
                  302825
Seq. No.
                  fwa700101927.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063694
BLAST score
                  252
E value
                  3.0e-22
Match length
                  60
% identity
                  75
NCBI Description
                 (AL022537) putative protein [Arabidopsis thaliana]
                  302826
Seq. No.
Seq. ID
                  fwa700101954.h1
Method
                  BLASTN
NCBI GI
                  g22155
BLAST score
                  69
E value
                  7.0e-31
                  100
Match length
                  92
% identity
NCBI Description Z.mays mRNA for alpha-tubulin
                  302827
Seq. No.
Seq. ID
                  fxb700397435.h1
Method
                  BLASTX
NCBI GI
                  g2213600
BLAST score
                  259
E value
                  1.0e-22
Match length
                  98
                  56
% identity
NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]
                  302828
Seq. No.
                  fxb700397438.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1929998
```

Method BLASTX
NCBI GI g1929998
BLAST score 234
E value 9.0e-20
Match length 92
% identity 53

NCBI Description (U77463) NADPH-dependent HC-toxin reductase [Hordeum

vulgare]

NCBI Description

Seq. No.

Seq. ID

Method

302834

BLASTX

gct701167149.h1



```
Seq. No.
                    302829
                    fxb700397446.h1
 Seq. ID
                    BLASTX
 Method
                    g3122724
 NCBI GI
                    304
 BLAST score
 E value
                    5.0e-28
 Match length
                    69
                    84
 % identity
                    60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal
 NCBI Description
                    protein L38 isolog [Arabidopsis thaliana]
 Seq. No.
                    302830
                    fxb700397554.h1
 Seq. ID
                    BLASTN
 Method
                    q484257
 NCBI GI
                    126
 BLAST score
 E value
                    5.0e-65
 Match length
                    126
 % identity
                    Human PMP2 gene for peripheral myelin protein 2, exon
 NCBI Description
                    302831
 Seq. No.
                    fxb700397574.h1
 Seq. ID
 Method
                    BLASTX
                    q1076660
 NCBI GI
                    207
 BLAST score
                    6.0e-17
 E value
                    47
 Match length
                    81
  % identity
                    D13F(MYBST1) protein - potato >gi_786426_bbs_159122
  NCBI Description
                    (S74753) MybSt1=Myb-related transcriptional activator
                    {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                    leaf, Peptide, 342 aa] [Solanum tuberosum]
                    302832
  Seq. No.
                    fxb700397576.h1
  Seq. ID
  Method
                    BLASTX
                    q4455203
  NCBI GI
  BLAST score
                    170
                    2.0e-12
  E value
  Match length
                    88
                    24
  % identity
                    (AL035440) putative protein [Arabidopsis thaliana]
  NCBI Description
                    302833
  Seq. No.
                    fxb700397595.h1
  Seq. ID
  Method
                    BLASTN
                    g2239257
  NCBI GI
  BLAST score
                    128
                    7.0e-66
  E value
                    162
  Match length
                    96
  % identity
                    Zea mays mRNA for cinnamyl alcohol dehydrogense
```

42765



```
q3114615
NCBI GI
BLAST score
                  160
E value
                  3.0e-11
Match length
                   40
                   80
% identity
                   (AF052483) 40S ribosomal protein S12 [Erysiphe graminis f.
NCBI Description
                  sp. hordei]
                   302835
Seq. No.
                   qct701167164.h1
Seq. ID
Method
                   BLASTX
                   q3560227
NCBI GI
BLAST score
                   192
                   6.0e-15
E value
                   77
Match length
                   47
% identity
                  (AL031530) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   302836
Seq. No.
                   gct701167183.h1
Seq. ID
                   BLASTX
Method
                   q4499900
NCBI GI
                   210
BLAST score
                   4.0e-17
E value
                   82
Match length
                   44
% identity
                   (AJ133736) BM-40 [Drosophila melanogaster]
NCBI Description
Seq. No.
                   302837
                   gct701167187.h1
Seq. ID
                   BLASTX
Method
                   g2760155
NCBI GI
                   182
BLAST score
E value
                   6.0e-14
                   67
Match length
                   57
 % identity
                   (AB010048) ribosomal protein L19 [Schizosaccharomyces
NCBI Description
                   pombe]
                   302838
 Seq. No.
                   gct701167214.hl
 Seq. ID
                   BLASTX
 Method
                   g730464
 NCBI GI
 BLAST score
                   188
                   2.0e-22
 E value
                   80
 Match length
                   72
 % identity
                   40S RIBOSOMAL PROTEIN RS16 HOMOLOG (RP61R HOMOLOG)
 NCBI Description
                   >gi_2119075_pir__S67619 ribosomal protein S16.e.B - yeast
                    (Saccharomyces cerevisiae) >gi_606441_emb_CAA87357_
                    (Z47071) putative ribosomal protein [Saccharomyces]
                    cerevisiae] >gi_1431106_emb_CAA98649_ (Z74131) ORF YDL083c
                    [Saccharomyces cerevisiae]
```

302839

BLASTX

gct701167225.h1

Seq. No.

Seq. ID

Method

```
NCBI GI
                  q4322946
BLAST score
                  157
                  2.0e-11
E value
Match length
                  44
% identity
NCBI Description
                  (AF096318) cyclophilin-like peptidyl prolyl cis-trans
                  isomerase [Aspergillus niger]
                  302840
Seq. No.
Seq. ID
                  gct701167233.h1
Method
                  BLASTX
NCBI GI
                  g1723187
BLAST score
                  189
                  9.0e-24
E value
Match length
                  86
% identity
                  73
                  112.3 KD PROTEIN IN PYK1-SNC1 INTERGENIC REGION
NCBI Description
                  >gi 2131258 pir S70292 FUN12 protein - yeast
                   (Saccharomyces cerevisiae) >gi_1326056 (U12980) Fun12p:
                  97kDa protein, function unknown [Saccharomyces cerevisiae]
                  302841
Seq. No.
                  gct701167268.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1709638
                  147
BLAST score
E value
                  7.0e-18
Match length
                  72
% identity
                  58
                  CARBOXYPEPTIDASE CPDS PRECURSOR >gi 976221 dbj BAA04974
NCBI Description
                   (D25288) carboxypeptidase [Aspergillus phoenicis]
                  302842
Seq. No.
Seq. ID
                  gct701167335.h1
                  BLASTX
Method
NCBI GI
                  q3641836
BLAST score
                  142
                  1.0e-18
E value
                  93
Match length
% identity
                  48
NCBI Description
                  (AL023094) putative serine/threonine protein kinase
                  [Arabidopsis thaliana]
                  302843
Seq. No.
                  gct701167349.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499451
```

BLAST score 237 E value 2.0e-20 Match length 77 % identity 60

PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP NCBI Description

OXIDASE) >gi_532815 (U13876) similar to pyridoxamine

5'-phosphate oxidase [Caenorhabditis elegans]

Seq. No. 302844

Seq. ID gct701167358.h1



```
BLASTX
Method
NCBI GI
                  g3249084
BLAST score
                  206
                  1.0e-16
E value
                  90
Match length
                  23
% identity
NCBI Description
                  (AC004473) Similar to red-1 (related to thioredoxin) gene
                  gb X92750 from Mus musculus. ESTs gb AA712687 and
                  gb Z37223 come from this gene [Arabidopsis thaliana]
Seq. No.
                  302845
Seq. ID
                  gct701167379.h1
Method
                  BLASTX
NCBI GI
                  g2827663
BLAST score
                  173
E value
                  1.0e-12
Match length
                  92
                  5
% identity
                  (AL021637) membrane-associated salt-inducible-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  302846
Seq. No.
                  gct701167388.h1
Seq. ID
Method
                  BLASTX
                  g3386604
NCBI GI
BLAST score
                  150
E value
                  2.0e-17
Match length
                  74
% identity
                  65
NCBI Description
                  (AC004665) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  302847
Seq. ID
                  gct701167450.h1
                  BLASTN
Method
NCBI GI
                  g2245648
BLAST score
                  48
E value
                  4.0e-18
Match length
                  56
% identity
                  96
NCBI Description
                  Zea mays discolored-1 (mutant allele dsc1-Ref::Mu1) gene,
                  partial sequence
Seq. No.
                  302848
Seq. ID
                  gct701167571.h1
Method
                  BLASTX
NCBI GI
                  g1710589
BLAST score
                  260
E value
                  6.0e-23
Match length
                  62
                  87
% identity
```

NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P1 (ALLERGEN CLA H 12) (CLA H XII) >gi_1143425_emb_CAA59463_ (X85180) ribosomal protein

P1 [Cladosporium herbarum]

Seq. No. 302849

Seq. ID gct701167581.h1

Method BLASTX

```
NCBI GI
BLAST score
                  209
E value
                  6.0e-17
Match length
                  59
% identity
NCBI Description
                  (AC006260) unknown protein [Arabidopsis thaliana]
                  302850
Seq. No.
Seq. ID
                  qct701167588.hl
Method
                  BLASTX
                  g3894197
NCBI GI
BLAST score
                  221
                  2.0e-18
E value
Match length
                  85
% identity
                  51
NCBI Description
                 (AC005662) hypothetical protein [Arabidopsis thaliana]
                  302851
Seq. No.
                  gct701167622.h1
Seq. ID
Method
                  BLASTN
                  g2623247
NCBI GI
BLAST score
                  74
                  1.0e-33
E value
Match length
                  122
% identity
                  90
NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds
                  302852
Seq. No.
Seq. ID
                  gct701167659.h1
Method
                  BLASTX
NCBI GI
                  g3645898
BLAST score
                  361
E value
                  8.0e-35
                  83
Match length
% identity
                  83
                  (U68408) in-frame stop codon; possibly a post-transposition
NCBI Description
                  mutation [Zea mays]
```

Seq. No. 302853

Seq. ID gct701167743.h1

Method BLASTX NCBI GI q549689 BLAST score 183 6.0e-14 E value Match length · 65 % identity 54

HYPOTHETICAL 19.7 KD PROTEIN IN LHS1-NUP100 INTERGENIC NCBI Description REGION >gi 539174 pir S37891 hypothetical protein YKL069w

- yeast (Saccharomyces cerevisiae) >gi_433630_emb_CAA53405_

(X75780) A180 [Saccharomyces cerevisiae]

>gi_486097_emb_CAA81906_ (Z28069) ORF YKL069w

[Saccharomyces cerevisiae] >gi_1587574_prf__2206496F ORF

[Saccharomyces cerevisiae]

Seq. No. 302854

gct701167750.h1 Seq. ID

Method BLASTX

```
q3702317
NCBI GI
BLAST score
                  165
                  9.0e-12
E value
                  38
Match length
% identity
NCBI Description
                  (AC005397) unknown protein [Arabidopsis thaliana]
                  >qi 4559376 qb AAD23036.1 AC006526 1 (AC006526) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  302855
Seq. ID
                  gct701167751.h1
Method
                  BLASTX
                  g172260
NCBI GI
                  224
BLAST score
E value
                  1.0e-25
Match length
                  84
                  76
% identity
                  (M96667) proteosome-related protein [Saccharomyces
NCBI Description
                  cerevisiae]
Seq. No.
                  302856
                  gct701167777.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024525
BLAST score
                  205
                  2.0e-16
E value
Match length
                  69
                  52
% identity
NCBI Description
                  RAS-RELATED PROTEIN RAB-1C (GTP-BINDING PROTEIN RAY)
                  >gi_1082425_pir__JC2488 GTP-binding protein H-ray - human
                  >gi_763122_emb_CAA56177_ (X79781) ray [Homo sapiens]
                  >gi_3970972 (AC004812) GTP-binding protein H-ray [Homo
                  sapiens]
Seq. No.
                  302857
Seq. ID
                  gct701167790.h1
                  BLASTX
Method
NCBI GI
                  g2865394
BLAST score
                  331
E value
                  3.0e-31
                  85
Match length
                  71
% identity
                 (AF036949) basic leucine zipper protein [Zea mays]
NCBI Description
                  302858
Seq. No.
Seq. ID
                  gct701167820.hl
Method
                  BLASTX
NCBI GI
                  g2501846
```

BLAST score 235 E value 5.0e-20 Match length 84 58 % identity

NCBI Description (AF004397) chromo-helicase-DNA-binding on the Z chromosome

protein [Gallus gallus]

302859 Seq. No.

Seq. ID gct701167841.h1

Match length

57

```
BLASTX
Method
                   q2244926
NCBI GI
                   145
BLAST score
                   2.0e-09
E value
                   43
Match length
                   65
% identity
                   (Z97339) glutaredoxin [Arabidopsis thaliana]
NCBI Description
                   302860
Seq. No.
                   gct701167850.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2262173
BLAST score
                   368
                   1.0e-35
E value
                   89
Match length
                   82
% identity
                   (AC002329) NADPH thioredoxin reductase [Arabidopsis
NCBI Description
                   thaliana]
                   302861
Seq. No.
                   gct701167875.h1
Seq. ID
                   BLASTX
Method
                   g2739382
NCBI GI
BLAST score
                   146
                   8.0e-10
E value
                   53
Match length
                   49
% identity
                   (AC002505) myosin heavy chain-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   302862
Seq. No.
                   gct701167890.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4539455
                   215
BLAST score
E value
                   7.0e-18
Match length
                   56
                   75
% identity
                   (AL049500) T5C23.70 [Arabidopsis thaliana]
NCBI Description
                   302863
Seq. No.
                   gct701167910.h1
Seq. ID
                   BLASTX
Method
                   g2224663
NCBI GI
BLAST score
                   155
                   7.0e-11
E value
                   60
Match length
 % identity
                   48
                   (AB002359) KIAA0361 [Homo sapiens]
NCBI Description
 Seq. No.
                   302864
                   gct701167914.h1
 Seq. ID
 Method
                   BLASTX
                   g1432056
 NCBI GI
 BLAST score
                   231
                   9.0e-20
 E value
```

42771



```
% identity
NCBI Description (U56834) WRKY3 [Petroselinum crispum]
                  302865
Seq. No.
                  gct701168093.hl
Seq. ID
                  BLASTX
Method
                  g3080421
NCBI GI
                  206
BLAST score
                  1.0e-16
E value
                  86
Match length
                  44
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
                  302866
Seq. No.
                  gct701168114.hl
Seq. ID
                  BLASTX
Method
                  g2252634
NCBI GI
                  176
BLAST score
                   5.0e-13
E value
                  70
Match length
                   46
% identity
                  (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   302867
Seq. No.
                   gct701168165.hl
Seq. ID
                   BLASTX
Method
                   g4580463
NCBI GI
                   160
BLAST score
                   4.0e-11
E value
                   40
Match length
                   70
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   302868
Seq. No.
                   gct701168187.h1
Seq. ID
                   BLASTX
Method
                   q2578818
NCBI GI
                   140
BLAST score
                   7.0e-09
E value
                   89
Match length
                   38
% identity
                   (AB000121) TBPIP [Mus musculus]
NCBI Description
                   302869
Seq. No.
                   gct701168208.h1
Seq. ID
                   BLASTX
Method
                   q2623311
NCBI GI
                   280
BLAST score
E value
                   3.0e-25
                   74
Match length
 % identity
                   78
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
```

>gi 3402720 (AC004261) unknown protein [Arabidopsis

thaliana]

302870 Seq. No.

qct701168210.h1 Seq. ID

42772

Seq. ID

Method

```
Method
                  BLASTX
NCBI GI
                  g168918
BLAST score
                  306
E value
                  2.0e-28
Match length
                  88
% identity
                  65
                  (M13630) beta-tubulin [Neurospora crassa]
NCBI Description
                  302871
Seq. No.
                  gct701168294.h1
Seq. ID
Method
                  BLASTX
                  g481923
NCBI GI
BLAST score
                  174
E value
                  7.0e-13
Match length
                  66
                  52
% identity
NCBI Description
                  glutathione transferase (EC 2.5.1.18) - nematode
                   (Onchocerca volvulus)
                  302872
Seq. No.
Seq. ID
                  gct701168304.h1
Method
                  BLASTX
                  g585661
NCBI GI
BLAST score
                  211
E value
                  4.0e-17
Match length
                  65
                  60
% identity
NCBI Description
                  PEROXIDASE PRECURSOR >gi 287401 dbj BAA03644 (D14997)
                  peroxidase [Oryza sativa]
                  302873
Seq. No.
Seq. ID
                  gct701168314.h1
Method
                  BLASTX
                  g2330871
NCBI GI
BLAST score
                  209
                  6.0e-17
E value
Match length
                  86
% identity
                  44
                  (Z98603) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                  302874
Seq. ID
                  gct701168319.hl
Method
                  BLASTX
NCBI GI
                  g125271
BLAST score
                  170
                  2.0e-12
E value
                  33
Match length
                  100
% identity
NCBI Description
                  CASEIN KINASE II, ALPHA CHAIN (CK II) (CK2-ALPHA)
                  >gi_100860 pir_ S19726 casein kinase II (EC 2.7.1.-) alpha
                  chain - maize >gi_3318993_pdb_1A60_ Protein Kinase Ck2
                   (Catalytic Subunit) From Zea Mays >gi_22117_emb_CAA43659_
                   (X61387) casein kinase II alpha subunit [Zea mays]
Seq. No.
                  302875
```

42773

gct701168594.h1

BLASTX

```
q2213629
NCBI GI
BLAST score
                  285
                   6.0e-26
E value
                  84
Match length
                   64
% identity
NCBI Description (AC000103) F21J9.21 [Arabidopsis thaliana]
                 . 302876
Seq. No.
                  gct701168609.h1
Seq. ID
                  BLASTX
Method
                   q3540206
NCBI GI
                   235
BLAST score
                   5.0e-20
E value
                   52
Match length
% identity
NCBI Description (AC004260) Hypothetical protein [Arabidopsis thaliana]
                   302877
Seq. No.
                   qct701168771.h1
Seq. ID
                   BLASTX
Method
                   g3152596
NCBI GI
                   144
BLAST score
                   5.0e-10
E value
Match length
                   62
                   63
% identity
                  (AC002986) YUP8H12R.36 [Arabidopsis thaliana]
NCBI Description
                   302878
Seq. No.
                   gct701168773.hl
Seq. ID
                   BLASTX
Method
                   q4544449
NCBI GI
                   285
BLAST score
                   6.0e-26
E value
Match length
                   84
                   65
 % identity
                   (AC006592) putative peroxidase [Arabidopsis thaliana]
NCBI Description
                   302879
 Seq. No.
                   gct701168787.hl
 Seq. ID
 Method
                   BLASTN
                   q1304265
 NCBI GI
                   41
 BLAST score
                   3.0e-14
 E value
                   105
 Match length
 % identity
                   85
                   Triticum aestivum mRNA for HALF-1, complete cds
 NCBI Description
                   302880
 Seq. No.
                   gct701168865.hl
 Seq. ID
 Method
                   BLASTX
                   g2627440
 NCBI GI
                   175
 BLAST score
                    5.0e-13
 E value
                   71
 Match length
 % identity
                    48
                    (AF019112) protein disulfide isomerase; PDI; P5-like
 NCBI Description
                    [Dictyostelium discoideum]
```

```
302881
Seq. No.
                  gct701168874.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832680
BLAST score
                  185
                  3.0e-14
E value
Match length
                  65
                  26
% identity
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
Seq. No.
                  302882
Seq. ID
                  gct701168903.hl
Method
                  BLASTX
NCBI GI
                  q3746069
BLAST score
                  159
E value
                  4.0e-11
Match length
                  88
                  32
% identity
                  (AC005311) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  302883
Seq. ID
                  gct701168909.hl
Method
                  BLASTN
NCBI GI
                  q3851002
BLAST score
                  101
                  8.0e-50
E value
Match length
                  171
                  99
% identity
                  Zea mays pyruvate dehydrogenase E1 beta subunit isoform 3
NCBI Description
                  mRNA, nuclear gene encoding mitochondrial protein, complete
                  cds
                  302884
Seq. No.
Seq. ID
                  gct701168944.h1
Method
                  BLASTX
NCBI GI
                  g3492806
BLAST score
                  193
                  4.0e-15
E value
Match length
                  82
% identity
                  49
                  (AJ225045) adventitious rooting related oxygenase [Malus
NCBI Description
                  domestica]
                  302885
Seq. No.
Seq. ID
                  gct701168951.hl
Method
                  BLASTX
NCBI GI
                  q127111
BLAST score
                  176
E value
                   4.0e-13
                  83
Match length
                   45
% identity
                  MAK11 PROTEIN >gi 101430 pir A29938 MAK11 protein - yeast
NCBI Description
                   (Saccharomyces cerevisiae) >gi 171877 (J03506) MAK11
                  protein [Saccharomyces cerevisiae] >gi_486013_emb_CAA81856_
```

....

42775

(Z28021) ORF YKL021c [Saccharomyces cerevisiae]



```
Seq. No.
                  302886
                  gct701169008.h1
Seq. ID
                  BLASTX
Method
                  q2865171
NCBI GI
                   291
BLAST score
                   1.0e-26
E value
Match length
                   73
                   75
% identity
                   (AB010901) ribosomal protein L21 homolog
NCBI Description
                   [Schizosaccharomyces pombe]
                   302887
Seq. No.
                   gct701169011.hl
Seq. ID
                   BLASTX
Method
                   q3668074
NCBI GI
                   259
BLAST score
                   8.0e-23
E value
                   73
Match length
                   60
% identity
                   (AC004667) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   302888
Seq. No.
                   gct701169046.h1
Seq. ID
                   BLASTX
Method
                   g3600052
NCBI GI
                   314
BLAST score
                   3.0e-29
E value
                   79
Match length
                   71
% identity
                   (AF080120) contains similarity to glycosyl hydrolases
NCBI Description
                   family 9 (Pfam: glycosyl_hydro5.hmm, score: 88.03)
                   [Arabidopsis thaliana]
                   302889
Seq. No.
                   gct701169086.hl
Seq. ID
Method
                   BLASTX
                   q3688209
NCBI GI
                   278
BLAST score
E value
                   5.0e-25
Match length
                   85
                   67
% identity
                   (AJ010093) MAP3K beta 1 protein kinase [Brassica napus]
NCBI Description
                   302890
Seq. No.
                   gct701169105.h1
Seq. ID
                   BLASTN
Method
                   q168406
NCBI GI
BLAST score
                   38
                   4.0e-12
E value
Match length
                   146
                   70
 % identity
                   Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,
NCBI Description
                   complete cds
```

302891

gct701169111.h1

Seq. No.

Seq. ID



```
BLASTX
Method
NCBI GI
                   q462665
                    271
BLAST score
E value
                    2.0e-24
Match length
                    84
                    71
 % identity
                   MAJOR VAULT PROTEIN ALPHA (MVP-ALPHA)
 NCBI Description
                    >gi_539069_pir__A47132 major vault protein alpha - slime
                   mold (Dictyostelium discoideum) >gi_167960 (L08646) major
                    vault protein-alpha [Dictyostelium discoideum]
                    302892
 Seq. No.
 Seq. ID
                    gct701169132.hl
                    BLASTX
 Method
                    q4567305
 NCBI GI
                    293
 BLAST score
                    8.0e-27
 E value
                    88
 Match length
 % identity
                    60
                    (AC005956) hypothetical protein [Arabidopsis thaliana]
"NCBI Description
                    302893
 Seq. No.
                    gct701169152.hl
 Seq. ID
 Method
                    BLASTX
                    q4490342
 NCBI GI
 BLAST score
                    284
                    5.0e-26
 E value
                    84
 Match length
 % identity
                    70
                    (AL035656) putative protein [Arabidopsis thaliana]
 NCBI Description
                    302894
 Seq. No.
                    gct701169206.h1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4539301
                    145
 BLAST score
                    2.0e-09
 E value
 Match length
                    71
                    41
 % identity
                    (AL049480) putative mitochondrial protein [Arabidopsis
 NCBI Description
                    thaliana]
                    302895
 Seq. No.
                    gct701169219.hl
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g22364
 BLAST score
                    38
 E value
                    3.0e-12
                    42
 Match length
  % identity
                    98
                    Zea mays (Bz-McC allele) bz1 gene for UFGT
  NCBI Description
                    (UDPglucose:flavonol 3-0-glucosyltransferase)
```

Seq. No. 302896

Seq. ID gct701169255.h1

Method BLASTX NCBI GI g3183094

Method

NCBI GI

BLASTX

q4581108



```
183
BLAST score
                  6.0e-14
E value
                  40
Match length
                   90
% identity
                  ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE)
NCBI Description
                   (ORNITHINE TRANSCARBAMYLASE) >gi 971168 (U13684) ornithine
                  carbamoyltransferase [Pisum sativum]
                  302897
Seq. No.
Seq. ID
                  gct701169332.h1
Method
                  BLASTN
NCBI GI
                  g4160401
BLAST score
                   56
E value
                   7.0e-23
Match length
                   128
                   87
% identity
NCBI Description
                  Zea mays eIF-5 gene, exons 1-2
                   302898
Seq. No.
                   gct701169348.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3183130
BLAST score
                   325
E value
                   1.0e-30
Match length
                   84
                   70
% identity
                   PROBABLE GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK)
NCBI Description
                   >qi 2330720 emb CAB11222 (Z98597) hypothetical glutamate
                   5-kinase [Schizosaccharomyces pombe]
                   302899
Seq. No.
Seq. ID
                   gct701169427.h1
Method
                   BLASTX
NCBI GI
                   g4056506
BLAST score
                   167
                   3.0e-12
E value
                   53
Match length
                   55
% identity
                   (AC005896) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   302900
Seq. No.
Seq. ID
                   gct701169448.hl
                   BLASTX
Method
NCBI GI
                   g3193302
BLAST score
                   151
                   2.0e-10
E value
                   54
Match length
                   57
% identity
                   (AF069298) contains similarity to a protein kinase domain
NCBI Description
                   (Pfam: pkinase.hmm, score: 166.20) and to legume lectins
                   beta domain (Pfam: lectin_legB.hmm, score: 139.32)
                   [Arabidopsis thaliana]
                   302901
Seq. No.
Seq. ID
                   qct701169476.h1
```

42778



```
BLAST score
E value
                   1.0e-14
Match length
                   52
                   65
% identity
                   (AC005825) putative chloroplast outer membrane protein
NCBI Description
                   86, also very similar to GTP-inding protein from pea
                   (GB:L36857) [Arabidopsis thaliana]
                   302902
Seq. No.
                   gct701169484.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g404364
BLAST score
                   89
E value
                   7.0e-43
                   132
Match length
% identity
                   preprotrypsin [Fusarium oxysporum, mycelium, mRNA, 998 nt]
NCBI Description
                   >gi_2297153_emb_A41499.1_A41499 Sequence 1 from Patent
                   W09426925 >gi 3013433 gb 177279 177279 Sequence 1 from patent US 5693520 >gi 3206709 gb 186991 186991 Sequence 1
                   from patent US
                   302903
Seq. No.
                    gct701169512.h1
Seq. ID
Method
                   BLASTX
                    g2130196
NCBI GI
                    156
BLAST score
                    6.0e-11
E value
                    50
Match length
                    64
% identity
                   E6-AP-like protein ubiquitin ligase Pub1 - fission yeast
NCBI Description
                    (Schizosaccharomyces pombe) >gi_1502364_emb_CAA68867_
                    (Y07592) ubiquitin--protein ligase [Schizosaccharomyces
                    pombe] >gi 1519444 (U66716) E6-AP-like protein ubiquitin
                    ligase [Schizosaccharomyces pombe]
                    302904
Seq. No.
                    gct701169578.h1
Seq. ID
                    BLASTN
Method
NCBI GI
                    q168394
                    132
BLAST score
                    2.0e-68
E value
                    136
Match length
                    99
% identity
NCBI Description Wuglu; Zea mays; ; 1292 base-pairs
                    302905
Seq. No.
                    qct701170759.h1
Seq. ID
```

Method BLASTX q3757525 NCBI GI BLAST score 217 7.0e-18 E value Match length 76 50 % identity

(AC005167) tetracycline transporter-like protein, 3' NCBI Description

partial [Arabidopsis thaliana]



```
302906
Seq. No.
                    act701170773.hl
Seq. ID
                    BLASTX
Method
                    q127980
NCBI GI
                     286
BLAST score
                     6.0e-26
E value
                     78
Match length
                     69
% identity
                    NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE) (ABNORMAL
NCBI Description
                     WING DISCS PROTEIN) (KILLER-OF-PRUNE PROTEIN)
                    >gi_84896_pir__S01908 awd protein - fruit fly (Drosophila
                     melanogaster) >gi_515218_pdb_1NDL_A Drosophila melanogaster
                     >gi_515219_pdb_1NDL_B Drosophila melanogaster
                     >gi_515220_pdb_1NDL_C Drosophila melanogaster
                    >gi_1065372 pdb_1NSQ_A Drosophila melanogaster
>gi_1065373 pdb_1NSQ_B Drosophila melanogaster
>gi_1065374 pdb_1NSQ_C Drosophila melanogaster
>gi_7635_emb_CAA31500_ (X13107) put. awd protein
                     [Drosophila melanogaster]
                     302907
Seq. No.
                     gct701170816.h1
Seq. ID
                     BLASTX
Method
                     g543842
NCBI GI
BLAST score
                     236
                     4.0e-20
E value
                     48
Match length
                     98
% identity
                     ADP-RIBOSYLATION FACTOR 1 >gi_477617_pir__A49520
NCBI Description
                     ADP-ribosylation factor 1 - fruit fly (Drosophila
                     melanogaster) >gi_385340_bbs_133334 (S62079)
                     ADP-ribosylation \overline{f}actor \overline{1}, A\overline{R}F 1 [Drosophila melanogaster,
                     Peptide, 182 aa] [Drosophila melanogaster]
                     302908
Seq. No.
                     gct701170834.h1
Seq. ID
Method
                     BLASTN
                     a577818
NCBI GI
                     33
BLAST score
E value
                     4.0e-09
Match length
                     53
                     91
% identity
NCBI Description Z.mays gene for H2B histone (gH2B4)
Seq. No.
                     302909
                     gct701170868.h1
Seq. ID
                     BLASTX
Method
                     q4309698
NCBI GI
BLAST score
                     151
E value
                     4.0e-10
Match length
                     58
                     52
% identity
                      (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                     thaliana]
```

302910

gct701170901.h1

Seq. No.

Seq. ID



```
BLASTX
Method
                   q1706492
NCBI GI
                   144
BLAST score
                   2.0e-09
E value
                   54
Match length
                   59
% identity
NCBI Description DPY-30 PROTEIN >gi_733065 (U21302) nuclear protein
                   essential for dosage compensation [Caenorhabditis elegans]
                   >gi_3881834_emb_CAB01452_ (Z78019) predicted using
Genefinder; Identity to C.elegans DPY-30 protein
                   (TR:G733065); cDNA EST CEMSB57R comes from this gene; cDNA
                   EST EMBL: D71517 comes from this gene; cDNA EST EMBL: D73128
                   comes from this gene; cDNA EST EMBL
                   302911
Seq. No.
                   gct701170944.h1
Seq. ID
                   BLASTX
Method
                   g136053
NCBI GI
                   201
BLAST score
                   5.0e-16
E value
                   73
Match length
                   51
% identity
                   TRIOSEPHOSPHATE ISOMERASE (TIM) >gi 68427 pir_ISASTN
NCBI Description
                   triose-phosphate isomerase (EC 5.3.1.1) - Emericella
                   nidulans >gi_217921_dbj_BAA00908_ (D10019) triosephosphate
                   isomerase [Emericella nidulans]
                   302912
Seq. No.
                   gct701170947.h1
Seq. ID
                   BLASTX
Method
                   g4154352
NCBI GI
                   182
BLAST score
                    7.0e-14
E value
                    77
Match length
                    49
% identity
                   (AF110333) PrMC3 [Pinus radiata]
NCBI Description
                    302913
Seq. No.
                    gct701170977.h1
Seq. ID
                    BLASTX
Method
                    q2500378
NCBI GI
                    143
BLAST score
                    2.0e-09
E value
                    30
Match length
                    80
 % identity
NCBI Description 60S RIBOSOMAL PROTEIN L37
                    302914
 Seq. No.
                    gct701170992.hl
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q1171666
```

Method BLASTX
NCBI GI g1171666
BLAST score 159
E value 3.0e-11
Match length 46
% identity 63

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 14.8 KD SUBUNIT (COMPLEX I-14.8KD) (CI-14.8KD) >gi_1084978_pir__S43840 NADH

dehydrogenase (ubiquinone) (EC 1.6.5.3) - Neurospora crassa
>gi_475915_emb_CAA53963_ (X76344) NADH dehydrogenase
(ubiquinone) [Neurospora crassa]

302915 Seq. No. gct701171005.h1 Seq. ID BLASTX Method q4218120 NCBI GI 218 BLAST score E value 5.0e-18 65 Match length % identity 60 (AL035353) Proline-rich APG-like protein [Arabidopsis NCBI Description thaliana] 302916 Seq. No. gct701171045.h1 Seq. ID BLASTX Method

Method BLASTX
NCBI GI g4510345
BLAST score 154
E value 1.0e-10
Match length 47

% identity 57

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 302917

Seq. ID gct701171088.h1

Method BLASTX
NCBI GI g2541876
BLAST score 183
E value 6.0e-14
Match length 82
% identity 44

NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein

[Nicotiana tabacum]

Seq. No. 302918

Seq. ID gct701172304.h1

Method BLASTX
NCBI GI g4455274
BLAST score 159
E value 4.0e-17
Match length 72
% identity 67

NCBI Description (AL035527) spliceosome associated protein-like [Arabidopsis

thaliana]

Seq. No. 302919

Seq. ID gct701172318.h1

Method BLASTN
NCBI GI g699622
BLAST score 45
E value 3.0e-16
Match length 45
% identity 100

NCBI Description Maize mRNA for glutamine synthetase, complete cds

NCBI Description



```
Seq. No.
                  302920
                  gct701172321.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2935344
BLAST score
                  337
E value
                  6.0e-32
Match length
                  86
                  72
% identity
NCBI Description (AF044313) anion channel protein [Arabidopsis thaliana]
Seq. No.
                  302921
Seq. ID
                  qct701172331.h1
Method
                  BLASTX
NCBI GI
                  q2829672
BLAST score
                   148
E value
                   9.0e-10
                   46
Match length
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 >gi 4240113_dbj_BAA74836_
NCBI Description
                   (AB001574) SUI1 homologue [Schizosaccharomyces pombe]
                   302922
Seq. No.
Seq. ID
                   gct701172436.h1
Method
                  BLASTX
                   q4263510
NCBI GI
                   222
BLAST score
                   1.0e-18
E value
                   57
Match length
% identity
                   79
NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   302923
Seq. ID
                   gct701172459.h1
Method
                   BLASTX
NCBI GI
                   g1346521
BLAST score
                   338
                   4.0e-32
E value
Match length
                   71
% identity
                   92
                   S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
                   >gi 2133316_pir__S65800 methionine adenosyltransferase (EC
                   2.5.1.6) - Neurospora crassa >gi_882335 (U21547)
                   S-adenosylmethionine synthetase [Neurospora crassa]
                   >gi 1589103 prf 2210293A Met(S-adenosyl) synthetase
                   [Neurospora crassa]
                   302924
Seq. No.
                   gct701172538.h1
Seq. ID
                   BLASTX
Method
                   g4455285
NCBI GI
                   141
BLAST score
E value
                   2.0e-20
                   81
Match length
                   67
% identity
```

(AL035527) hypothetical protein [Arabidopsis thaliana]



```
302925
Seq. No.
                  gct701172545.hl
Seq. ID
Method
                  BLASTN
                  g3819267
NCBI GI
                  68
BLAST score
                  5.0e-30
E value
Match length
                  116
                  90
% identity
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0526.uni
                   302926
Seq. No.
                  gct701172659.h1
Seq. ID
Method
                  BLASTX
                   q2708309
NCBI GI
BLAST score
                   210
                   5.0e-17
E value
                   55
Match length
                   67
% identity
                   (AF016371) U-snRNP-associated cyclophilin [Homo sapiens]
NCBI Description
                   >gi_3647230 (AF036331) cyclophilin [Homo sapiens]
                   302927
Seq. No.
                   gct701172715.h2
Seq. ID
Method
                   BLASTX
                   g3046695
NCBI GI
                   273
BLAST score
                   2.0e-24
E value
                   76
Match length
                   68
% identity
                   (AL022224) putative protein [Arabidopsis thaliana]
NCBI Description
                   302928
Seq. No.
                   gct701172735.h2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2286153
BLAST score
                   258
                   1.0e-22
E value
                   76
Match length
% identity
                   70
                   (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                   302929
Seq. No.
                   gct701172739.h2
Seq. ID
                   BLASTX
Method
                   g2660670
NCBI GI
                   293
BLAST score
                   8.0e-27
E value
                   85
Match length
 % identity
                   (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
NCBI Description
                   thaliana]
                   302930
 Seq. No.
                   gct701172814.h2
 Seq. ID
                   BLASTX
Method
                   g4262232
 NCBI GI
```

BLAST score



```
6.0e-12
E value
Match length
                  86
                   43
% identity
                   (AC006200) putative ribosomal protein L7 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   302931
                   gct701172834.h2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2851483
BLAST score
                   240
E value
                   1.0e-20
Match length
                   78
                   68
% identity
                   HEAT SHOCK PROTEIN HSP1 (65 KD IGE-BINDING PROTEIN)
NCBI Description
                   >gi_1930153 (U92465) heat shock protein [Aspergillus
                   fumigatus]
                   302932
Seq. No.
Seq. ID
                   qct701172919.h2
Method
                   BLASTX
NCBI GI
                   q3395440
BLAST score
                   188
E value
                   2.0e-14
                   68
Match length
                   47
% identity
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   302933
                   gct701172937.h2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3513738
BLAST score
                   259
                   8.0e-23
E value
Match length
                   80
% identity
                   57
                   (AF080118) similar to the GDSL family of lipolytic enzymes
NCBI Description
                   [Arabidopsis thaliana]
                   302934
Seq. No.
                   gct701173011.h2
Seq. ID
                   BLASTX
Method
                   g1769887
NCBI GI
                   272
BLAST score
                   1.0e-24
E value
                   60
Match length
                   78
% identity
                   (X95736) amino acid permease 6 [Arabidopsis thaliana]
NCBI Description
                   302935
Seq. No.
Seq. ID
                   gct701173070.h2
                   BLASTX
Method
NCBI GI
                   g4239696
                   215
BLAST score
                   1.0e-17
E value
                   59
Match length
```

% identity



```
(AJ132767) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  302936
Seq. No.
                  gct701173093.h2
Seq. ID
                  BLASTX
Method
                  q3845301
NCBI GI
BLAST score
                  160
                  4.0e-11
E value
                  52
Match length
                  67
% identity
                  (AE001422) ribosomal protein S30 [Plasmodium falciparum]
NCBI Description
                  302937
Seq. No.
                  qct701173127.h1
Seq. ID
                  BLASTX
Method
                  q4539301
NCBI GI
                  259
BLAST score
                  8.0e-23
E value
                  73
Match length
                   64
% identity
                  (AL049480) putative mitochondrial protein [Arabidopsis
NCBI Description
                  thaliana]
                   302938
Seq. No.
                   gct701173167.h1
Seq. ID
                   BLASTX
Method
                   g4587556
NCBI GI
                   302
BLAST score
                   8.0e-28
E value
                   89
Match length
                   63
% identity
                   (AC006577) Similar to gi 1653162 (p)ppGpp
NCBI Description
                   3-pyrophosphohydrolase from Synechocystis sp genome
                   gb_D90911. EST gb_W43807 comes from this gene.
                   [Arabidopsis thaliana]
                   302939
Seq. No.
                   gct701173218.h2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1170092
                   190
BLAST score
                   1.0e-14
E value
                   45
Match length
                   73
% identity
                   GLUTATHIONE S-TRANSFERASE IV (GST-IV) (GST-27) (CLASS PHI)
NCBI Description
                   >qi 1076807 pir S52037 glutathione transferase (EC
                   2.5.1.18) 27K chain - maize >gi_529015 (U12679) glutathione
                   S-transferase IV [Zea mays] >gi_695789_emb_CAA56047_
                   (X79515) glutathione transferase [Zea mays]
                   >gi 1094866_prf__2106424A glutathione
                   S-transferase: ISOTYPE=IV [Zea mays]
                   302940
 Seq. No.
                   gct701173267.h2
 Seq. ID
 Method
                   BLASTN
```

42786

g21810

.34

NCBI GI

BLAST score

```
7.0e-10
E value
                  38
Match length
                  97
% identity
                  T.aestivum mRNA for heat shock protein 26.6B
NCBI Description
                  302941
Seq. No.
                  gct701173270.h2
Seq. ID
Method
                  BLASTX
                  g218511
NCBI GI
                  181
BLAST score
E value
                  1.0e-13
Match length
                  53
% identity
                  (D10226) ribosomal protein YL16 [Saccharomyces cerevisiae]
NCBI Description
                  302942
Seq. No.
                   gct701173358.h2
Seq. ID
Method
                  BLASTX
                   g2826786
NCBI GI
                   173
BLAST score
                   7.0e-13
E value
                   42
Match length
% identity
                   79
                  (Y10905) RAPB protein [Oryza sativa]
NCBI Description
                   302943
Seq. No.
                   qct701173469.h2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3551960
                   329
BLAST score
                   4.0e-31
E value
                   76
Match length
% identity
                   (AF082033) senescence-associated protein 15 [Hemerocallis
NCBI Description
                   hybrid cultivar]
                   302944
Seq. No.
                   gct701173560.h1
Seq. ID
Method
                   BLASTX
                   g1170140
NCBI GI
                   247
BLAST score
                   4.0e-41
E value
                   85
Match length
                   96
% identity
                   PUTATIVE ENDOGLUCANASE TYPE K PRECURSOR
NCBI Description
                   (ENDO-1,4-BETA-GLUCANASE) (CELLULASE) >gi_520823 (L29381)
                   K-family cellulase homologue [Fusarium oxysporum]
                   302945
Seq. No.
                   gct701173585.h1
Seq. ID
                   BLASTX
Method
                   g1346945
NCBI GI
BLAST score
                   152
                   7.0e-15
E value
                   60
Match length
                   67
 % identity
NCBI Description 60S RIBOSOMAL PROTEIN YL35 (L37A) >gi_1084777_pir__S54068
```



ribosomal protein L37a.e - yeast (Saccharomyces cerevisiae) >gi 805027_emb_CAA89164_ (Z49219) unknown [Saccharomyces cerevisiae] >gi 1314115_emb_CAA94991_ (Z71255) unknown [Saccharomyces cerevisiae] >gi_1370300_emb_CAA97993_ (Z73616) 10 kDa protein of 60S ribosomal subunit [Saccharomyces cerevisiae] >gi_2131104_emb_CAA89623_ (Z49594) ORF YJR094w-a [Saccharomyces cerevisiae] >gi 2131105 emb CAA89625_ (Z49595) ORF YJR094w-a [Saccharomyces cerevisiae]

302946 Seq. No. act701173616.hl Seq. ID Method BLASTX q2499488 NCBI GI BLAST score 299

3.0e-30 E value 89 Match length 73 % identity

PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE NCBI Description

ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))

(PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)

(PPI-PFK) >gi_483547 emb_CAA83682_ (Z32849)

pyrophosphate-dependent phosphofructokinase alpha subunit

[Ricinus communis]

302947 Seq. No.

gct701173618.hl Seq. ID

BLASTX Method q1049374 NCBI GI 201 BLAST score 5.0e-16 E value 62 Match length 68 % identity

(U39649) possible psuedogene, similar to blt101 NCBI Description

protein-barley PIR:S40406 and ZK632.10 Swiss Prot: P34655

[Caenorhabditis elegans]

302948 Seq. No.

gct701173648.hl Seq. ID

Method BLASTX q416615 NCBI GI 330 BLAST score 4.0e-31 E value 92 Match length % identity

ALKALINE PROTEINASE PRECURSOR (ALP) >gi_419912_pir__S32905 NCBI Description

serine proteinase (EC 3.4.21.-) prb1 precursor - fungus (Trichoderma harzianum) >gi_170539 (M87516) alkaline proteinase [Trichoderma harzianum] >gi 170545 (M87518)

alkaline proteinase [Trichoderma harzianum]

302949 Seq. No.

gct701173678.h1 Seq. ID

BLASTX Method g516118 NCBI GI 254 BLAST score 2.0e-30 E value

```
Match length
                   72
% identity
                   (L08469) envelope Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
                   302950
Seq. No.
                   gct701173691.hl
Seq. ID
                    BLASTX
Method
                   q1352223
NCBI GI
                    250
BLAST score
                    9.0e-22
E value
                    85
Match length
                    52
% identity
                   ORNITHINE DECARBOXYLASE (ODC) >gi 67992 pir DCHYOC
NCBI Description
                   ornithine decarboxylase (EC 4.1.1.17) - Chinese hamster >gi_49440 emb_CAA34784_ (X16910) ornithine decarboxylase
                    (AA 1-455) [Cricetus cricetus]
                    302951
Seq. No.
                    gct701173708.h1
Seq. ID
                    BLASTX
Method
                    g729823
NCBI GI
                    319
BLAST score
                    9.0e-30
E value
                    92
Match length
                    67
% identity
                    INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
NCBI Description
                    >gi_1084977_pir__S55278 translation initiation factor
                    eIF-5A - Neurospora crassa >gi_409567 (U02638) initiation
                    factor 5a [Neurospora crassa]
                    302952
Seq. No.
                    gct701173745.h1
Seq. ID
                    BLASTX
Method
                    g3075400
NCBI GI
                    152
BLAST score
                    3.0e-10
E value
                    43
Match length
% identity
                    60
```

NCBI Description (AC004484) putative thromboxane-A synthase [Arabidopsis thaliana] >gi_3413720 (AC004747) putative thromboxin-A

synthase [Arabidopsis thaliana]

Seq. No. 302953

Seq. ID gct701173762.h1

Method BLASTX
NCBI GI g1710760
BLAST score 235
E value 6.0e-20
Match length 54
% identity 87

NCBI Description PROBABLE 40S RIBOSOMAL PROTEIN S28 (S33)

>gi_1256529_emb_CAA94635_ (Z70691) ribosomal protein S28
[Schizosaccharomyces pombe] >gi_3581915_emb_CAA20854_

(AL031545) probable 40s ribosomal protein 28s

[Schizosaccharomyces pombe]

Seq. No. 302954

Seq. ID

Method



```
gct701173778.h1
Seq. ID
Method
                   BLASTN
                   q4160401
NCBI GI
                   48
BLAST score
                   4.0e-18
E value
                   88
Match length
% identity
                   Zea mays eIF-5 gene, exons 1-2
NCBI Description
                   302955
Seq. No.
                   gct701173786.hl
Seq. ID
                   BLASTX
Method
                   g3236247
NCBI GI
BLAST score
                   176
                   4.0e-13
E value
                   78
Match length
                   44
% identity
                   (AC004684) SCARECROW-like protein [Arabidopsis thaliana]
NCBI Description
                   302956
Seq. No.
                   gct701173804.h1
Seq. ID
                   BLASTX
Method
                   g3123215
NCBI GI
                   214
BLAST score
                   2.0e-17
E value
                   67
Match length
                   60
% identity
                   DNAJ PROTEIN >gi 1514439 dbj_BAA12282_ (D84222) DnaJ
NCBI Description
                   homologue [Thermus thermophilus] >gi_1542950_emb_CAA69161_
                    (Y07826) DnaJ-homologue [Thermus thermophilus]
                   302957
Seq. No.
                   gct701173857.h1
Seq. ID
                   BLASTX
Method
                   g4559380
NCBI GI
BLAST score
                   181
E value
                    4.0e-19
                    76
Match length
 % identity
                    (AC006526) putative auxin-responsive GH3 protein
 NCBI Description
                    [Arabidopsis thaliana]
                    302958
 Seq. No.
                    gct701173877.h1
 Seq. ID
 Method
                    BLASTX
                    g2702277
 NCBI GI
                    143
 BLAST score
                    3.0e-09
 E value
 Match length
                    71
 % identity
                    45
                    (AC003033) putative cyclin g-associated kinase [Arabidopsis
 NCBI Description
                    thaliana] >gi 2914689 (AC003974) putative cyclin
                    g-associated \overline{k}inase [Arabidopsis thaliana]
                    302959
 Seq. No.
```

42790

gct701173894.h1

BLASTX

```
q4646223
NCBI GI
                  210
BLAST score
                  2.0e-19
E value
                  81
Match length
% identity
                   (AC007295) hypothetical protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
                  302960
Seq. No.
                  gct701173901.h1
Seq. ID
                  BLASTX
Method
                  g431762
NCBI GI
                   237
BLAST score
                  3.0e-20
E value
                  73
Match length
% identity
                  56
                  (L22494) cytochrome b5 [Saccharomyces cerevisiae]
NCBI Description
                   302961
Seq. No.
                   gct701173909.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2104536
BLAST score
                   177
                   2.0e-13
E value
Match length
                   45
                   64
% identity
                   (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                   thaliana]
                   302962
Seq. No.
                   gct701173932.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3218543
                   397
BLAST score
                   6.0e-39
E value
                   86
Match length
                   90
% identity
                   (AB004813) alternative oxidase [Oryza sativa]
NCBI Description
                   >qi 3218548 dbj BAA28774 (AB004865) alternative oxidase
                   [Oryza sativa]
                   302963
Seq. No.
Seq. ID
                   gct701174166.h1
                   BLASTX
Method
NCBI GI
                   g1708191
                   184
BLAST score
                   6.0e-14
E value
                   47
Match length
                   64
% identity
                   HEXOSE CARRIER PROTEIN HEX6 >gi 467319 (L08188) hexose
NCBI Description
                   carrier protein [Ricinus communis]
```

Seq. No. 302964 gct701174188.h1 Seq. ID

BLASTN Method

NCBI GI g2226330 BLAST score 73

Match length

NCBI Description

% identity

93

48



```
2.0e-33
E value
Match length
                   102
% identity
                   Zea mays physical impedance induced protein (IIG2) mRNA,
NCBI Description
                   complete cds
                   302965
Seq. No.
                   gct701174191.h1
Seq. ID
                   BLASTX
Method
                   g2275204
NCBI GI
BLAST score
                   266
                   1.0e-23
E value
Match length
                   82
% identity
                   56
                   (AC002337) DNA binding protein isolog [Arabidopsis
NCBI Description
                   thaliana]
                   302966
Seq. No.
                   gct701174253.h1
Seq. ID
                   BLASTX
Method
                   g4406761
NCBI GI
                   338
BLAST score
                   5.0e-32
E value
                                              W.
                   84
Match length
% identity
                   79
                   (AC006836) putative ubiquinone biosynthesis protein
NCBI Description
                   [Arabidopsis thaliana]
                   302967
Seq. No.
                   gct701174261.hl
Seq. ID
Method
                   BLASTX
                   g2980768
NCBI GI
                   178
BLAST score
E value
                   3.0e-13
                   45
Match length
                   78
% identity
                   (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                   302968
Seq. No.
Seq. ID
                   gct701174304.h1
                   BLASTX
Method
                   g3341696
NCBI GI
                   299
BLAST score
                   2.0e-27
E value
Match length
                   96
                   60
% identity
                   (AC003672) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   302969
                    qct701174319.h1
Seq. ID
Method
                   BLASTX
                   g4079632
NCBI GI
                   246
BLAST score
                   3.0e-21
E value
```

(AJ131722) hypothetical protein [Arabidopsis thaliana]

```
302970
Seq. No.
                   gct701174339.h1
Seq. ID
                   BLASTX
                   g3420004
NCBI GI
```

208 9.0e-17

92

% identity (AF000305) steroid sulfotransferase 1 [Brassica napus] NCBI Description

Seq. No. 302971 Seq. ID gct701174365.hl Method BLASTX

NCBI GI q4558558 BLAST score 224 E value 1.0e-18 Match length 87 47 % identity

Method

E value Match length

BLAST score

(AC007138) putative polygalacturonidase [Arabidopsis NCBI Description

thaliana]

Seq. No. 302972

Seq. ID gct701174367.hl

Method BLASTX NCBI GI q1574946 BLAST score 222 E value 2.0e-18 Match length 53 77 % identity

(U38612) caffeoyl-coenzymeA O-methyltransferase [Nicotiana NCBI Description

tabacum]

302973 Seq. No.

Seq. ID gct701174387.h1

Method BLASTX q1841864 NCBI GI BLAST score 142 E value 4.0e-09 Match length 52 % identity

(U87108) nucleic acid binding protein [Trypanosoma NCBI Description

equiperdum]

302974 Seq. No.

Seq. ID gct701174755.h1

Method BLASTX NCBI GI g2598575 BLAST score 216 7.0e-18 E value 59 Match length 66 % identity

(Y15293) MtN21 [Medicago truncatula] NCBI Description

302975 Seq. No.

Seq. ID gct701174816.hl

BLASTX Method



```
g3289002
NCBI GI
BLAST score
                  410
                  2.0e-40
E value
Match length
                  83
                   94
% identity
NCBI Description (AF073522) CRP1 [Zea mays]
                  302976
Seq. No.
```

gct701174842.h1 Seq. ID Method BLASTX NCBI GI q3687251 BLAST score 171 E value 2.0e-12 69 Match length

% identity 54

NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

```
Seq. No.
                   302977
                   gct701174874.h1
Seq. ID
Method
                   BLASTX
                   q548584
NCBI GI
                   332
BLAST score
```

E value 2.0e-31 Match length 78 72 % identity

SERINE/THREONINE PROTEIN PHOSPHATASE PPE1 (PHOSPHATASE NCBI Description

ESP1) >gi_477056_pir__A47727 cell shape control protein phosphatase ppel - fission yeast (Schizosaccharomyces pombe) >gi_312020_emb_CAA79358_ (Z18925) type2A-like

protein phosphatase [Schizosaccharomyces pombe]

>gi 391946 dbj BAA02865 (D13712) protein phosphatase [Schizosaccharomyces pombe] >gi_3581888_emb_CAA20786_

(AL031540) serine-threonine protein phosphatase

[Schizosaccharomyces pombe]

Seq. No. 302978

gct701174884.h1 Seq. ID

Method BLASTX NCBI GI q2501499 BLAST score 275 1.0e-24 E value Match length 85 % identity

NCBI Description INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE (IAA-GLU

SYNTHETASE) ((URIDINE

5'-DIPHOSPHATE-GLUCOSE: INDOL-3-YLACETYL)-BETA-D-GLUCOSYL TRANSFERASE) >gi_626043_pir__A54739 indole-3-acetate beta-glucosyltransferase (EC 2.4.1.121) - maize >gi_548195

(L34847) IAA-glu synthetase [Zea mays]

302979 Seq. No.

Seq. ID gct701174937.hl

Method BLASTX g2961466 NCBI GI BLAST score 154 1.0e-10 E value Match length 46



```
% identity
                   (U97699) LIM domain protein [Dictyostelium discoideum]
 NCBI Description
                    302980
 Seq. No.
                    gct701175046.h1
 Seq. ID
                    BLASTX
 Method
                    g3522943
 NCBI GI
                    313
 BLAST score
                    4.0e-29
 E value
                    89
 Match length
                    41
 % identity
                    (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
 NCBI Description
                    302981
 Seq. No.
                    gct701175062.h1
 Seq. ID
                    BLASTX
 Method
                    g2829918
 NCBI GI
                    230
 BLAST score
                    3.0e-19
 E value
                    70
 Match length
                    66
  % identity
                    (AC002291) similar to "tub" protein gp_U82468_2072162
 NCBI Description
                    [Arabidopsis thaliana]
                    302982
  Seq. No.
                    gct701175119.h1
  Seq. ID
                    BLASTX
  Method -
                    g282881
  NCBI GI
                    270
  BLAST score
                    4.0e-24
  E value
                    84
  Match length
                    62
  % identity
                    receptor-like protein kinase precursor - Arabidopsis
  NCBI Description
                    thaliana >gi_166846 (M84658) receptor-like protein kinase
                    [Arabidopsis thaliana]
                    302983
  Seq. No.
                    gct701175136.h1
  Seq. ID
                    BLASTX
  Method
                    q3776559
  NCBI GI
                    261
  BLAST score
                    4.0e-23
  E value
                    84
  Match length
                    58
  % identity
                    (AC005388) Strong similarity to gene F14J9.26 gi_3482933
  NCBI Description
                     cdc2 protein kinase homolog from A. thaliana BAC
                     gb AC003970. ESTs gb_Z35332 and gb_F19907 come from this
                     gene. [Arabidopsis thaliana]
```

302984 Seq. No.

gct701175205.h1 Seq. ID

BLASTX Method q2276396 NCBI GI 191 BLAST score 7.0e-15E value 73 Match length 53 % identity



```
NCBI Description (U72514) C2f [Homo sapiens]
                  302985
Seq. No.
                  qct701175217.h1
Seq. ID
                  BLASTX
Method
                  g3367793
NCBI GI
BLAST score
                  260
                   6.0e-23
E value
                   59
Match length
                   83
% identity
                   (AL031154) 40s ribosomal protein s27 type
NCBI Description
                   [Schizosaccharomyces pombe]
                   302986
Seq. No.
                   gct701175240.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3935148
BLAST score
                   197
                   1.0e-15
E value
                   71
Match length
                   62
% identity
                   (AC005106) T25N20.12 [Arabidopsis thaliana]
NCBI Description
                   302987
Seq. No.
                   gct701175261.h1
Seq. ID
Method
                   BLASTX
                   q1905775
NCBI GI
                   326
BLAST score
                   1.0e-30
E value
                   75
Match length
                   69
% identity
                   (Y11930) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   302988
Seq. No.
                   gct701175267.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3023178
                   242
BLAST score
                   7.0e-21
E value
Match length
                   62
% identity
                   84
                   14-3-3 PROTEIN EPSILON (SUPPRESSOR OF RAS1 3-9) >gi_1814377
NCBI Description
                   (U84897) 14-3-3 epsilon isoform [Drosophila melanogaster]
                   >gi 1814382 (U84898) 14-3-3 epsilon isoform [Drosophila
                   melanogaster]
                   302989
Seq. No.
                   gct701175335.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4006918
BLAST score
                   187
E value
                   2.0e-14
                   62
Match length
                   60
% identity
                   (Z99708) peroxidase like protein [Arabidopsis thaliana]
NCBI Description
```

42796

302990

Seq. No.

BLAST score

E value

260 6.0e-23

```
gct701175417.hl
Seq. ID
                  BLASTX
Method
                  q4432822
NCBI GI
                  246
BLAST score
                  3.0e-21
E value
                  86
Match length
                  56
% identity
                  (AC006593) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  302991
Seq. No.
                  gct701175616.h1
Seq. ID
                  BLASTX
Method
                  g3659509
NCBI GI
                   199
BLAST score
                   1.0e-15
E value
                   77
Match length
                   42
% identity
                   (AF055919) putative serine/threonine protein kinase MAK-V
NCBI Description
                   [Mus musculus]
                   302992
Seq. No.
                   gct701175712.h1
Seq. ID
                   BLASTX
Method
                   q4539383
NCBI GI
                   174
BLAST score
                   6.0e-13
E value
                   83
Match length
                   37
% identity
                   (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   302993
Seq. No.
                   gct701175873.h1
Seq. ID
                   BLASTX
Method
                   g4508079
NCBI GI
                   180
BLAST score
                   1.0e-13
E value
                   75
Match length
                   48
 % identity
                   (AC005882) 66284 [Arabidopsis thaliana]
NCBI Description
                   302994
 Seq. No.
                   gct701175887.h1
 Seq. ID
                   BLASTX
Method
                   g2827528
 NCBI GI
 BLAST score
                   184
                   5.0e-14
 E value
                   83
 Match length
                   43
 % identity
                   (AL021633) predicted protein [Arabidopsis thaliana]
 NCBI Description
                   302995
 Seq. No.
                   gct701175904.h1
 Seq. ID
                   BLASTX
 Method
                   g1362150
 NCBI GI
```



```
Match length
% identity
                  72
                  hypothetical protein (clone AFN3) - wild oat (fragment)
NCBI Description
                  >gi 726478 (U20000) putative ORF1 [Avena fatua]
                  302996
Seq. No.
                  gct701175962.h1
Seq. ID
Method
                  BLASTN
                  g4512215
NCBI GI
BLAST score
                  94
E value
                  2.0e-45
Match length
                  224
% identity
                  86
                  Zea mays ZmRR1 mRNA for response regulator, complete cds
NCBI Description
                  302997
Seq. No.
                  gct701175975.h1
Seq. ID
Method
                  BLASTX
                  g4432860
NCBI GI
BLAST score
                  184
                  5.0e-14
E value
                  91
Match length
                  12
% identity
NCBI Description
                   (AC006300) putative glucose-induced repressor protein
                   [Arabidopsis thaliana]
                  302998
Seq. No.
                  gct701176012.h1
Seq. ID
Method
                  BLASTN
                  q2463510
NCBI GI
                   54
BLAST score
                  1.0e-21
E value
                  173
Match length
% identity
                  Z.mays small nuclear RNA genes snoR1.1, snoR2.2, snoR3.2,
NCBI Description
                  U14.1a, U14.1b, U14.1c and U14.1d
                   302999
Seq. No.
                   gct701176046.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q282382
BLAST score
                   157
E value
                   8.0e-11
Match length
                   86
% identity
                   36
                  pyruvate kinase (EC 2.7.1.40) (version 1) - Bacillus
NCBI Description
                   stearothermophilus >gi_47828_emb_CAA40994 (X57859)
                  pyruvate kinase [Bacillus stearothermophilus]
Seq. No.
                   303000
                   gct701176080.h1
Seq. ID
                   BLASTX
Method
```

NCBI GI G4262147
BLAST score 175
E value 6.0e-13
Match length 87
% identity 44



(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No. 303001

NCBI Description

Seq. ID gct701176123.hl

Method BLASTX
NCBI GI g4099090
BLAST score 178
E value 2.0e-13
Match length 42
% identity 79

NCBI Description (U83178) unknown [Arabidopsis thaliana]

Seq. No. 303002

Seq. ID gct701176142.h1

Method BLASTX
NCBI GI g1946361
BLAST score 145
E value 2.0e-09
Match length 70
% identity 40

NCBI Description (U93215) C3HC4 zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 303003

Seq. ID gct701176152.h1

Method BLASTX
NCBI GI g2306977
BLAST score 283
E value 1.0e-25
Match length 87
% identity 57

NCBI Description (AF010145) hexose transporter [Aspergillus parasiticus]

Seq. No. 303004

Seq. ID gct701176158.h1

Method BLASTX
NCBI GI 94585873
BLAST score 317
E value 1.0e-29
Match length 84
% identity 69

NCBI Description (AC005850) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 303005

Seq. ID gct701176165.h1

Method BLASTX
NCBI GI g4455176
BLAST score 207
E value 1.0e-16
Match length 70
% identity 60

NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 303006

Seq. ID gct701176318.h1

Method BLASTX

```
g3152596
NCBI GI
BLAST score
                  180
                  2.0e-13
E value
Match length
                  92
                  50
% identity
                  (AC002986) YUP8H12R.36 [Arabidopsis thaliana]
NCBI Description
                  303007
Seq. No.
                  gct701176320:h1
Seq. ID
Method
                  BLASTX
                  g1351122
NCBI GI
                  203
BLAST score
                  3.0e-16
E value
Match length
                  80
% identity
                  51
                  THIAZOLE BIOSYNTHETIC ENZYME (STRESS-INDUCIBLE PROTEIN
NCBI Description
                  STI35) >gi 280494 pir B37767 stress-inducible protein
                  sti35 - fungus (Fusarium oxysporum) >gi 168164 (M33643)
                  STI35 protein [Fusarium oxysporum]
                  303008
Seq. No.
                  gct701176332.h1
Seq. ID
                  BLASTX
Method
                  g2865394
NCBI GI
BLAST score
                  438
                  1.0e-43
E value
                  94
Match length
                  95
% identity
                  (AF036949) basic leucine zipper protein [Zea mays]
NCBI Description
                  303009
Seq. No.
                  gct701176334.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455223
BLAST score
                   161
E value
                   3.0e-11
                   52
Match length
% identity
                   65
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   303010
Seq. No.
                   gct701176373.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4206305
                   83
BLAST score
                   5.0e-39
E value
Match length
                   267
                   84
% identity
                  Zea mays retrotransposon Cinful-1, complete sequence
NCBI Description
                   303011
Seq. No.
                   gct701176378.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1173198
```

Method BLASTX
NCBI GI g1173198
BLAST score 344
E value 8.0e-33



```
Match length
                   81
% identity
                   40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal protein S13.e - garden pea >gi_396639_emb_CAA80974_
NCBI Description
                   (Z25509) ribosomal protein S13 [Pisum sativum]
                   303012
Seq. No.
                   gct701176379.h1
Seq. ID
Method
                   BLASTX
                   g2137741
NCBI GI
                   166
BLAST score
                   6.0e-12
E value
                   58
Match length
% identity
                   62
                   ribosomal protein fau - mouse >gi_50950_emb_CAA46715
NCBI Description
                   (X65922) fau [Mus musculus] >gi_497611 (L33715) Fau gene
                   product [Mus musculus] >gi_1060927_dbj_BAA05655_ (D26610)
                   monoclonal nonspecific suppressor factor beta [Mus
                   musculus]
                   303013
Seq. No.
                   gct701176393.h1
Seq. ID
                   BLASTX
Method
                   g3024706
NCBI GI
BLAST score
                   265
                   2.0e-23
E value
Match length
                   83
                   59
% identity
                   TRANSCRIPTION INITIATION FACTOR TFIID 18 KD SUBUNIT
NCBI Description
                   (TAFII-18) (TAFII18) >gi_1362894_pir__S54782 PolII
                   transcription factor TFIID chain hTAFII18 - human
                   >gi 791053 emb CAA58827 (X84003) PolII transcription
                   factor TFIID [Homo sapiens]
Seq. No.
                   303014
                   gct701176395.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q168487
                   93
BLAST score
                   2.0e-45
E value
Match length
                   112
% identity
NCBI Description Maize glutathione S-transferase gene (GST-I), exons 2 and 3
                   303015
Seq. No.
                   gct701176462.h1
Seq. ID
Method
                   BLASTX
                   g2047324
NCBI GI
BLAST score
                   142
                    4.0e-09
E value
```

Match length 38 71 % identity

(U80192) HAL3 homolog [Arabidopsis thaliana] NCBI Description

303016 Seq. No.

gct701176501.h1 Seq. ID

Method BLASTX



NCBI GI g2500647 BLAST score 175 E value 7.0e-13 Match length 53 % identity 58

NCBI Description SMALL NUCLEAR RIBONUCLEOPROTEIN E HOMOLOG SME1

>gi_2133142_pir__S67047 SME1 protein - yeast (Saccharomyces cerevisiae) >gi_1293719 (U55020) similar to the mammalian snRNP-E involved in splicing, CAI: 0.12; snRNPE homolog [Saccharomyces cerevisiae] >gi_1420395_emb_CAA99365_

(Z75067) ORF YOR159c [Saccharomyces cerevisiae]

>gi 1694906 emb CAA63198_ (X92449) core snRNP protein E

[Saccharomyces cerevisiae]

Seq. No. 303017

Seq. ID gct701176522.h1

Method BLASTX
NCBI GI 94115914
BLAST score 303
E value 6.0e-28
Match length 84
% identity 63

NCBI Description (AF118222) contains similarity to Iron/Ascorbate family of

oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana] >gi_4539410_emb_CAB40043.1_(AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis

thaliana]

Seq. No. 303018

Seq. ID gct701176526.hl

Method BLASTX
NCBI GI g2072023
BLAST score 361
E value 9.0e-35
Match length 86
% identity 80

NCBI Description (U93506) symbiosis-related protein [Laccaria bicolor]

Seq. No. 303019

Seq. ID gct701176532.h1

Method BLASTX
NCBI GI g3941414
BLAST score 280
E value 2.0e-25
Match length 74
% identity 78

NCBI Description (AF062861) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 303020

Seq. ID gct701176578.h1

Method BLASTX
NCBI GI g4539406
BLAST score 249
E value 1.0e-21
Match length 69
% identity 70

NCBI Description



```
(AL049524) putative retrotransposon [Arabidopsis thaliana]
NCBI Description
                  303021
Seq. No.
Seq. ID
                  qct701176670.hl
Method
                  BLASTN
                  g2804611
NCBI GI
BLAST score
                  37
                  2.0e-11
E value
                  49
Match length
% identity
                  94
                  Podospora anserina suppressor of vegetative incompatibility
NCBI Description
                  MOD-E (mod-E) gene, complete cds
                  303022
Seq. No.
Seq. ID
                  gct701176695.h1
Method
                  BLASTX
                  q3688123
NCBI GI
                  147
BLAST score
                  6.0e-10
E value
Match length
                  64
% identity
                  53
                  (AJ006293) granule-bound starch synthase [Antirrhinum
NCBI Description
                  majus]
                  303023
Seq. No.
Seq. ID
                  gct701176735.h1
Method
                  BLASTX
NCBI GI
                  g547627
BLAST score
                  211
                  3.0e-17
E value
                  53
Match length
                  74
% identity
                  HES1 PROTEIN >gi 630294 pir S42677 HES1 protein - yeast
NCBI Description
                   (Saccharomyces cerevisiae) >gi_433365 (U03914) Hes1p
                   [Saccharomyces cerevisiae] >gi_1420543_emb_CAA99458_
                   (Z75145) ORF YOR237w [Saccharomyces cerevisiae]
                   303024
Seq. No.
                   gct701176738.hl
Seq. ID
Method
                  BLASTX
                   g626100
NCBI GI
BLAST score
                   269
                   5.0e-24
E value
                  78
Match length
                   65
% identity
                  aminopeptidase Y (EC 3.4.11.-) precursor - yeast
NCBI Description
                   (Saccharomyces cerevisiae)
                   303025
Seq. No.
                   gct701176827.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2494132
BLAST score
                   165
                   7.0e-12
E value
                   41
Match length
% identity
                   66
```

42803

(AC002376) Contains similarity to human dimethylaniline

Seq. No.

303031



monooxygenase (gb_M64082). [Arabidopsis thaliana]

```
Seq. No.
                   303026
                   gct701176828.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   `q3980380
BLAST score
                   291
                   1.0e-26
E value
Match length
                   80
% identity
                   62
                  (AC004561) putative enolase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303027
                   gct701177012.h1
Seq. ID
Method
                   BLASTX
                   g2494165
NCBI GI
BLAST score
                   343
                   1.0e-32
E value
Match length
                   81
                   75
% identity
NCBI Description DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))
                   >gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana
                   >gi 1359495 emb CAA66599 (X97924) DNA ligase [Arabidopsis
                   thaliana]
Seq. No.
                   303028
                   gct701177013.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g543217
BLAST score
                   256
                   2.0e-22
E value
Match length
                   68
                   68
% identity
                   ribosomal protein S24 - mouse >gi_437878_emb_CAA50792_
NCBI Description
                   (X71972) mrp S24 [Mus musculus]
                   303029
Seq. No.
                   gct701177043.h1
Seq. ID
Method
                   BLASTX
                   g3337367
NCBI GI
BLAST score
                   171
                   1.0e-12
E value
                   44
Match length
% identity
                   68
                  (AC004481) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   303030
Seq. No.
                   gct701177052.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q21447
BLAST score
                   68
E value
                   5.0e-30
Match length
                   68
% identity
                   100
NCBI Description S.tuberosum gene for U6 small nuclear RNA
```



```
gct701177062.hl
Seq. ID
                  BLASTX
Method
                  g3236235
NCBI GI
BLAST score
                  142
                  3.0e-09
E value
                  58
Match length
                   47
% identity
                   (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4056501 (AC005896) unknown protein [Arabidopsis
                  thaliana]
                   303032
Seq. No.
                   gct701177106.h1
Seq. ID
                   BLASTX
Method
                   g4097094
NCBI GI
BLAST score
                   279
                   4.0e-25
E value
                   79
Match length
                   75
% identity
                   (U45447) vacuolar proton-ATPase subunit D [Oryctolagus
NCBI Description
                   cuniculus]
                   303033
Seq. No.
                   gct701177121.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4220485
BLAST score
                   253
E value
                   4.0e-22
Match length
                   80
                   56
% identity
                   (AC006069) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
                   303034
Seq. No.
                   gct701177124.h1
Seq. ID
                   BLASTX
Method
                   g2135893
NCBI GI
                   145
BLAST score
                   2.0e-09
E value
Match length
                   59
                   47
% identity
                   peptidylprolyl isomerase (EC 5.2.1.8) A - human
NCBI Description
                   >gi_4406227_gb_AAD19906_ (AF104012) peptidyl-prolyl
                   cis-trans isomerase E [Homo sapiens]
                   303035
Seq. No.
                   gct701177165.h1
Seq. ID
                   BLASTX
Method
                   g3127857
NCBI GI
BLAST score
                   162
                   2.0e-11
E value
Match length
                   78
```

46 % identity

(AJ005837) putative progesterone binding protein [Rattus NCBI Description

norvegicus]

303036 Seq. No.

```
gct701177190.hl
Seq. ID
                  BLASTX
Method
                  g3193309
NCBI GI
                  232
BLAST score
                  1.0e-19
E value
                  96
Match length
% identity
                   (AF069300) No definition line found [Arabidopsis thaliana]
NCBI Description
                  303037
Seq. No.
                   gct701177216.h1
Seq. ID
                  BLASTX
Method
                   g584892
NCBI GI
                   351
BLAST score
                   1.0e-33
E value
                   89
Match length
                   76
% identity
                   SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
NCBI Description
                   >gi_629805_pir__S43516 serine carboxypeptidase I - rice
                   >gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I
                   [Oryza sativa]
                   303038
Seq. No.
                   gct701177218.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2739371
BLAST score
                   396
E value
                   7.0e-39
Match length
                   90
                   83
% identity
                   (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                   303039
Seq. No.
                   gct701177233.h1
Seq. ID
                   BLASTX
Method
                   g4467116
NCBI GI
                   203
BLAST score
                   3.0e-16
E value
Match length
                   56
                   59
% identity
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   303040
Seq. No.
                   gct701177255.h1
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g3182916
BLAST score 180
E value 6.0e-16
Match length 65
% identity 65

NCBI Description ADP-RIBOSYLATION FACTOR >gi_1565278_emb_CAB02498_ (Z80359) ADP-ribosylation factor [Plasmodium falciparum] >gi_1932731

(U57370) ADP-ribosylation factor [Plasmodium falciparum]

eg. No. 303041

Seq. No. 303041 Seq. ID gct701177261.h1

Method BLASTX

```
g3805845
NCBI GI
                  242
BLAST score
                  8.0e-21
E value
                  79
Match length
                  57
% identity
                  (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
                  303042
Seq. No.
                  gct701177262.h1
Seq. ID
Method
                  BLASTX
                  g4006892
NCBI GI
                   226
BLAST score
                   6.0e-19
E value
                   80
Match length
% identity
                   61
                   (Z99708) glucosyltransferase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   303043
Seq. No.
                   gct701177287.h1
Seq. ID
Method
                   BLASTX
                   g1168489
NCBI GI
BLAST score
                   211
                   2.0e-20
E value
Match length
                   81
% identity
                   56
                  ADP-RIBOSYLATION FACTOR >gi 727191 (M54910)
NCBI Description
                   ADP-ribosylation factor [Candida albicans]
                   303044
Seq. No.
                   gct701177378.hl
Seq. ID
                   BLASTX
Method
                   g4580472
NCBI GI
                   155
BLAST score
                   8.0e-11
E value
                   48
Match length
                   54
% identity
                   (AC006081) DNA binding protein; similar to CDC27 and nuclear
NCBI Description
                   scaffold proteins [Arabidopsis thaliana]
Seq. No.
                   303045
                   gct701177393.h1
Seq. ID
Method
                   BLASTN
                   g22435
NCBI GI
BLAST score
                   35
                   2.0e-10
E value
Match length
                   47
                   94
% identity
NCBI Description Z.mays PK1 gene for receptor-like protein kinase
```

Seq. No. 303046

Seq. ID gct701177430.h1

Method BLASTX
NCBI GI g4581120
BLAST score 146
E value 1.0e-09
Match length 86



```
% identity
                  (AC005825) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  303047
Seq. No.
                  gct701177459.h1
Seq. ID
Method
                  BLASTX
                  g416935
NCBI GI
BLAST score
                  344
                  7.0e-33
E value
                  80
Match length
```

% identity 78
NCBI Description ELONGATION FACTOR 2 (EF-2) >gi_283128_pir__A41778

translation elongation factor eEF-2 - yeast (Saccharomyces cerevisiae) >gi_171442 (M59370) translation elongation factor 2 [Saccharomyces cerevisiae] >gi_549849 (M59369) translation elongation factor 2 [Saccharomyces cerevisiae] >gi_927318 (U32274) Eft2p: translation elongation factor 2

(EF-2); CAI: 0.80 [Saccharomyces cerevisiae]

>gi 1050821 emb CAA62116 (X90518) ORF 03317 [Saccharomyces cerevisiae] >gi 1164977 emb CAA64052 (X94335) YOR3317w [Saccharomyces cerevisiae] >gi 1420342 emb CAA99332 (775041) OPF VOR133v [Saccharomyces cerevisiae]

(Z75041) ORF YOR133w [Saccharomyces cerevisiae]

```
      Seq. No.
      303048

      Seq. ID
      gct701177475.h1

      Method
      BLASTX

      NCBI GI
      g4506715

      BLAST score
      205

      E value
      1.0e-16
```

E value 1.0
Match length 58
% identity 71

NCBI Description ribosomal protein S28 >gi_133903_sp_P25112_RS28_HUMAN 40S RIBOSOMAL PROTEIN S28 >gi_71049_pir_R3RT28_ribosomal

protein S28 - rat >gi_57726_emb_CAA41967_ (X59277) ribosomal protein S28 [Rattus rattus] >gi_337403 (L05091) ribosomal protein S28 [Homo sapiens] >gi_508266 (U11248) ribosomal protein S28 [Mus musculus] >gi_1518637 (U58682) ribosomal protein S28 [Homo sapiens] >gi_4050094 (AF110520)

RPS28 [Mus musculus]

 Seq. No.
 303049

 Seq. ID
 gct701177525.h1

 Method
 BLASTX

 NCBI GI
 g3894158

 BLAST score
 143

BLAST score 143 E value 3.0e-09 Match length 66 % identity 44

NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis

thaliana]

Seq. No. 303050

Seq. ID gct701177555.h1

Method BLASTX
NCBI GI g2589164
BLAST score 396
E value 6.0e-39

```
Match length
                  88
                  84
% identity
                  (D88452) aldehyde oxidase-2 [Zea mays]
NCBI Description
                  303051
Seq. No.
                  gct701177607.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4506605
                  283
BLAST score
                  1.0e-25
E value
                  80
Match length
                  71
% identity
                  ribosomal protein L23 >gi_266927_sp_P23131_RL23_HUMAN 60S
NCBI Description
                  RIBOSOMAL PROTEIN L23 (L17) >gi_71229_pir_R5RT23 ribosomal
                  protein L23 - rat >gi_34194_emb_CAA39417_
                                                             (X55954) HL23
                  ribosomal protein [Homo sapiens] >gi_36126_emb_CAA37023_
                  (X52839) ribosomal protein L17 [Homo sapiens]
                  >qi 57688 emb CAA41177 (X58200) ribosomal protein L23
                  [Rattus rattus]
                  303052
Seq. No.
                  gct701177610.h1
Seq. ID
Method
                  BLASTX
                  g3249567
NCBI GI
BLAST score
                  217
                  7.0e-18
E value
Match length
                  77
% identity
                  52
                  (AF047694) glutaredoxin [Vernicia fordii]
NCBI Description
Seq. No.
                  303053
                  gct701177804.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1652387
BLAST score
                  196
E value
                  2.0e-15
Match length
                  91
% identity
                  41
                  (D90905) hypothetical protein [Synechocystis sp.]
NCBI Description
```

Seq. No.

303054

Seq. ID

gct701177830.h1 BLASTX

Method NCBI GI

q3875294

BLAST score

250

E value

1.0e-21

Match length

88 55

% identity NCBI Description

(Z66560) similar to glutathione S-transferase

[Caenorhabditis elegans]

Seq. No.

303055

Seq. ID

gct701177882.h1

Method NCBI GI BLAST score E value

BLASTX g1710760 241 1.0e-20



```
Match length
                  56
% identity
                  PROBABLE 40S RIBOSOMAL PROTEIN S28 (S33)
NCBI Description
                  >gi_1256529_emb_CAA94635_ (Z70691) ribosomal protein S28
                  [Schizosaccharomyces pombe] >gi_3581915_emb_CAA20854_
                   (AL031545) probable 40s ribosomal protein 28s
                   [Schizosaccharomyces pombe]
                  303056
Seq. No.
                  gct701177962.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4755086
BLAST score
                  80
E value
                  3.0e-37
Match length
                  109
                  96
% identity
                  Zea mays aluminum-induced protein (Zmall) mRNA, complete
NCBI Description
                  303057
Seq. No.
                  gct701177965.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4416300
BLAST score
                  199
E value
                  1.0e-108
Match length
                  250
                  95
% identity
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                  region, complete sequence
                  303058
Seq. No.
                  gct701177966.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1707981
BLAST score
                  184
E value
                  5.0e-14
Match length
                  62
                  55
% identity
                  GLUTAREDOXIN >gi 1076561 pir S54825 glutaredoxin - castor
NCBI Description
Seq. No.
                  303059
                  gct701178035.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3063471
BLAST score
                  154
E value
                  2.0e-10
Match length
                  82
```

% identity

NCBI Description (AC003981) F22013.33 [Arabidopsis thaliana]

303060 Seq. No.

qct701178074.h1 Seq. ID

Method BLASTX NCBI GI g4581108 244 BLAST score E value 2.0e-23



```
Match length 83
% identity 66
NCBI Description (AC005825) putative chloroplast outer membrane protein 86,also very similar to GTP-inding protein from pea (GB:L36857) [Arabidopsis thaliana]
Seq. No. 303061
```

Seq. ID gct701178078.h1
Method BLASTX
NCBI GI g4263048
BLAST score 231
E value 1.0e-19
Match length 52
% identity 79

NCBI Description (AC005142) putative hydrolase [Arabidopsis thaliana]

 Seq. No.
 303062

 Seq. ID
 gct701178181.h1

 Method
 BLASTX

 NCBI GI
 g2132183

 BLAST score
 229

NCBI GI G213218.
BLAST score 229
E value 3.0e-19
Match length 89
% identity 47

NCBI Description hypothetical protein YPL088w - yeast (Saccharomyces cerevisiae) >gi_1151238 (U43281) Lpg20p [Saccharomyces

cerevisiae]

Seq. No. 303063

Seq. ID gct701178191.h1

Method BLASTN
NCBI GI g4115614
BLAST score 38
E value 4.0e-12
Match length 136
% identity 82

NCBI Description Zea mays mRNA for root cap-specific glycine-rich protein,

complete cds

Seq. No. 303064

Seq. ID gct701178225.h1

Method BLASTX
NCBI GI g3914915
BLAST score 206
E value 3.0e-18
Match length 87
% identity 52

NCBI Description 40S RIBOSOMAL PROTEIN S3A (V-FOS TRANSFORMATION EFFECTOR

PROTEIN) >gi_3037139 (AF056328) V-Fos transformation

effector [Oryzias latipes]

Seq. No. 303065

Seq. ID gct701178227.h1

Method BLASTN
NCBI GI g3702724
BLAST score 35
E value 2.0e-10



47 Match length % identity 94 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K17N15, complete sequence [Arabidopsis thaliana] 303066 Seq. No. gct701178232.h1 Seq. ID BLASTX Method g4263790 NCBI GI BLAST score 177 2.0e-13 E value Match length 62 56 % identity (AC006068) putative ch-TOG protein [Arabidopsis thaliana] NCBI Description Seq. No. 303067 gct701178236.h1 Seq. ID BLASTX Method g4006855 NCBI GI BLAST score 260 E value 6.0e-23 Match length 84 % identity 64 (Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis NCBI Description thaliana] 303068 Seq. No. Seq. ID gct701178237.hl Method BLASTX g4115379 NCBI GI BLAST score 154 2.0e-10 E value 60 Match length 55 % identity (AC005967) putative carbonyl reductase [Arabidopsis NCBI Description thaliana] 303069 Seq. No. gct701178286.h1 Seq. ID Method BLASTX NCBI GI g4455294 278 BLAST score 4.0e-25 E value 88 Match length 21 % identity (AL035528) putative protein [Arabidopsis thaliana] NCBI Description 303070 Seq. No. gct701178370.h1 Seq. ID Method BLASTX NCBI GI g4262225

Method BLASTX
NCBI GI g4262225
BLAST score 179
E value 1.0e-13
Match length 42
% identity 76

NCBI Description (AC006200) putative phosphatidic acid phosphatase

[Arabidopsis thaliana]



```
303071
Seq. No.
                  qct701178420.hl
Seq. ID
Method
                  BLASTX
                  g3152591
NCBI GI
                  258
BLAST score
                  9.0e-23
E value
                  77
Match length
                  58
% identity
                  (AC002986) Similar to hypothetical protein gb_Z97336 from
NCBI Description
                  A. thaliana. This gene is probably cut off. [Arabidopsis
                  thaliana]
                  303072
Seq. No.
Seq. ID
                  gct701178424.h1
Method
                  BLASTX
NCBI GI
                  g2130080
BLAST score
                  173
                  6.0e-13
E value
Match length
                  46
% identity
                  63
                  Nramp1 protein - rice >gi_1470320 bbs_177441 (S81897)
NCBI Description
                  OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa,
                  indica, cv. IR 36, etiolated shoots, Peptide, 517 aa]
                   [Oryza sativa] >gi 2231132 (L41217) integral membrane
                  protein [Oryza sativa]
Seq. No.
                  303073
Seq. ID
                  gct701178449.h1
Method
                  BLASTX
                  g4539660
NCBI GI
BLAST score
                  264
                  2.0e-23
E value
                  82
Match length
                  57
% identity
                  (AF061282) polyprotein [Sorghum bicolor]
NCBI Description
                  303074
Seq. No.
                   gct701178504.h1
Seq. ID
Method
                  BLASTX
                   g464255
NCBI GI
BLAST score
                   158
                   7.0e-11
E value
                   94
Match length
                   34
% identity
                  NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-39KD) (CI-39KD) >gi_89674_pir__S17676 NADH
```

dehydrogenase (ubiquinone) (EC $^{-}1.6.5.3$) $\overline{39}$ K chain precursor - bovine >gi_228_emb_CAA42053_ (X59418) NADH dehydrogenase

(ubiquinone) 42 kDa subunit [Bos taurus]

Seq. No. 303075

gct701178554.h1 Seq. ID

Method BLASTN g22378 NCBI GI BLAST score 60 3.0e-25 E value



```
128
Match length
                   88
% identity
                  Z.mays gene for nucleic acid binding protein
NCBI Description
Seq. No.
                   303076
                   qct701178675.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4512105
BLAST score
                   220
E value
                   3.0e-18
Match length
                   64
% identity
                   (AF121962) alliinase [Allium cepa]
NCBI Description
                   303077
Seq. No.
Seq. ID
                   gct701178730.h2
Method
                   BLASTX
NCBI GI
                   g1709515
BLAST score
                   197
                   1.0e-32
E value
Match length
                   86
% identity
                   74
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT
NCBI Description
                   >qi 2117987 pir S60471 phosphoprotein phosphatase (EC
                   3.1.3.16) type 2A catalytic chain - Neurospora crassa
                   >gi 1360076 emb CAA58573 (X83593) phosphoprotein
                   phosphatase [Neurospora crassa]
Seq. No.
                   303078
Seq. ID
                   gct701178735.h2
Method
                   BLASTX
NCBI GI
                   q4539423
BLAST score
                   139
E value
                   7.0e-11
Match length
                   43
% identity
                   91
                   (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                   [Arabidopsis thaliana]
                   303079
Seq. No.
Seq. ID
                   gct701178812.h1
Method
                   BLASTN
                   g499013
NCBI GI
BLAST score
                   123
                   8.0e-63
E value
                   268
Match length
% identity
                   93
                   T.aestivum (Capitole) mitochondrial orf240 gene
NCBI Description
                   303080
Seq. No.
                   gct701178844.h1.
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1077211
BLAST score
                   162
E value
                   2.0e-11
Match length
                   90
% identity
                   40
```



hypothetical protein YDR175c - yeast (Saccharomyces NCBI Description cerevisiae) >gi_1289290_emb_CAA86680_ (Z46727) unknown [Saccharomyces cerevisiae]

Seq. No. 303081

qct701178847.h1 Seq. ID

Method BLASTX NCBI GI q4510348 BLAST score 229 3.0e-19 E value Match length 92

% identity

(AC006921) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

303082 Seq. ID qct701178927.h1

Method BLASTX NCBI GI q1350954 275 BLAST score 1.0e-24 E value Match length 81 68 % identity

40S RIBOSOMAL PROTEIN S15A >gi 422493 pir_S33498 ribosomal NCBI Description

protein DS15a - fruit fly (Drosophila melanogaster) >gi 311606 emb CAA79771 (Z21673) ribosomal protein 15a

(40S subunit) [Drosophila melanogaster]

303083 Seq. No.

gct701178948.h1 Seq. ID

Method BLASTX q4038055 NCBI GI 173 BLAST score E value 6.0e-13 62 Match length 53 % identity

(AC005897) putative cytochrome P450 [Arabidopsis thaliana] NCBI Description >gi_4557077_gb_AAD22516.1_AC007045_16 (AC007045) putative

cytochrome p450 [Arabidopsis thaliana]

303084 Seq. No.

Seq. ID gct701178949.h1

Method BLASTX NCBI GI g3080398 BLAST score 177 2.0e-13 E value Match length 57 % identity

(AL022603) putative protein [Arabidopsis thaliana] NCBI Description

303085 Seq. No.

gct701178972.h1 Seq. ID

BLASTX Method NCBI GI g1076755 270 BLAST score 3.0e-24 E value Match length 81 59 % identity



```
NCBI Description protein kinase - rice >gi_450300 (L27821) protein kinase
                   [Oryza sativa]
                   303086
Seq. No.
                   gct701178978.h1
Seq. ID
Method
                   BLASTX
                   q4506633
NCBI GI
BLAST score
                   250
                   8.0e-22
E value
                   83
Match length
% identity
                   57
                   ribosomal protein L31 >gi_132881_sp_P12947_RL31_HUMAN 60S RIBOSOMAL PROTEIN L31 >gi_71328_pir__R5HU31 ribosomal
NCBI Description
                   protein L31 - human >gi_71329_pir__R5RT31 ribosomal protein
                   L31 - rat >gi_36130_emb_CAA34066_ (X15940) ribosomal
                   protein L31 (AA 1-125) [Homo sapiens]
                    >gi_57115_emb_CAA28500_ (X04809) ribosomal protein L31 (AA
                    1-1\overline{2}5) [Rattus norvegicus]
                    303087
Seq. No.
                    gct701179114.hl
Seq. ID
Method
                    BLASTN
                    g1777706
NCBI GI
                    122
BLAST score
                    2.0e-62
E value
                    146
Match length
% identity
                    96
                    Zea mays 18S ribosomal RNA gene, partial sequence
NCBI Description
Seq. No.
                    303088
                    gct701179120.hl
Seq. ID
                    BLASTX
Method
NCBI GI
                    q445612
BLAST score
                    158
                    3.0e-11
E value
                    50
Match length
% identity
                    64
NCBI Description ribosomal protein S19 [Solanum tuberosum]
                    303089
Seq. No.
                    qct701179138.h1
Seq. ID
                    BLASTX
Method
                    q3413706
NCBI GI
                    190
BLAST score
                    6.0e-15
E value
                    49
Match length
% identity
                    (AC004747) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    303090
Seq. No.
                    gct701179163.h1
Seq. ID
                    BLASTX
Method
                    g1711534
NCBI GI
                    152
BLAST score
```

42816

2.0e-10

47

62

E value

Match length

% identity



NCBI Description

```
SUCCINIC SEMIALDEHYDE DEHYDROGENASE)
                  >qi 2136207 pir A55773 succinate-semialdehyde
                  dehydrogenase (EC 1.2.1.24) - human (fragment) >gi_556221
                  (L34820) succinate semialdehyde dehydrogenase [Homo
                  sapiens]
                  303091
Seq. No.
                  gct701179230.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406764
                  159
BLAST score
                  3.0e-11
E value
Match length
                  51
% identity
                  (AC006836) putative uridylyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                  303092
Seq. No.
                  gct701179256.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3063465
                  191
BLAST score
                  5.0e-15
E value
Match length
                  46
% identity
NCBI Description (AC003981) F22013.27 [Arabidopsis thaliana]
                  303093
Seq. No.
Seq. ID
                  gct701179274.h1
                  BLASTX
Method
                  q3738302
NCBI GI
BLAST score
                  163
                  9.0e-12
E value
                  41
Match length
                  73
% identity
                  (AC005309) tubby-like protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4249398 (AC006072) putative tubby protein [Arabidopsis
                  thaliana]
Seq. No.
                  303094
                  gct701179328.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2494246
BLAST score
                   424
                   4.0e-42
E value
Match length
                  89
% identity
                  84
                  ELONGATION FACTOR 2 (EF-2) >gi_1184958 (U46663) elongation
NCBI Description
                   factor 2 [Gallus gallus]
                   303095
Seq. No.
Seq. ID
                   gct701179363.h1
Method
                  BLASTX
                  g4506661
NCBI GI
BLAST score
                   291
                  1.0e-26
E value
```

SUCCINATE SEMIALDEHYDE DEHYDROGENASE (NAD(+)-DEPENDENT



Match length 71 % identity 75

NCBI Description ribosomal protein L7a >gi_133014_sp_P11518_RL7A_HUMAN 60S

RIBOSOMAL PROTEIN L7A (PLA-X POLYPEPTIDE) (SURF-3)
>gi_71116_pir__R5HU7A ribosomal protein L7a - human
>gi_71117_pir__R5RT7A ribosomal protein L7a - rat

>gi_34203_emb_CAA36383 (X52138) L7a protein [Homo sapiens]
>gi_35512_emb_CAA29889 (X06705) PLA-X polypeptide [Homo sapiens] >gi_36647_emb_CAA43925 (X61923) ribosomal protein
L7a [Homo sapiens] >gi_56956_emb_CAA33117 (X15013)

ribosomal protein L7a (AA 1-266) [Rattus rattus] >gi_337495 (M36072) ribosomal protein L7a large subunit [Homo sapiens]

>gi_1584354_prf__2122395A nuclear hormone receptor-associated protein [Homo sapiens]

Seq. No. 303096

Seq. ID gct701179408.h1

Method BLASTX
NCBI GI g3929337
BLAST score 224
E value 1.0e-18
Match length 67
% identity 58

NCBI Description AMINO ACID PERMEASE 2 >gi 2995851 (AF053231) amino acid

permease [Neurospora crassa]

Seq. No. 303097

Seq. ID gct701179414.h1

Method BLASTX
NCBI GI g4138265
BLAST score 153
E value 1.0e-10
Match length 32
% identity 91

NCBI Description (AJ006228) Avr9 elicitor response protein [Nicotiana

tabacum]

Seq. No. 303098

Seq. ID gct701179431.h1

Method BLASTX
NCBI GI 94587556
BLAST score 166
E value 4.0e-12
Match length 36
% identity 81

NCBI Description (AC006577) Similar to gi_1653162 (p)ppGpp

3-pyrophosphohydrolase from Synechocystis sp genome gb D90911. EST gb_W43807 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 303099

Seq. ID gct701179511.h1

Method BLASTX
NCBI GI g4455250
BLAST score 197
E value 1.0e-15
Match length 83



46

% identity

NCBI Description

```
% identity
                  (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                  303100
Seq. No.
Seq. ID
                  gct701179522.h1
Method
                  BLASTX
NCBI GI
                  q3242789
BLAST score
                  155
E value
                  3.0e-12
Match length
                  78
% identity
                  (AF055357) respiratory burst oxidase protein D [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  303101
Seq. ID
                  qct701179577.h1
Method
                  BLASTX
NCBI GI
                  q3172542
BLAST score
                  218
E value
                  4.0e-18
                  77
Match length
% identity
                  56
NCBI Description (AF067648) isoprenylated v-SNARE protein [Xenopus laevis]
                  303102
Seq. No.
Seq. ID
                  qct701179594.h1
Method
                  BLASTX
NCBI GI
                  q4559334
BLAST score
                  144
E value
                  2.0e-09
Match length
                  37
% identity
                  59
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]
                  303103
Seq. No.
                  gct701179627.h1
Seq. ID
Method
                  BLASTX
                  g1169211
NCBI GI
BLAST score
                  212
                  3.0e-17
E value
Match length
                  73
                  56
% identity
                  DEFENDER AGAINST CELL DEATH 1 (DAD-1)
NCBI Description
                  >gi 627261 pir B54437 apoptotic cell death regulator DAD1
                  - African clawed frog >gi 914964 dbj BAA03652 (D15059)
                  DAD-1 [Xenopus laevis]
                  303104
Seq. No.
                  gct701179711.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4127346
BLAST score
                  150
                  5.0e-10
E value
Match length
                  61
```

(AJ010448) glutathione transferase [Alopecurus myosuroides]

Match length

NCBI Description

% identity

93 62



```
Seq. No.
                  303105
Seq. ID
                  gct701179745.h1
Method
                  BLASTX
NCBI GI
                  q4325354
BLAST score
                  180
E value
                  2.0e-13
                  89
Match length
                  42
% identity
                  (AF128395) contains similarity to retrovirus-related
NCBI Description
                  polyproteins and to CCHC zinc finger protein (Pfam:
                  PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]
                  303106
Seq. No.
                  gct701179752.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3947880
BLAST score
                  266
E value
                  1.0e-23
                   94
Match length
                   59
% identity
                   (AL034382) putative ras-related GTP-binding protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   303107
Seq. No.
                  gct701179783.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4454484
BLAST score
                   341
                   2.0e-32
E value
Match length
                   89
% identity
NCBI Description
                   (AC006234) putative diacylglycerol kinase [Arabidopsis
                   thaliana]
Seq. No.
                   303108
                   gct701179806.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1174783
BLAST score
                   207
                   1.0e-16
E value
Match length
                   95
                   52
% identity
                  TRYPTOPHAN SYNTHASE ALPHA CHAIN PRECURSOR
NCBI Description
                   >gi 1362207 pir S56665 tryptophan synthase (EC 4.2.1.20)
                   alpha chain - maize >gi_440171_emb CAA54131_ (X76713)
                   tryptophan synthase, alpha subunit [Zea mays]
                   303109
Seq. No.
                   gct701179846.h1
Seq. ID
Method
                   BLASTX
                   g2252824
NCBI GI
BLAST score
                   290
E value
                   2.0e-26
```

(AF013293) No definition line found [Arabidopsis thaliana]



58

% identity

NCBI Description

```
303110
Seq. No.
Seq. ID
                  gct701179930.h1
                  BLASTX
Method
                  g3142303
NCBI GI
BLAST score
                  366
E value
                  2.0e-35
                  88
Match length
% identity
                  78
                  (AC002411) Strong similarity to MRP-like ABC transporter
NCBI Description
                  gb U92650 from A. thaliana and canalicular multi-drug
                  resistance protein gb L49379 from Rattus norvegicus.
                   [Arabidopsis thaliana]
                  303111
Seq. No.
                  gct701179944.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3135543
BLAST score
                  193
                   4.0e-15
E value
Match length
                   38
% identity
NCBI Description
                  (AF062393) aquaporin [Oryza sativa]
                   303112
Seq. No.
                   gct701179956.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g122094
BLAST score
                   173
                   1.0e-12
E value
Match length
                   36
% identity
                   HISTONE H4.2 >gi_101786_pir__S11940 histone H4.2 -
NCBI Description
                   Emericella nidulans >gi 296339 emb CAA39156 (X55550)
                   histone H4.2 [Emericella nidulans] >gi_529957 (U12631)
                   histone H4.2 [Emericella nidulans] >gi_227598_prf__1707275D
                   histone H4.2 [Emericella nidulans]
Seq. No.
                   303113
                   gct701179995.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1707645
BLAST score
                   215
E value
                   1.0e-17
                   83
Match length
% identity
                   46
                   (X99514) mexF [Pseudomonas aeruginosa]
NCBI Description
Seq. No.
                   303114
                   gct701180001.h1
Seq. ID
                   BLASTX
Method
                   g119164
NCBI GI
BLAST score
                   215
                   1.0e-17
E value
Match length
                   67
```

42821

>gi_84607_pir__S00162 translation elongation factor eEF-1

ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA)



gamma chain - brine shrimp >gi_161172 (M28020) elongation factor 1-gamma [Artemia sp.]

Seq. No. 303115

Seq. ID gct701180012.h1

Method BLASTX
NCBI GI g2119042
BLAST score 210
E value 5.0e-17
Match length 75
% identity 55

NCBI Description glycine-rich RNA-binding protein RGP-la - wood tobacco

>gi_469070_dbj_BAA03741_ (D16204) RNA-binding glycine-rich

protein-1 (RGP-1a) [Nicotiana sylvestris]

Seq. No. 303116

Seq. ID gct701180076.h1

Method BLASTX
NCBI GI g4049534
BLAST score 305
E value 3.0e-28
Match length 78
% identity 68

NCBI Description (AL034564) 40s ribosomal protein [Schizosaccharomyces

pombe] >gi 4481957 emb CAB38515.1 (AL035637) ribosomal

protein subunit s18. [Schizosaccharomyces pombe]

Seq. No. 303117

Seq. ID gct701180082.h1

Method BLASTX
NCBI GI g4585925
BLAST score 163
E value 1.0e-11
Match length 82
% identity 48

NCBI Description (AC007211) unknown protein [Arabidopsis thaliana]

Seq. No. 303118

Seq. ID gct701180106.h1

Method BLASTX
NCBI GI g584806
BLAST score 211
E value 3.0e-17
Match length 54
% identity 83

NCBI Description ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_83764_pir__JC1111 H+-transporting ATP synthase (EC
3.6.1.34) alpha chain - Neurospora crassa >gi_168759
(M84191) mitochondrial ATPase alpha-subunit [Neurospora

crassa]

Seq. No. 303119

Seq. ID gct701180169.h1

Method BLASTX
NCBI GI g2494112
BLAST score 239
E value 2.0e-20



Match length 46 87 % identity (AC002376) Match to Arabidopsis ATHKCP (gb L40948). ESTs NCBI Description gb ATTS0764, gb R90646, gb AA389809, gb_ATTS2615 come from this gene. [Arabidopsis thaliana] >gi_3126868 (AF061570) potassium channel beta subunit homolog [Arabidopsis thaliana] 303120 Seq. No. Seq. ID gct701180196.h1 Method BLASTX NCBI GI g3702331 BLAST score 189 E value 1.0e-14 80 Match length % identity NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana] 303121 Seq. No. Seq. ID gct701180205.h1 Method BLASTX NCBI GI g4580462 BLAST score 282 E value 2.0e-25 88 Match length 57 % identity NCBI Description (AC006081) hypothetical protein [Arabidopsis thaliana] 303122 Seq. No. Seq. ID gct701180234.h1 Method BLASTX NCBI GI g3261633 BLAST score 201 5.0e-16 E value Match length 83 % identity NCBI Description (Z79700) fadE13 [Mycobacterium tuberculosis] Seq. No. 303123 Seq. ID qct701180246.h1 Method BLASTN NCBI GI q2245648 BLAST score 172 E value 4.0e-92 Match length 196 % identity 97 Zea mays discolored-1 (mutant allele dsc1-Ref::Mu1) gene, NCBI Description partial sequence Seq. No. 303124 gct701180267.h1 Seq. ID Method BLASTX NCBI GI g2194139 BLAST score 170 2.0e-12 E value

42823

73

56

Match length

% identity



NCBI Description (AC002062) EST gb_ATTS0887 comes from this gene. [Arabidopsis thaliana]

Seq. No. 303125

Seq. ID gct701180282.h1

Method BLASTX
NCBI GI g2462749
BLAST score 265
E value 2.0e-23
Match length 87
% identity 61

NCBI Description (AC002292) Putative Serine/Threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 303126

Seq. ID gct701180336.h1

Method BLASTX
NCBI GI g3461822
BLAST score 223
E value 1.0e-18
Match length 81
% identity 51

NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 303127

Seq. ID gct701180341.h1

Method BLASTX
NCBI GI g4416301
BLAST score 279
E value 3.0e-25
Match length 84
% identity 74

NCBI Description (AF105716) gag protein [Zea mays]

Seq. No. 303128

Seq. ID gct701180359.h1

Method BLASTX
NCBI GI g1730777
BLAST score 155
E value 1.0e-10
Match length 82
% identity 38

NCBI Description HYPOTHETICAL 119.3 KD PROTEIN IN FPR1-TOM22 INTERGENIC

REGION >gi 1078050 pir S55151 probable membrane protein

YNL132w - yeast (Saccharomyces cerevisiae)

>gi_854505_emb_CAA86893_ (Z46843) orf16 [Saccharomyces
cerevisiae] >gi 1302072 emb CAA96014 (Z71408) ORF YNL132w

[Saccharomyces cerevisiae]

Seq. No. 303129

Seq. ID gct701180367.h1

Method BLASTX
NCBI GI g1351129
BLAST score 370
E value 7.0e-36
Match length 84
% identity 85



MITOGEN-ACTIVATED PROTEIN KINASE STY1 (MAP KINASE STY1) NCBI Description >qi 2130460 pir S57930 MAP kinase - fission yeast (Schizosaccharomyces pombe) >gi_2130485_pir__S62551 STY1 protein - fission yeast (Schizosaccharomyces pombe) >qi 1488373 bbs 175803 Phh1p=Hog1-like MAP kinase [Schizosaccharomyces pombe=fission yeast, L972, Peptide, 349 aa] >gi 897810_emb CAA61537_ (X89262) MAP kinase [Schizosaccharomyces pombe] >gi_1022685 (U26739) Spc1p [Schizosaccharomyces pombe] >gi 1061294 emb CAA91771 (Z67757) Stylp [Schizosaccharomyces pombe] 303130 Seq. No. gct701180481.h1 Seq. ID BLASTX Method g532813 NCBI GI 269 BLAST score 5.0e-24 E value 82 Match length % identity (U13875) C26E6.9 gene product [Caenorhabditis elegans] NCBI Description 303131 Seq. No. gct701180482.h1 Seq. ID Method BLASTX q2585775 NCBI GI 238 BLAST score 2.0e-20 E value Match length 81 % identity (AF022853) multidrug resistance protein [Homo sapiens] NCBI Description 303132 Seq. No. Seq. ID gct701180576.h1 Method BLASTX q4558558 NCBI GI 255 BLAST score 3.0e-22 E value Match length 86 % identity (AC007138) putative polygalacturonidase [Arabidopsis NCBI Description thaliana] Seq. No. 303133 Seq. ID act701180618.hl BLASTX Method q960280 NCBI GI BLAST score 239 2.0e-20 E value Match length 84 % identity (L46867) TPBF gene product [Acanthamoeba castellanii] NCBI Description Seq. No. 303134

Seq. ID gct701180621.h1

Method BLASTX NCBI GI g4586107 BLAST score 317



E value 1.0e-29 Match length 86 % identity 11

NCBI Description (AL049638) putative disease resistance protein [Arabidopsis

thaliana]

Seq. No. 303135

Seq. ID gct701180624.hl

Method BLASTX
NCBI GI g3219966
BLAST score 170
E value 2.0e-12
Match length 86
% identity 37

NCBI Description PROBABLE 60S RIBOSOMAL PROTEIN C2E11.04

>gi_3395568_emb_CAA20151_ (AL031181) 60s ribosomal protein
L28 [Schizosaccharomyces pombe] >gi_4106660_emb_CAA22600_
(AL035064) 60s ribosomal protein 128 [Schizosaccharomyces

pombe]

Seq. No. 303136

Seq. ID gct701180648.h1

Method BLASTX
NCBI GI g1723715
BLAST score 158
E value 6.0e-11
Match length 88
% identity 39

NCBI Description HYPOTHETICAL 67.6 KD PROTEIN IN PASS-CBF2 INTERGENIC REGION

>gi_2132616_pir__S64447 probable membrane protein YGR138c yeast (Saccharomyces cerevisiae) >gi_1323230_emb_CAA97151_

(Z72923) ORF YGR138c [Saccharomyces cerevisiae]

Seq. No. 303137

Seq. ID gct701180653.h1

Method BLASTX
NCBI GI g4406768
BLAST score 216
E value 8.0e-18
Match length 84
% identity 46

NCBI Description (AC006836) putative flavonol sulfotransferase [Arabidopsis

thaliana]

Seq. No. 303138

Seq. ID gct701180657.h1

Method BLASTX
NCBI GI g4646206
BLAST score 182
E value 9.0e-14
Match length 40
% identity 78

NCBI Description (AC007230) Contains similarity to gb D13630 KIAA0005 gene

from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene.

[Arabidopsis thaliana]



```
Seq. No.
                  303139
Seq. ID
                  gct701180692.h1
Method
                  BLASTX
NCBI GI
                  g115699
BLAST score
                  333
E value
                  2.0e-31
Match length
                  86
% identity
                  70
                  CATALASE (PXP-9) >gi_83928_pir__S00231 catalase (EC
NCBI Description
                  1.11.1.6), peroxisomal - yeast (Candida tropicalis)
                  >qi 2656 emb CAA32159 (X13978) catalase (AA 1 - 485)
                  [Candida tropicalis] >gi 2677 emb CAA29859 (X06660)
                  catalase (AA 1 - 485) [Candida tropicalis]
                  >gi 225914 prf 1403293A peroxisomal catalase [Candida
                  tropicalis]
Seq. No.
                  303140
Seq. ID
                  gw1700612303.h1
Method
                  BLASTN
NCBI GI
                  g3242306
BLAST score
                  131
E value
                  6.0e-68
                  139
Match length
                  99
% identity
NCBI Description Rattus norvegicus mRNA for protein tyrosine phosphatase
Seq. No.
                  303141
Seq. ID
                  gw1700612313.h1
Method
                  BLASTN
NCBI GI
                  q168650
BLAST score
                  181
                  1.0e-97
E value
                  197
Match length
                  98
% identity
NCBI Description Zea mays ubiquitin fusion protein (UBF9) gene, complete cds
                  303142
Seq. No.
Seq. ID
                  gw1700612325.h1
Method
                  BLASTN
NCBI GI
                  q206203
BLAST score
                  105
E value
                  2.0e-52
Match length
                  113
                  98
% identity
NCBI Description Rat pyruvate kinase M1 and M2 subunit genes, complete cds
Seq. No.
                  303143
Seq. ID
                  gwl700612351.h1
Method
                  BLASTN
NCBI GI
                  q1209700
```

Method BLASTN
NCBI GI g1209700
BLAST score 139
E value 1.0e-72
Match length 147
% identity 99

303144

NCBI Description Zea mays ribosomal protein L12 mRNA, complete cds

Seq. No.



```
Seq. ID
                  gw1700612356.h1
                  BLASTX
Method
NCBI GI
                  g3184283
                  213
BLAST score
                  1.0e-17
E value
Match length
                  61
% identity
                  (AC004136) putative TBP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  303145
Seq. No.
Seq. ID
                  gw1700612392.h1
Method
                  BLASTX
NCBI GI
                  g417154
                  174
BLAST score
                  4.0e-13
E value
                  36
Match length
                  100
% identity
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                                                               ** 5
Seq. No.
                  303146
                  gw1700612464.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2914700
BLAST score
                  188
E value
                  1.0e-14
                  48
Match length
                   71
% identity
                   (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   303147
Seq. ID
                   gw1700612661.h1
                  BLASTN
Method
NCBI GI
                   g3980350
BLAST score
                  56
E value
                   3.0e-23
Match length
                  96
                   90
% identity
                  Human DNA sequence from clone 227L5 on chromosome
NCBI Description
                  Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18
                   (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete
                   sequence [Homo sapiens]
                   303148
Seq. No.
Seq. ID
                   qw1700612679.h1
Method
                  BLASTN
NCBI GI
                   g507844
                   68
```

NCBI GI g507844
BLAST score 68
E value 4.0e-30
Match length 168
% identity 85

NCBI Description Zea mays A188 retrotransposon gag gene, complete cds



```
Seq. No.
                  303149
                  gw1700612741.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1806283
                  369
BLAST score
                  1.0e-35
E value
                  82
Match length
                  90
% identity
NCBI Description
                  (Z79637) Histone H4 homologue [Sesbania rostrata]
Seq. No.
                  303150
Seq. ID
                  gwl700612749.h1
Method
                  BLASTX
NCBI GI
                  q1730674
BLAST score
                  151
E value
                  6.0e-10
Match length
                  66
% identity
                  52
NCBI Description
                  HYPOTHETICAL 62.7 KD PROTEIN IN SEC12-SSK2 INTERGENIC
                  REGION >gi_2132801_pir__$63361 probable membrane protein
                  YNR030w - yeast (Saccharomyces cerevisiae)
                  >gi_1302525_emb_CAA96310_ (Z71645) ORF YNR030w
                   [Saccharomyces cerevisiae]
                  303151
Seq. No.
Seq. ID
                  gw1700612763.h1
Method
                  BLASTX
NCBI GI
                  g182424
BLAST score
                  270
E value
                   4.0e-24
Match length
                  83
% identity
NCBI Description
                  (J00127) alpha-fibrinogen precursor [Homo sapiens]
Seq. No.
                   303152
Seq. ID
                   gw1700612807.h1
Method
                  BLASTX
                   g3128225
NCBI GI
BLAST score
                  177
E value
                  2.0e-13
Match length
                   41
% identity
                  85
                  (AC004077) unknown protein [Arabidopsis thaliana]
NCBI Description
                  303153
Seq. No.
Seq. ID
                   gw1700612864.h1
Method
                  BLASTN
                   q300082
NCBI GI
BLAST score
                   36
E value
                   3.0e-11
Match length
                   52
                   92
% identity
NCBI Description
                  hsp82=82 kda heat shock protein [Zea mays, seedling,
                  leaves, Genomic, 3468 nt]
```

42829

303154

gw1700612908.h1

Seq. No. Seq. ID

BLAST score

E value

147

1.0e-09



```
Method
                   BLASTX
NCBI GI
                   q4262222
BLAST score
                   317
E value
                   1.0e-29
Match length
                   85
% identity
                   71
                   (AC006200) putative RNA helicase A, 3' partial [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   303155
Seq. ID
                   gw1700612910.h1
Method
                   BLASTX
NCBI GI
                   q141605
BLAST score
                   189
E value
                   9.0e-24
Match length
                   67
% identity
                   94
NCBI Description
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
                   >gi_72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                   303156
Seq. ID
                   gwl700613010.h1
Method
                  BLASTX
NCBI GI
                   g2564205
BLAST score
                   201
E value
                   9.0e-16
Match length
                  82
% identity
                   59
NCBI Description (AF025506) prenylated rab acceptor 1 [Rattus norvegicus]
Seq. No.
                  303157
Seq. ID
                   gw1700613059.h1
Method
                  BLASTN
NCBI GI
                  g2623247
BLAST score
                  74
E value
                  2.0e-33
Match length
                  121
% identity
                  92
NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds
Seq. No.
                  303158
Seq. ID
                  gw1700613072.h1
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                  89
E value
                  1.0e-42
Match length
                  165
% identity
                  10
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  303159
Seq. ID
                  gw1700613086.h1
Method
                  BLASTX
NCBI GI
                  g1350736
```



```
Match length
                  79
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L37 >qi 629673 pir S44313 ribosomal
                  protein L37 - tomato >gi 483586 emb CAA55674 (X79074)
                  ribosomal protein L37 [Lycopersicon esculentum]
                  303160
Seq. No.
                  gw1700613114.h1
Seq. ID
Method
                  BLASTX
                  g2832247
NCBI GI
BLAST score
                  331
E value
                  5.0e-31
                  103
Match length
                  37
% identity
NCBI Description
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
                  303161
Seq. No.
Seq. ID
                  gw1700613162.h1
Method
                  BLASTN
NCBI GI
                  g4007864
BLAST score
                   90
                  1.0e-43
E value
                   98
Match length
                  19
% identity
                  Zea mays HRGP gene, AC1503 line
NCBI Description
                   303162
Seq. No.
                   gwl700613192.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3395431
BLAST score
                   199
                   1.0e-15
E value
                   53
Match length
% identity
                   62
NCBI Description
                   (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   303163
Seq. ID
                   gw1700613220.h1
Method
                   BLASTX
NCBI GI
                   g2911073
BLAST score
                   150
E value
                   2.0e-17
Match length
                   79
                   62
% identity
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303164
                   gw1700613222.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4567283
                   180
```

NCBI GI g4567283
BLAST score 180
E value 2.0e-13
Match length 64
% identity 66

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No. 303165



```
qw1700613231.h1
Seq. ID
                  BLASTX
Method
                  g548774
NCBI GI
                  172
BLAST score
                  5.0e-23
E value
                  57
Match length
% identity
                  81
                  60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal
NCBI Description
                  protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
                  ribosomal protein L7A [Oryza sativa]
Seq. No.
                  303166
                   gw1700613246.h1
Seq. ID
Method
                  BLASTX
                  g3549667
NCBI GI
                  253
BLAST score
E value
                   6.0e-22
Match length
                   108
% identity
                   57
                   (AL031394) Arabidopsis dynamin-like protein ADL2
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   303167
                   gw1700613284.h1
Seq. ID
Method
                  BLASTX
                   g3355486
NCBI GI
BLAST score
                   234
E value
                   1.0e-19
                   106
Match length
                   52
% identity
                  (AC004218) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303168
Seq. ID
                   gw1700613285.h1
Method
                   BLASTX
NCBI GI
                   g2282584
BLAST score
                   239
                   4.0e-40
E value
                   89
Match length
                   89
% identity
                  (U76259) elongation factor 1-alpha [Zea mays]
NCBI Description
                   303169
Seq. No.
Seq. ID
                   gw1700613360.h1
Method
                   BLASTX
NCBI GI
                   q3914212
BLAST score
                   161
E value
                   2.0e-11
Match length
                   45
                   73
% identity
                   5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE)
NCBI Description
```

(5-OPASE) >gi 1732065 (U70825) 5-oxo-L-prolinase [Rattus

norvegicus]

Seq. No. 303170

Seq. ID gwl700613408.h1

Method BLASTX



```
NCBI GI
                  142
BLAST score
E value
                  6.0e-09
Match length
                  45
                   67
% identity
                  (X55722) 22kD zein [Zea mays]
NCBI Description
                  303171
Seq. No.
Seq. ID
                  gwl700613433.h1
                  BLASTX
Method
                  g2245378
NCBI GI
BLAST score
                  174
                  5.0e-13
E value
                  45
Match length
                  78
% identity
NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]
                  303172
Seq. No.
Seq. ID
                  gw1700613478.h1
Method
                  BLASTX
                  g123593
NCBI GI
BLAST score
                  293
E value
                  7.0e-27
                  59
Match length
                  97
% identity
NCBI Description
                  HEAT SHOCK 70 KD PROTEIN >gi 82697 pir A25089 heat shock
                  protein 70 - maize
                  303173
Seq. No.
Seq. ID
                   gw1700613614.h1
Method
                  BLASTX
                   g3451068
NCBI GI
BLAST score
                   181
                   2.0e-13
E value
                   53
Match length
% identity
                   68
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303174
Seq. ID
                   gw1700613656.h1
Method
                  BLASTX
NCBI GI
                   q2190419
BLAST score
                   162
                   2.0e-15
E value
Match length
                   94
% identity
                   49
NCBI Description
                  (Y13632) dem [Lycopersicon esculentum]
Seq. No.
                   303175
Seq. ID
                   gw1700613664.h1
Method
                   BLASTX
NCBI GI
                   g1708107
BLAST score
                   211
E value
                   2.0e-17
Match length
                   61
% identity
                   75
```

NCBI Description HISTONE H2B >gi 473605 (U08226) histone H2B [Zea mays]



```
Seq. No.
                  303176
Seq. ID
                  gw1700613749.h1
Method
                  BLASTX
NCBI GI
                  g1705678
BLAST score
                   354
                   7.0e - 34
E value
                   91
Match length
% identity
                  80
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                  PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
                  valosin-containing protein [Glycine max]
Seq. No.
                  303177
Seq. ID
                  gwl700613791.h1
Method
                  BLASTN
NCBI GI
                  g37570
BLAST score
                   72
E value
                  1.0e-32
Match length
                  155
% identity
                  87
NCBI Description
                  H.sapiens Uba80 mRNA for ubiquitin
Seq. No.
                  303178
Seq. ID
                  gw1700613833.h1
Method
                  BLASTN
                  g762884
NCBI GI
BLAST score
                   67
E value
                  8.0e-30
Match length
                  122
% identity
NCBI Description
                  Human plakoglobin (PLAK) mRNA, complete cds
Seq. No.
                  303179
Seq. ID
                  qw1700613880.h1
Method
                  BLASTX
                  g2137774
NCBI GI
BLAST score
                  161
E value
                   2.0e-11
Match length
                   32
% identity
                  siah-1A protein - mouse >gi_297035_emb_CAA79630_ (Z19579)
NCBI Description
                  siah-1A protein [Mus musculus]
Seq. No.
                  303180
Seq. ID
                  gwl700613957.h1
Method
                  BLASTX
NCBI GI
                  g1174483
BLAST score
                  177
                  2.0e-13
E value
Match length
                  51
```

% identity 69

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (SUI1ISO1)

>gi 543015 pir JC2042 translation initiation factor eIF-2A - human >gi 450281 (L26247) isolog of yeast suil and rice

gos2; putative [Homo sapiens]



```
Seq. No.
                  303181
Seq. ID
                  gw1700613974.h1
Method
                  BLASTX
NCBI GI
                  g4056502
BLAST score
                  236
E value
                  4.0e-20
Match length
                  66
% identity
                  70
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
                  303182
Seq. No.
Seq. ID
                  gw1700613996.h1
Method
                  BLASTX
NCBI GI
                  g125554
BLAST score
                  249
                  7.0e-22
E value
                  47
Match length
                  100
% identity
                  PROTEIN KINASE C, DELTA TYPE (NPKC-DELTA)
NCBI Description
                  >gi 66730 pir KIRTCD protein kinase C (EC 2.7.1.-) delta -
                  rat >gi 206181 (M18330) protein kinase C delta subspecies
                  [Rattus sp.]
Seq. No.
                  303183
Seq. ID
                  gw1700614022.h1
Method
                  BLASTX
NCBI GI
                  g2062169
BLAST score
                  302
E value
                  1.0e-27
Match length
                  93
% identity
                  59
NCBI Description
                  (ACO01645) ABC transporter (PDR5-like) isolog [Arabidopsis
                  thaliana]
                  303184
Seq. No.
Seq. ID
                  gw1700614055.h1
Method
                  BLASTX
NCBI GI
                  g4263787
BLAST score
                  294
                  1.0e-26
E value
Match length
                  86
                  76
% identity
NCBI Description
                  (AC006068) unknown protein [Arabidopsis thaliana]
Seq. No.
                  303185
Seq. ID
                  gw1700614213.h1
Method
                  BLASTX
NCBI GI
                  g2245020
BLAST score
                  178
E value
                  3.0e-13
Match length
                  69
% identity
                  48
NCBI Description
                  (Z97341) growth regulator homolog [Arabidopsis thaliana]
```

42835

303186

BLASTX

gw1700614245.h1

Seq. No.

Seq. ID Method

% identity

```
NCBI GI
                  g2914706
                  169
BLAST score
                  2.0e-12
E value
                  59
Match length
% identity
                  56
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]
                  303187
Seq. No.
Seq. ID
                  gw1700614263.h1
                                                 ٠.٠
Method
                  BLASTX
NCBI GI
                  g3914557
BLAST score
                  245
                  2.0e-21
E value
                  51
Match length
                  98
% identity
                  RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED
NCBI Description
                  PROTEIN) >gi_1155265 (U40219) possible apospory-associated
                  protein [Pennisetum ciliare]
Seq. No.
                  303188
Seq. ID
                  gwl700614326.h1
Method
                  BLASTN
                  g3777616
NCBI GI
                  162
BLAST score
                  3.0e-86
E value
                  182
Match length
                  97
% identity
NCBI Description Homo sapiens serine protease (PRSS11) mRNA, partial cds
                  303189
Seq. No.
Seq. ID
                  gwl700614327.h1
                  BLASTX
Method
NCBI GI
                  g1771158
BLAST score
                  201
                  4.0e-16
E value
Match length
                  83
                  48
% identity
NCBI Description (Y07861) MFP1 protein [Lycopersicon esculentum]
                  303190
Seq. No.
Seq. ID
                  gw1700614363.h1
Method
                  BLASTN
                  g192911
NCBI GI
BLAST score
                  34
E value
                  4.0e-10
                  50
Match length
                  92
% identity
NCBI Description Mouse cystatin C mRNA, complete cds
Seq. No.
                  303191
                  gwl700614372.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351014
BLAST score
                  211
E value
                  2.0e-17
Match length
                  41
```



NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No. 303192

Seq. ID gwl700614488.h1

Method BLASTX
NCBI GI g1363492
BLAST score 325
E value 2.0e-30
Match length 90
% identity 64

NCBI Description outer envelope membrane protein OEP75 precursor - garden

pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No. 303193

Seq. ID gwl700614529.h1

Method BLASTX
NCBI GI g4220514
BLAST score 479
E value 2.0e-48
Match length 113
% identity 77

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 303194

Seq. ID gwl700614739.h1

Method BLASTN
NCBI GI g397395
BLAST score 168
E value 1.0e-89
Match length 172
% identity 99

NCBI Description Z.mays MNB1b mRNA for DNA-binding protein

Seq. No. 303195

Seq. ID gwl700614836.hl

Method BLASTX
NCBI GI g464863
BLAST score 217
E value 4.0e-18
Match length 50
% identity 84

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 8 (TAT-BINDING PROTEIN

HOMOLOG 10) >gi_422297_pir__JN0610 probable transcription factor DdTBP10 - slime mold (Dictyostelium discoideum) (fragment) >gi_290057 (L16579) HIV1 TAT-binding protein

[Dictyostelium discoideum]

Seq. No. 303196

Seq. ID gwl700614850.h1

Method BLASTN
NCBI GI g3646023
BLAST score 210
E value 1.0e-114
Match length 294



% identity 97

NCBI Description Human DNA sequence from clone 1033B10 on chromosome

6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of

the BING4 gene, the gene for GalT3

(beta3-Galactosyltransferase), the RPS18 (40S ribosomal

protein S18) gene,

Seq. No. 303197

Seq. ID gwl700614909.h1

Method BLASTX
NCBI GI g2558654
BLAST score 184
E value 9.0e-14
Match length 62
% identity 47

NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No. 303198

Seq. ID gwl700614942.h1

Method BLASTN
NCBI GI g22326
BLAST score 80
E value 3.0e-37
Match length 80
% identity 100

NCBI Description Z.mays gene for Hageman factor inhibitor

Seq. No. 303199

Seq. ID gwl700614970.h1

Method BLASTN
NCBI GI g2267596
BLAST score 66
E value 6.0e-29

Match length 114 % identity 89

NCBI Description Oryza sativa 10 kDa chaperonin mRNA, complete cds

Seq. No. 303200

Seq. ID gwl700614995.h1

Method BLASTN
NCBI GI g1503995
BLAST score 79
E value 2.0e-36
Match length 229
% identity 92

NCBI Description Human mRNA for KIAA0206 gene, partial cds

Seq. No. 303201

Seq. ID gwl700615049.h1

Method BLASTX
NCBI GI g3882231
BLAST score 169
E value 4.0e-12
Match length 73
% identity 44

NCBI Description (AB018298) KIAA0755 protein [Homo sapiens]



Seq. No. 303202

Seq. ID gwl700615060.h1

Method BLASTX
NCBI GI g1184774
BLAST score 366
E value 3.0e-35
Match length 76
% identity 92

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 303203

Seq. ID gwl700615084.h1

Method BLASTX
NCBI GI g4512704
BLAST score 191
E value 1.0e-16
Match length 71
% identity 54

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 303204

Seq. ID gwl700615120.h1

Method BLASTX
NCBI GI g140400
BLAST score 141
E value 3.0e-09
Match length 40
% identity 70

NCBI Description HYPOTHETICAL 37.2 KD PROTEIN IN CHA1-PRD1 INTERGENIC REGION

>gi_83176_pir__S19389 hypothetical protein YCL059c - yeast
(Saccharomyces cerevisiae) >gi 5300 emb CAA42386 (X59720)

YCL059c, len:316 [Saccharomyces cerevisiae]

Seq. No. 303205

Seq. ID gwl700615187.h1

Method BLASTX
NCBI GI g3928084
BLAST score 207
E value 1.0e-16
Match length 50
% identity 74

NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis

thaliana]

Seq. No. 303206

Seq. ID gwl700615191.h1

Method BLASTX
NCBI GI g730536
BLAST score 203
E value 2.0e-16
Match length 42

% identity 95

NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi 310933 (L18915) 60S ribosomal

protein subunit L17 [Nicotiana tabacum]

Seq. No. 303207



```
gw1700615249.h1
Seq. ID
Method
                  BLASTN
                  g902526
NCBI GI
BLAST score
                  104
                  7.0e-52
E value
Match length
                  132
% identity
                  95
                  Zea mays clone MubG7 ubiquitin fusion protein gene,
NCBI Description
                  complete cds
Seq. No.
                  303208
                  gw1700615283.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22657
BLAST score
                   42
                  9.0e-15
E value
                  102
Match length
                  87
% identity
                  A.thaliana mRNA for ubiquitin-conjugating enzyme
NCBI Description
Seq. No.
                  303209
                  gw1700615290.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2231312
BLAST score
                  146
                  9.0e-10
E value
Match length
                  39
                  74
% identity
                  (U75603) AtRab18 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  303210
                   gw1700615315.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3184283
BLAST score
                  140
E value
                   4.0e-09
Match length
                   40
% identity
                  72
NCBI Description
                   (AC004136) putative TBP-binding protein [Arabidopsis
                   thaliana]
                   303211
Seq. No.
Seq. ID
                   gw1700615322.h1
Method
                  BLASTX
NCBI GI
                  g141605
BLAST score
                  150
                   6.0e-10
E value
Match length
                   30
% identity
                  100
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
```

maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]

303212 Seq. No.

qw1700615442.h1 Seq. ID

Method BLASTN NCBI GI g2431766



BLAST score 105 E value 4.0e-52 Match length 137 % identity 96

NCBI Description Zea mays acidic ribosomal protein P3a (rpp3a) mRNA,

complete cds

Seq. No. 303213

Seq. ID gwl700615448.h1

Method BLASTX
NCBI GI g129916
BLAST score 148
E value 5.0e-10
Match length 31
% identity 94

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY

phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_(X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

Seq. No. 303214

Seq. ID gwl700615469.h1

Method BLASTN
NCBI GI g22163
BLAST score 46
E value 4.0e-17
Match length 62

% identity 95

NCBI Description Z.mays MANT2 mRNA for adenine nucleotide translocator

(ADP/ATP translocase)

3.0

Seq. No. 303215

Seq. ID gwl700615472.h1

Method BLASTN
NCBI GI g22215
BLAST score 43
E value 2.0e-15
Match length 50
% identity 98

NCBI Description Z.mays ZSF4C1 gene for zein

Seq. No. 303216

Seq. ID gwl700615493.h1

Method BLASTN
NCBI GI g432367
BLAST score 36
E value 6.0e-11
Match length 91
% identity 86

NCBI Description Rice mRNA for elongation factor 1 beta, complete cds

Seq. No. 303217

Seq. ID gwl700615502.h1

Method BLASTX
NCBI GI g2347187
BLAST score 147
E value 2.0e-09



```
Match length
                  36
                  81
% identity
                  (ACO02338) putative malonyl-CoA:Acyl carrier protein
NCBI Description
                  transacylase, 3' partial [Arabidopsis thaliana]
                  303218
Seq. No.
                  qw1700615506.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  42
                  2.0e-14
E value
                  70
Match length
                  90
% identity
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                  complete sequence
                  303219
Seq. No.
                  gw1700615527.h1
Seq. ID
Method
                  BLASTX
                  g3643600
NCBI GI
BLAST score
                  214
                  2.0e-17
E value
Match length
                  54
                  70
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
                  303220
Seq. No.
Seq. ID
                  gw1700615534.h1
Method
                  BLASTN
                  q533094
NCBI GI
BLAST score
                  90
                  1.0e-43
E value
                  106
Match length
% identity
                  96
NCBI Description
                  Human G2 protein mRNA, partial cds
                  303221
Seq. No.
                  gw1700615609.h1
Seq. ID
Method
                  BLASTX
                  g2190992
NCBI GI
BLAST score
                  305
                  2.0e-34
E value
Match length
                  110
% identity
                   65
                   (AF004358) glutathione S-transferase TSI-1 [Aegilops
NCBI Description
                  tauschii]
                  303222
Seq. No.
                  gwl700615701.h1
Seq. ID
Method
                  BLASTX
                  g119791
NCBI GI
BLAST score
                  262
                  2.0e-23
E value
```

Match length 68

% identity 76

NCBI Description 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR

(3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)



>gi_1084385_pir__S22450 3-oxoacyl-[acyl-carrier-protein]
reductase (EC 1.1.1.100) precursor - Cuphea lanceolata
>gi_18046_emb_CAA45866_ (X64566) 3-oxoacyl-[acyl-carrier
protein] reductase [Cuphea lanceolata]
>gi_228929_prf__1814446A beta ketoacyl-ACP reductase
[Cuphea lanceolata]

Seq. No. 303223

Seq. ID gw1700615773.h1

Method BLASTX
NCBI GI g1296955
BLAST score 163
E value 9.0e-12
Match length 32
% identity 88

NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]

Seq. No. 303224

Seq. ID gwl700615779.h1

Method BLASTN
NCBI GI g1419369
BLAST score 104
E value 1.0e-51
Match length 179
% identity 90

NCBI Description Z.mays ZmABP3 mRNA for actin depolymerizing factor

Seq. No. 303225

Seq. ID gwl700615879.hl

Method BLASTX
NCBI GI g112994
BLAST score 245
E value 1.0e-36
Match length 87

% identity 95

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi 22313 emb CAA31077 (X12564)

ABA-inducible gene protein [Zea mays]

>gi 226091 prf 1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 303226

Seq. ID gwl700615901.h1

Method BLASTN
NCBI GI g2605605
BLAST score 79
E value 8.0e-37
Match length 166
% identity 87

NCBI Description Rattus norvegicus mRNA for RANP-1, complete cds

Seq. No. 303227

Seq. ID gwl700615935.h1

Method BLASTX
NCBI GI g2130090
BLAST score 163



```
9.0e-12
E value
Match length
                  50
% identity
                  72
NCBI Description
                  2-oxoglutarate/malate translocator (clone OMT134),
                  mitochondrial membrane - proso millet
                  >gi 1100739 dbj BAA08103 (D45073) 2-oxoglutarate/malate
                  translocator [Panicum miliaceum] >gi 1100741 dbj BAA08104
                   (D45074) 2-oxoglutarate/malate translocator [Panicum
                  miliaceum]
Seq. No.
                  303228
Seq. ID
                  gw1700615955.h1
Method
                  BLASTX
NCBI GI
                  q2498077
BLAST score
                  208
E value
                  9.0e-17
Match length
                  53
% identity
                  87
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                   (PP18) >gi 1777930 (U55019) nucleoside diphosphate kinase
                  [Saccharum officinarum]
Seq. No.
                  303229
Seq. ID
                  gw1700615995.h1
Method
                  BLASTX
NCBI GI
                  g1143864
BLAST score
                  164
                  7.0e-12
E value
Match length
                  44
% identity
                  66
NCBI Description
                  (U28047) beta glucosidase [Oryza sativa]
Seq. No.
                  303230
Seq. ID
                  qw1700616006.h1
Method
                  BLASTX
NCBI GI
                  g2281090
BLAST score
                  239
E value
                  2.0e-20
Match length
                  108
% identity
                  51
NCBI Description
                  (AC002333) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  303231
                  gw1700616114.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2950394
BLAST score
                  45
                  2.0e-16
E value
Match length
                  96
                  96
% identity
NCBI Description
                  Zea mays me gene, exons 1 to
```

Seq. No. 303232

Seq. ID gwl700616118.h1

Method BLASTX NCBI GI g4586049 BLAST score 211

E value

Match length

4.0e-09 29

```
E value
                  5.0e-17
Match length
                  78
% identity
NCBI Description
                  (AC007020) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  303233
                  gw1700616130.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3249071
BLAST score
                  234
                  7.0e-20
E value
                  89
Match length
% identity
                  48
NCBI Description
                  (AC004473) Contains similarity to protein-tyrosine
                  phosphatase 2 gb_L15420 from Dictyostelium discoideum. EST
                  gb_N38718 comes from this g [Arabidopsis thaliana]
Seq. No.
                  303234
Seq. ID
                  gw1700616172.h1
Method
                  BLASTX
NCBI GI
                  g3122724
BLAST score
                  159
E value
                  3.0e-11
Match length
                  48
                  69
% identity
                  60S RIBOSOMAL PROTEIN L38 >gi 2289009 (AC002335) ribosomal
NCBI Description
                  protein L38 isolog [Arabidopsis thaliana]
Seq. No.
                  303235
Seq. ID
                  gw1700616180.h1
                  BLASTX
Method
NCBI GI
                  g1076389
BLAST score
                  291
E value
                  1.0e-26
Match length
                  78
                  73
% identity
                  protein phosphatase 2A pDF1 - Arabidopsis thaliana
NCBI Description
                  >qi 683502 emb CAA57528 (X82002) protein phosphatase 2A 65
                  kDa regulatory subunit [Arabidopsis thaliana]
Seq. No.
                  303236
                  qw1700616211.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q511870
BLAST score
                  144
E value
                  2.0e-13
Match length
                  64
% identity
                  70
NCBI Description
                  (M23537) zein protein [Zea mays]
Seq. No.
                  303237
Seq. ID
                  gw1700616222.h1
Method
                  BLASTX
                  g464986
NCBI GI
BLAST score
                  140
```



% identity 86

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi 421857_pir__S32674 ubiquitin--protein ligase (EC

6.3.2.19) UBC9 - Arabidopsis thaliana

>gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)

ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No. 303238

Seq. ID gwl700616266.h1

Method BLASTN
NCBI GI g3108052
BLAST score 61
E value 4.0e-26
Match length 77
% identity 95

NCBI Description Zea mays myo-inositol 1-phosphate synthase mRNA, complete

cds

Seq. No. 303239

Seq. ID gwl700616291.hl

Method BLASTX
NCBI GI g3023934
BLAST score 154
E value 2.0e-10
Match length 55
% identity 60

NCBI Description HISTONE DEACETYLASE 2 (HD2) (YY1 TRANSCRIPTION FACTOR

BINDING PROTEIN) >gi 1667396 (U31758) transcriptional

regulator homolog RPD3 [Mus musculus]

Seq. No. 303240

Seq. ID gwl700616425.h1

Method BLASTN
NCBI GI g602605
BLAST score 115
E value 3.0e-58
Match length 154
% identity 94

NCBI Description Zea mays tandem genes for alphal-tubulin and alpha2-tubulin

Seq. No. 303241

Seq. ID gwl700616426.h1

Method BLASTN
NCBI GI g168492
BLAST score 132
E value 2.0e-68
Match length 213
% identity 92

NCBI Description Corn histone H3 (H3C3) gene, complete cds

Seq. No. 303242

BLAST score

E value Match length 49 6.0e-19

65



```
gw1700616478.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3269285
BLAST score
                  222
E value
                  2.0e-18
Match length
                  78
% identity
                  (AL030978) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  303243
Seq. No.
Seq. ID
                  gw1700616495.h1
                  BLASTN
Method
                  g4160401
NCBI GI
BLAST score
                  92
                   3.0e-44
E value
Match length
                  180
% identity
                   88
                  Zea mays eIF-5 gene, exons 1-2
NCBI Description
                  303244
Seq. No.
                   gw1700616516.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2462640
BLAST score
                   147
                   1.0e-12
E value
Match length
                   66
% identity
                   48
                  (Y13370) reverse transcriptase [Oryza sativa]
NCBI Description
                   303245
Seq. No.
                   gwl700616620.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                   q609289
BLAST score
                   53
E value
                   2.0e-21
Match length
                   128
                   86
% identity
                  Z.mays cultivar (LG11) ROA mRNA for replication origin
NCBI Description
                   activator protein
Seq. No.
                   303246
                   gw1700616658.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2558664
BLAST score
                   163
E value
                   1.0e-11
Match length
                   67
% identity
                  (AC002354) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303247
Seq. ID
                   qw1700616676.h1
Method
                   BLASTN
NCBI GI
                   g170746
```



% identity NCBI Description Wheat histone H4 TH091 gene, complete cds Seq. No. 303248 Seq. ID gwl700616714.hl Method BLASTX g141600 NCBI GI BLAST score 233 1.0e-20 E value Match length 60 % identity 90 ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1) NCBI Description >gi 72315 pir ZIZMB1 19K zein precursor (clone cZ19B1) $maize > gi 168\overline{67}4$ (M12143) 19 kDa zein protein [Zea mays] Seq. No. 303249 Seq. ID qw1700616715.h1 Method BLASTX NCBI GI q322750 BLAST score 295 E value 4.0e-27 Match length 58 95 % identity ubiquitin / ribosomal protein CEP52 - wood tobacco NCBI Description >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris] Seq. No. 303250 Seq. ID qw1700616723.h1 Method BLASTX NCBI GI g3924612 BLAST score 338 E value 6.0e-32 Match length 80 % identity 82 NCBI Description (AF069442) mitochondrial elongation factor Tu [Arabidopsis thaliana] >gi 4263511 gb AAD15337 (AC004044) mitochondrial elongation factor Tu [Arabidopsis thaliana] Seq. No. 303251 Seq. ID gw1700616785.h1 Method BLASTX NCBI GI q3859548 BLAST score 152 2.0e-10 E value Match length 29 % identity 97 NCBI Description (AF097182) protein phosphatase 2A catalytic subunit [Oryza sativa] 303252 Seq. No. gw1700616861.h1 Seq. ID Method BLASTX NCBI GI

Method BLASTX
NCBI GI g417154
BLAST score 163
E value 9.0e-12
Match length 38



% identity NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa] Seq. No. 303253 Seq. ID qw1700616866.h1 Method BLASTX NCBI GI q2344892 BLAST score 236 4.0e-20 E value Match length 58 79 % identity NCBI Description (AC002388) unknown protein [Arabidopsis thaliana] Seq. No. 303254 Seq. ID gwl700616895.h1 Method BLASTX NCBI GI g3850999 BLAST score 161 E value 2.0e-11 Match length 32 % identity 100 NCBI Description (AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1 [Zea mays] 303255 Seq. No. Seq. ID gwl700616908.h1 Method BLASTX NCBI GI g1172495 BLAST score 263 E value 5.0e-23 Match length 69 % identity 77 NCBI Description PHYTOCHROME A >gi 515749 (L34842) phytochrome A [Glycine max] >gi_515751 (L34844) phytochrome A [Glycine max] Seq. No. 303256 Seq. ID gw1700616913.h1 Method BLASTN NCBI GI g984307 BLAST score 86 E value 4.0e-41 Match length 134 % identity 92 Glycine max ribosomal protein S16 (rps16) gene, partial NCBI Description cds, beta-carboxyltransferase (accD), photosystem I

cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No.

303257

Seq. ID

gwl700616925.h1

Method NCBI GI BLASTX g3261775

BLAST score



E value 2.0e-16 Match length 94 45

NCBI Description (Z95584) hypothetical protein Rv1165 [Mycobacterium

tuberculosis]

Seq. No. 303258

Seq. ID gwl700616964.h1

Method BLASTX
NCBI GI g548852
BLAST score 329
E value 8.0e-31
Match length 72
% identity 83

NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal

protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S

subunit ribosomal protein [Oryza sativa]

Seq. No. 303259

Seq. ID gwl700616968.h1

Method BLASTX
NCBI GI g3892051
BLAST score 353
E value 1.0e-33
Match length 104
% identity 72

NCBI Description (AC002330) predicted NADH dehydrogenase 24 kD subunit

[Arabidopsis thaliana]

Seq. No. 303260

Seq. ID gwl700616978.h1

Method BLASTX
NCBI GI g1168411
BLAST score 152
E value 4.0e-10
Match length 57
% identity 61

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 303261

Seq. ID gwl700616996.h1

Method BLASTX
NCBI GI g120662
BLAST score 140
E value 4.0e-09
Match length 42
% identity 71

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,

CHLOROPLAST >gi_81621 pir_JQ1286

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - Arabidopsis thaliana >gi_336390 (M64115) glyceraldehyde 3-phosphate dehydrogenase B subunit [Arabidopsis thaliana]

Seq. No. 303262

Seq. ID gwl700617079.h1

Method BLASTX



```
NCBI GI
                  g730463
BLAST score
                  232
E value
                  2.0e-19
Match length
                  69
% identity
                  58
NCBI Description
                  60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
                  >qi 630323 pir S44069 ribosomal protein L35a.e.c15 - yeast
                  (Saccharomyces cerevisiae) >qi 484241 (L23923) ribosomal
                  protein L37 [Saccharomyces cerevisiae]
                  >gi 1420537 emb CAA99454 (Z75142) ORF YOR234c
                  [Saccharomyces cerevisiae]
Seq. No.
                  303263
Seq. ID
                  gwl700617080.h1
Method
                  BLASTX
NCBI GI
                  q4539408
BLAST score
                  193
E value
                  7.0e-15
                  45
Match length
% identity
                  87
                  (AL049524) putative alpha NAC [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  303264
Seq. ID
                  gw1700617088.h1
                  BLASTX
Method
NCBI GI
                  g3337361
BLAST score
                  272
                  1.0e-26
E value
Match length
                  100
% identity
                  59
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  303265
Seq. ID
                  qw1700617119.h1
Method
                  BLASTX
NCBI GI
                  q1914683
BLAST score
                  144
E value
                  1.0e-09
Match length
                  62
% identity
                  53
NCBI Description
                  (Y12013) RAD23, isoform I [Daucus carota]
Seq. No.
                  303266
Seq. ID
                  qw1700617125.h1
Method
                  BLASTX
NCBI GI
                  q4586592
BLAST score
                  367
E value
                  1.0e-35
Match length
                  76
% identity
                  96
NCBI Description
                  (AB025000) multicatalytic endopeptidase complex [Cicer
```

arietinum]

Seq. No. 303267

Seq. ID gw1700617228.h1

Method BLASTX NCBI GI g4455169

Match length

% identity

100

94



```
BLAST score
                  6.0e-09
E value
Match length
                  46
% identity
                  54
                  (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  303268
Seq. No.
Seq. ID
                  qw1700617235.h1
Method
                  BLASTN
NCBI GI
                  g577088
BLAST score
                  84
                  7.0e-40
E value
Match length
                  104
% identity
                  95
NCBI Description P.sativum mRNA for ribosomal protein L1
                  303269
Seq. No.
Seq. ID
                  qw1700617239.h1
Method
                  BLASTN
NCBI GI
                  q1732555
BLAST score
                  142
E value
                  3.0e-74
Match length
                  201
% identity
                  94
NCBI Description
                  Glycine max desiccation protective protein LEA5 (Lea5)
                  mRNA, complete cds
Seq. No.
                  303270
Seq. ID
                  gwl700617241.h1
Method
                  BLASTN
NCBI GI
                  q454881
BLAST score
                  35
                  1.0e-10
E value
Match length
                  59
% identity
                  90
NCBI Description Rice gene for thioredoxin h, complete cds
Seq. No.
                  303271
Seq. ID
                  gw1700617258.h1
Method
                  BLASTX
NCBI GI
                  g2191144
BLAST score
                  271
E value
                  4.0e-24
Match length
                  89
% identity
                  58
NCBI Description
                  (AF007269) A_IG002N01.24 gene product [Arabidopsis
                  thaliana]
Seq. No.
                  303272
Seq. ID
                  gw1700617324.h1
Method
                  BLASTN
NCBI GI
                  g22524
BLAST score
                  76
E value
                  3.0e-35
```



NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 303273

Seq. ID gwl700617404.h1

Method BLASTX
NCBI GI g3334441
BLAST score 166
E value 1.0e-11
Match length 48
% identity 58

NCBI Description HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II

>gi 2642161 (AC003000) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 303274

Seq. ID gwl700617456.hl

Method BLASTX
NCBI GI g3746060
BLAST score 247
E value 3.0e-21
Match length 61
% identity 75

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 303275

Seq. ID gwl700617477.hl

Method BLASTX
NCBI GI g1491931
BLAST score 280
E value 4.0e-25
Match length 108
% identity 55

NCBI Description (U52078) kinesin-like protein [Nicotiana tabacum]

Seq. No. 303276

Seq. ID gwl700617490.h1

Method BLASTX
NCBI GI g141608
BLAST score 255
E value 3.0e-22
Match length 55
% identity 93

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655

zein, 19K - maize >gi_22446_emb_CAA3765 $\overline{1}$ _ (X53 $\overline{5}$ 82) $\overline{1}$ 9 kDa

zein [Zea mays]

Seq. No. 303277

Seq. ID gwl700617492.h1

Method BLASTX
NCBI GI g2500380
BLAST score 445
E value 2.0e-44
Match length 88
% identity 93

NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi_2119128_pir__JC4923 ribosomal

protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal

protein L44 isoform a [Gossypium hirsutum] >gi 1553131



(U64678) ribosomal protein L44 isoform b [Gossypium hirsutum]

Seq. No. 303278

Seq. ID gwl700617529.h1

Method BLASTX
NCBI GI g4544443
BLAST score 230
E value 3.0e-19
Match length 104
% identity 52

NCBI Description (AC006592) putative mitochondrial uncoupling protein

[Arabidopsis thaliana]

Seq. No. 303279

Seq. ID gwl700617546.h1

Method BLASTX
NCBI GI g899610
BLAST score 149
E value 2.0e-18
Match length 88
% identity 63

NCBI Description (U29383) acidic ribosomal protein P2 [Zea mays]

Seq. No. 303280

Seq. ID gwl700617632.h1

Method BLASTX
NCBI GI g4371280
BLAST score 279
E value 2.0e-25
Match length 64
% identity 80

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.

Seq. ID gwl700617709.h1

303281

Method BLASTX
NCBI GI g3309086
BLAST score 211
E value 2.0e-34
Match length 82
% identity 90

NCBI Description (AF076253) calcineurin B-like protein 3 [Arabidopsis

thaliana]

Seq. No. 303282

Seq. ID gwl700617909.h1

Method BLASTX
NCBI GI g3461833
BLAST score 167
E value 3.0e-12
Match length 39
% identity 74

NCBI Description (AC004138) putative expansin [Arabidopsis thaliana]

Seq. No. 303283

Seq. ID gwl700617962.h1



```
Method
                  BLASTX
NCBI GI
                  g2497539
BLAST score
                  192
E value
                  5.0e-15
Match length
                  56
% identity
                  88
                  PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >qi 169703
NCBI Description
                  (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]
Seq. No.
                  303284
Seq. ID
                  gw1700618063.h1
Method
                  BLASTX
NCBI GI
                  q3687231
BLAST score
                  200
E value
                  1.0e-15
Match length
                  84
% identity
NCBI Description
                  (AC005169) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  303285
Seq. ID
                  qw1700618085.h1
Method
                  BLASTN
NCBI GI
                  g168500
BLAST score
                  54
E value
                  8.0e-22
Match length
                  106
% identity
                  88
NCBI Description
                  Maize (Zea mays) histone H4 gene (H4C14), complete cds
Seq. No.
                  303286
Seq. ID
                  gw1700618088.h1
Method
                  BLASTX
NCBI GI
                  g2833375
BLAST score
                  153
                  1.0e-10
E value
Match length
                  39
% identity
                  77
                  DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10)
NCBI Description
                   (RP10) (ABC10) >gi 533690 (U12133) RNA polymerase II
                  subunit RPB10 homolog; similar to yeast RNA polymerase II
                  subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica
                  napus]
                  303287
Seq. No.
                  gw1700618126.h1
Seq. ID
Method
                  BLASTX
                  g2853090
NCBI GI
BLAST score
                  376
                  3.0e-36
E value
Match length
                  89
```

% identity 83

NCBI Description (AL021768) small GTP-binding protein-like [Arabidopsis

thaliana]

Seq. No. 303288

Seq. ID gwl700618142.h1

Method BLASTX

```
g3420055
NCBI GI
BLAST score
                  308
E value
                   3.0e-28
                  67
Match length
% identity
                  (AC004680) cyclophilin [Arabidopsis thaliana]
NCBI Description
                  303289
Seq. No.
                  gwl700618172.hl
Seq. ID
                  BLASTX
Method
```

Method BLASTX
NCBI GI g1429226
BLAST score 208
E value 1.0e-16
Match length 45
% identity 80

NCBI Description (X98861) TFIIA [Arabidopsis thaliana]

Seq. No. 303290

Seq. ID gwl700618213.h1

Method BLASTX
NCBI GI g223430
BLAST score 154
E value 2.0e-10
Match length 27
% identity 100

NCBI Description dehydrogenase Adhl, alcohol [Zea mays]

Seq. No. 303291

Seq. ID gwl700618222.hl

Method BLASTN
NCBI GI g2293565
BLAST score 44
E value 1.0e-15

Match length 84 % identity 88

NCBI Description Oryza sativa ADP-ribosylation factor 1 (Os-ARF1) mRNA,

complete cds

Seq. No. 303292

Seq. ID gwl700618263.h1

Method BLASTN
NCBI GI g2443401
BLAST score 43
E value 2.0e-15
Match length 118
% identity 85

NCBI Description Oryza sativa mRNA for orthophosphate dikinase, complete cds

Seq. No. 303293

Seq. ID gwl700618295.h1

Method BLASTN
NCBI GI g1184775
BLAST score 89
E value 1.0e-42
Match length 173
% identity 90

NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4

NCBI GI

g132983



(gpc4) mRNA, complete cds

```
Seq. No.
                    303294
 Seq. ID
                    gw1700618357.h1
 Method
                    BLASTX
 NCBI GI
                    g4416302
 BLAST score
                    155
 E value
                    2.0e-10
 Match length
                    80
 % identity
                    42
                    (AF105716) copia-type pol polyprotein [Zea mays]
 NCBI Description
 Seq. No.
                    303295
 Seq. ID
                    gwl700618383.h1
 Method
                    BLASTX
 NCBI GI
                    q3641836
 BLAST score
                    147
 E value
                    2.0e-14
 Match length
                    60
                    72
 % identity
 NCBI Description
                    (AL023094) putative serine/threonine protein kinase
                    [Arabidopsis thaliana]
 Seq. No.
                    303296
 Seq. ID
                    gw1700618562.h1
 Method
                    BLASTN
 NCBI GI
                    g4234847
 BLAST score
                    101
 E value
                    1.0e-49
 Match length
                    153
                    92
  % identity
 NCBI Description
                    Zea mays copia-like retrotransposon Sto-3, partial sequence
                    303297
 Seq. No.
                    gw1700618671.h1
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4263783
 BLAST score
                    332
                    3.0e-31
 E value
 Match length
                    92
  % identity
                    (AC006068) putative DNAJ protein [Arabidopsis thaliana]
 NCBI Description
                    303298
 Seq. No.
                    gw1700618688.h1
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3402709
 BLAST score
                    287
                    5.0e-26
 E value
                    92
 Match length
% identity
                    61
 NCBI Description
                    (AC004261) hypothetical protein [Arabidopsis thaliana]
                    303299
 Seq. No.
                    hbs701180727.h1
 Seq. ID
 Method
                    BLASTX
```



```
BLAST score
E value
                  5.0e-33
Match length
                  87
% identity
                  72
NCBI Description
                  60S RIBOSOMAL PROTEIN L5A >gi_85843_pir__A33823 ribosomal
                  protein L5a - African clawed frog >gi 214754 (M29032) L5a
                  ribosomal protein [Xenopus laevis]
                  303300
Seq. No.
Seq. ID
                  hbs701180730.h1
Method
                  BLASTX
NCBI GI
                  g4582434
BLAST score
                  270
E value
                  4.0e-24
Match length
                  59
% identity
NCBI Description
                  (AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.
                  303301
                  hbs701180848.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263718
BLAST score
                  325
E value
                  1.0e-30
Match length
                  84
% identity
                  (AC006223) putative DNA topoisomerase III beta [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  303302
Seq. ID
                  hbs701180930.h1
Method
                  BLASTX
NCBI GI
                  g2281705
BLAST score
                  341
E value
                  3.0e-37
Match length
                  88
% identity
                  85
NCBI Description
                  (AF013979) ethylene responsive factor [Oryza sativa]
Seq. No.
                  303303
Seq. ID
                  hbs701180970.h1
Method
                  BLASTX
NCBI GI
                  g3063459
BLAST score
                  399
                  3.0e-39
E value
Match length
                  90
% identity
                  80
NCBI Description
                  (AC003981) F22013.21 [Arabidopsis thaliana]
Seq. No.
                  303304
Seq. ID
                  hbs701181114.hl
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3618316
BLAST score 228
E value 4.0e-19
Match length 94
% identity 50



```
NCBI Description
                  (AB001886) zinc finger protein [Oryza sativa]
Seq. No.
                  303305
Seq. ID
                  hbs701181131.h1
Method
                  BLASTX
NCBI GI
                  g2623307
BLAST score
                  338
E value
                  5.0e-32
Match length
                  93
% identity
                  71
NCBI Description
                  (AC002409) putative ubiquitin protease [Arabidopsis
                  303306
Seq. No.
Seq. ID
                  hbs701181166.hl
Method
                  BLASTX
NCBI GI
                  q2245004
BLAST score
                  177
E value
                  3.0e-13
Match length
                  46
% identity
                  70
NCBI Description
                  (Z97341) similarity to membrane transport protein
                  [Arabidopsis thaliana]
Seq. No.
                  303307
Seq. ID
                  hbs701181168.hl
Method
                  BLASTX
NCBI GI
                  q4063760
BLAST score
                  240
E value
                  1.0e-20
Match length
                  90
% identity
                  48
NCBI Description (AC005561) putative POL3 protein [Arabidopsis thaliana]
Seq. No.
                  303308
Seq. ID
                  hbs701181217.h1
Method
                  BLASTX
NCBI GI
                  g4191779
BLAST score
                  169
E value
                  3.0e-12
Match length
                  84
% identity
                  45
NCBI Description
                  (AC005917) putative recA protein [Arabidopsis thaliana]
                  303309
Seq. No.
                  hbs701181253.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4235644
BLAST score
                  159
E value
                  5.0e-11
Match length
                  65
% identity
                  48
NCBI Description (AF119040) polyprotein [Lycopersicon esculentum]
```

Seq. No. 303310

Seq. ID hbs701181317.h1

Method BLASTX

% identity

80



```
g2160161
NCBI GI
                   143
BLAST score
                   3.0e-09
E value
Match length
                   86
% identity
NCBI Description (AC000132) F21M12.7 gene product [Arabidopsis thaliana]
Seq. No.
                   303311
                  hbs701181412.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2245136
BLAST score
                   157
E value
                   4.0e-11
Match length
                   74
% identity
NCBI Description
                  (Z97344) trehalose-6-phosphate synthase homolog
                   [Arabidopsis thaliana]
Seq. No.
                   303312
Seq. ID
                   hbs701181477.h1
Method
                   BLASTX
NCBI GI
                   q2618689
BLAST score
                   170
E value
                   2.0e-12
Match length
                   57
% identity
                   63
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
Seq. No.
                   303313
Seq. ID
                   hbs701181556.h1
Method
                   BLASTX
NCBI GI
                   g1172809
BLAST score
                   154
                   1.0e-10
E value
Match length
                   41
                   73
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >gi 468056
                   (U06108) QM protein [Zea mays]
Seq. No.
                   303314
Seq. ID
                   hbs701181607.h1
                   BLASTX
Method
                   g3641868
NCBI GI
BLAST score
                   179
                   2.0e-13
E value
Match length
                   53
% identity
                  (AJ011012) hypothetical protein [Cicer arietinum]
NCBI Description
                   303315
Seq. No.
                   hbs701181625.h1
Seq. ID
Method
                   BLASTX
                   g1103318
NCBI GI
BLAST score
                   311
                   7.0e-29
E value
Match length
                   69
```



```
NCBI Description
                  (X78818) casein kinase I [Arabidopsis thaliana]
                  >gi 2244791 emb CAB10213.1 (Z97336) casein kinase I
                  [Arabidopsis thaliana]
Seq. No.
                  303316
                  hbs701181690.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4039155
BLAST score
                  259
E value
                  8.0e-23
Match length
                  82
% identity
                  57
                  (AF104258) putative copper-inducible 35.6 kDa protein
NCBI Description
                  [Festuca rubra]
Seq. No.
                  303317
Seq. ID
                  hbs701181703.h1
Method
                  BLASTN
NCBI GI
                  g22270
BLAST score
                  57
E value
                  7.0e-24
Match length
                  61
% identity
                  98
NCBI Description Maize mRNA from an embryogenic abscisic acid-inducible gene
Seq. No.
                  303318
Seq. ID
                  hbs701181707.hl
Method
                  BLASTX
NCBI GI
                  q3641252
BLAST score
                  203
E value
                  2.0e-16
Match length
                  73
% identity
                  55
NCBI Description
                  (AF053127) leucine-rich receptor-like protein kinase [Malus
                  domestica]
                  303319
Seq. No.
                  hbs701181813.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2809251
BLAST score
                  200
                  7.0e-16
E value
Match length
                  83
                  43
% identity
NCBI Description
                  (AC002560) F21B7.20 [Arabidopsis thaliana]
                  303320
Seq. No.
                  hbs701181901.h1
Seq. ID
Method
                  BLASTX
                  g2618699
NCBI GI
BLAST score
                  199
                  8.0e-16
E value
Match length
                  79
% identity
```

Seq. No. 303321

44

42861

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

```
hbs701181989.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4234845
                  38
BLAST score
E value
                  3.0e-12
Match length
                  38
% identity
                  100
                  Zea mays copia-like retrotransposon Sto-17, partial
NCBI Description
                  sequence
Seq. No.
                  303322
Seq. ID
                  hbs701182022.h1
                  BLASTX
Method
NCBI GI
                  g2735841
BLAST score
                  303
E value
                  5.0e-28
Match length
                  61
                  97
% identity
NCBI Description (AF010283) No definition line found [Sorghum bicolor]
                  303323
Seq. No.
Seq. ID
                  hbs701182047.h1
Method
                  BLASTX
                  g4582468
NCBI GI
BLAST score
                  224
E value
                  1.0e-21
Match length
                  79
% identity
                  63
NCBI Description (AC007071) putative 40S ribosomal protein; contains
                  C-terminal domain [Arabidopsis thaliana]
                  303324
Seq. No.
Seq. ID
                  hbs701182067.h1
Method
                  BLASTX
NCBI GI
                  g4579913
BLAST score
                  356
E value
                  3.0e-34
Match length
                  84 -
% identity
NCBI Description
                  (AB023423) sulfate transporter [Arabidopsis thaliana]
Seq. No.
                  303325
Seq. ID
                  hbs701182111.h1
                  BLASTX
Method
NCBI GI
                  q3859659
BLAST score
                  187
                  2.0e-14
E value
```

Match length 51 % identity 69

(AL031394) putative potassium transporter AtKT5p (AtKT5) NCBI Description

[Arabidopsis thaliana]

Seq. No. 303326

hbs701182117.h1 Seq. ID

Method BLASTN q1546918 NCBI GI

BLAST score 34

```
4.0e-10
E value
Match length
                  50
% identity
                  92
NCBI Description
                  Z.mays mRNA for translation initiation factor 5A
                  303327
Seq. No.
                  hbs701182315.hl
Seq. ID
Method
                  BLASTX
                  g2108252
NCBI GI
BLAST score
                  149
                  4.0e-10
E value
Match length
                  51
% identity
                  63
NCBI Description
                  (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
                  >gi 2108254 emb CAA71276 (Y10227) P-glycoprotein-2
                  [Arabidopsis thaliana] >gi 4538925 emb CAB39661.1
                  (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
Seq. No.
                  303328
Seq. ID
                  hbs701182331.h1
Method
                  BLASTN
NCBI GI
                  q4584956
BLAST score
                  34
E value
                  9.0e-10
Match length
                  46
                  93
% identity
NCBI Description
                  Zea mays heat shock protein 101 (HSP101) gene, complete cds
Seq. No.
                  303329
Seq. ID
                  hbs701182343.h1
Method
                  BLASTX
NCBI GI
                  g1707015
BLAST score
                  248
                  2.0e-21
E value
Match length
                  72
% identity
                  69
NCBI Description
                  (U78721) protein phosphatase 2C isolog [Arabidopsis
                  thaliana]
Seq. No.
                  303330
Seq. ID
                  hbs701182346.h1
Method
                  BLASTN
                  g2642212
NCBI GI
BLAST score
                  85
E value
                  3.0e-40
                  149
Match length
                  89
% identity
NCBI Description Zea mays nitrate-induced NOI protein gene, complete cds
                  303331
Seq. No.
                  hbs701182360.h1
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3913425
BLAST score 141
E value 5.0e-09
Match length 45
% identity 60



PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA NCBI Description HELICASE >gi 2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana] Seq. No. 303332 Seq. ID hbs701182425.h1 Method BLASTX NCBI GI g1531758 BLAST score 410 2.0e-40 E value Match length 93 % identity (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) NCBI Description unknown protein [Arabidopsis thaliana] Seq. No. 303333 hbs701182471.h1 Seq. ID Method BLASTN q3452305 NCBI GI BLAST score 98 6.0e-48 E value Match length 138 % identity 93 NCBI Description Zea mays retrotransposon Opie-3 3' LTR, partial sequence 303334 Seq. No. Seq. ID hbs701182490.h1 Method BLASTX g1350680 NCBI GI BLAST score 138 8.0e-09 E value Match length 43 % identity 58 60S RIBOSOMAL PROTEIN L1 NCBI Description 303335 Seq. No. Seq. ID hbs701182580.h1 BLASTX Method g1708424 NCBI GI BLAST score 301 E value 9.0e-28 Match length 86 % identity 60 ISOFLAVONE REDUCTASE HOMOLOG >qi 1230614 (U48590) NCBI Description

isoflavone reductase-like protein [Lupinus albus]

303336 Seq. No.

hbs701182621.h1 Seq. ID

Method BLASTX g4406820 NCBI GI BLAST score 263 E value 2.0e-23 Match length 81 69 % identity

(AC006201) putative ras superfamily member [Arabidopsis NCBI Description

thaliana]

Seq. ID

Method

NCBI GI



```
303337
Seq. No.
                  hbs701182710.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3033400
BLAST score
                  305
E value
                  3.0e-28
Match length
                  69
                  75
% identity
                  (AC004238) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                   303338
Seq. No.
Seq. ID
                  hbs701182729.h1
                  BLASTX
Method
NCBI GI
                   g4105772
                   280
BLAST score
                   3.0e-25
E value
                   62
Match length
                   76
% identity
NCBI Description (AF049917) PGP9B [Petunia x hybrida]
                   303339
Seq. No.
                   hbs701182779.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1109614
                   158
BLAST score
E value
                   6.0e-11
                   47
Match length
% identity
                   60
NCBI Description (D45078) MP28 [Cucurbita sp.]
                   303340
Seq. No.
Seq. ID
                   hbs701182981.h1
                   BLASTX
Method
                   q3600059
NCBI GI
                   186
BLAST score
                   2.0e-14
E value
Match length
                   50
% identity
                   66
                   (AF080120) contains similarity to WB domains, G-beta
NCBI Description
                   repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03)
                   [Arabidopsis thaliana]
Seq. No.
                   303341
                   hbs701183089.h1
Seq. ID
                   BLASTN
Method
                   q311238
NCBI GI
BLAST score
                   57
E value
                   2.0e-23
                   168
Match length
                   85
% identity
NCBI Description Z.mays cat1 gene for catalase
Seq. No.
                   303342
```

42865

hbs701183116.h1

BLASTX

g2984225



```
BLAST score
                   9.0e-17
E value
Match length
                  86
                  52
% identity
NCBI Description (AE000766) enolase-phosphatase E-1 [Aquifex aeolicus]
Seq. No.
                  303343
                  hbs701183140.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1946356
BLAST score
                  144
E value
                   2.0e-09
                   52
Match length
                   58
% identity
                   (U93215) hypothetical protein H1.2flk [Arabidopsis
NCBI Description
                   thaliana] >gi_2880041 (AC002340) hypothetical protein
                  H1.2flk [Arabidopsis thaliana]
                   303344
Seq. No.
Seq. ID
                   hbs701183148.h1
Method
                   BLASTN
NCBI GI
                   g3341647
BLAST score
                   49
                   4.0e-19
E value
                   65
Match length
                   94
% identity
                  Zea mays Ama gene encoding single-subunit RNA polymerase
NCBI Description
                   303345
Seq. No.
Seq. ID
                   hbs701183265.h1
Method
                   BLASTX
NCBI GI
                   q2832658
BLAST score
                   155
                   1.0e-10
E value
                   85
Match length
% identity
                  (AL021710) putative protein [Arabidopsis thaliana]
NCBI Description
                   303346
Seq. No.
Seq. ID
                   hbs701183302.h1
Method
                   BLASTN
NCBI GI
                   g2735016
BLAST score
                   226
E value
                   1.0e-124
                   238
Match length
                   99
% identity
                   Zea mays KI domain interacting kinase 1 (KIK1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   303347
                   hbs701183309.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2065021
BLAST score
                   245
                   4.0e-21
E value
                   77
Match length
```

61

% identity

Seq. ID



```
(Y12555) alanyl t-RNA synthetase [Arabidopsis thaliana]
NCBI Description
                   303348
 Seq. No.
 Seq. ID
                   hbs701183323.h1
Method
                   BLASTX
NCBI GI
                   q4539330
BLAST score
                   152
                   3.0e-10
E value
Match length
                   66
                   50
 % identity
NCBI Description
                   (AL035679) putative receptor-like protein kinase (fragment)
                   [Arabidopsis thaliana]
                   303349
 Seq. No.
                   hbs701183341.h1
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   g2293006
 BLAST score
                   145
                   2.0e-09
E value
Match length
                   48
 % identity
NCBI Description
                   (AJ000977) hypothetical protein [Rhodobacter sphaeroides]
                   303350
 Seq. No.
                   hbs701183366.h1
 Seq. ID
                   BLASTX
Method
                   g3176715
NCBI GI
 BLAST score
                   378
                   9.0e-37
 E value
Match length
                   89
 % identity
                   75
                    (AC002392) putative receptor-like protein kinase
NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                   303351
 Seq. ID
                   hbs701183381.h1
 Method
                   BLASTX
 NCBI GI
                   g3420052
 BLAST score
                   196
 E value
                   4.0e-26
 Match length
                   87
 % identity
                   74
 NCBI Description
                    (AC004680) putative ubiginone reductase [Arabidopsis
                   thaliana]
                   303352
 Seq. No.
                   hbs701183465.h1
 Seq. ID
 Method
                   BLASTN
                   g22101
 NCBI GI
 BLAST score
                   121
                   1.0e-61
 E value
Match length
                   255
 % identity
                   88
                   Maize 7SL RNA of signal recognition particle
 NCBI Description
                   303353
 Seq. No.
```

42867

hbs701183475.h1

```
BLASTX
Method
                  g1208496
NCBI GI
                  160
BLAST score
                   3.0e-11
E value
                  29
Match length
                   97
% identity
NCBI Description (D38124) EREBP-3 [Nicotiana tabacum]
                   303354
Seq. No.
                  hbs701183501.hl
Seq. ID
                  BLASTX
Method
                   g3327394
NCBI GI
                   353
BLAST score
                   9.0e-34
E value
                   93
Match length
% identity
NCBI Description (AC004483) putative RNA helicase [Arabidopsis thaliana]
                   303355
Seq. No.
                   hbs701183590.hl
Seq. ID
                   BLASTX
Method
                   g2586082
NCBI GI
                   229
BLAST score
                   3.0e-19
E value
                   87
Match length
                   53
% identity
NCBI Description (U72725) retrofit [Oryza longistaminata]
                   303356
Seq. No.
Seq. ID
                   hbs701183625.h1
                   BLASTX
Method
                   g4467137
NCBI GI
BLAST score
                   378
                   9.0e-37
E value
                   88
Match length
% identity
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   303357
Seq. No.
                   hbs701183718.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4512670
BLAST score
                   142
E value
                   3.0e-14
                   85
Match length
                   48
% identity
                   (AC006931) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303358
                   hbs701183728.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2062172
BLAST score
                   148
E value
                   8.0e-10
Match length
                   33
```

(AC001645) unknown protein [Arabidopsis thaliana]

73

% identity

NCBI Description

```
303359
Seq. No.
                  hbs701183753.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1076678
BLAST score
                  191
                  2.0e-20
E value
                  65
Match length
% identity
                  ubiquitin / ribosomal protein S27a - potato (fragment)
NCBI Description
                  303360
Seq. No.
Seq. ID
                  hbs701183863.h1
                  BLASTX
Method
                  g3004564
NCBI GI
BLAST score
                  177
                   2.0e-13
E value
                  71
Match length
% identity
                   (AC003673) putative receptor Ser/Thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   303361
Seq. No.
                   hbs701183864.h1
Seq. ID
                   BLASTX
Method
                   g3152613
NCBI GI
BLAST score
                   175
                   4.0e-13
E value
                   69
Match length
% identity
                  (AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303362
                   hbs701183876.h1
Seq. ID
                   BLASTX
Method
                   g549674
NCBI GI
BLAST score
                   200
E value
                   4.0e-16
                   73
Match length
                   49
% identity
                   HYPOTHETICAL 49.6 KD PROTEIN IN ELM1-PRI2 INTERGENIC REGION
NCBI Description
                   >gi 539160_pir__S37867 hypothetical protein YKL046c
                   precursor - yeast (Saccharomyces cerevisiae)
                   >gi 486062_emb_CAA81881_ (Z28046) ORF YKL046c
                   [Saccharomyces cerevisiae]
                   303363
Seq. No.
                   hbs701183921.hl
Seq. ID
                   BLASTX
Method
                   g2829916
NCBI GI
BLAST score
                   378
                   1.0e-36
E value
Match length
                   92
% identity
                   84
                   (AC002291) Unknown protein [Arabidopsis thaliana]
NCBI Description
```

303364

Seq. No.

Match length

NCBI Description

% identity

89

```
hbs701183976.h1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g3176686
                   359
 BLAST score
                   2.0e-34
 E value
                   90
 Match length
 % identity
                    (AC003671) Similar to high affinity potassium transporter,
 NCBI Description
                   HAK1 protein gb U22945 from Schwanniomyces occidentalis.
                    [Arabidopsis thaliana]
                    303365
 Seq. No.
 Seq. ID
                   hbs701184118.h1
 Method
                   BLASTX
 NCBI GI
                    g1169151
                    426
 BLAST score
                    2.0e-42
 E value
 Match length
                    94
                    86
 % identity
                   ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
 NCBI Description
                    CYCLASE) >gi 1070522_pir__OYBY adenylate cyclase (EC
                    4.6.1.1) - yeast (Saccharomyces cerevisiae)
                    >gi 1006714 emb CAA89295 (Z49280) ORF YJL005w
[Saccharomyces cerevisiae]
                    303366
 Seq. No.
                    hbs701184126.h1
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g3880563
                    197
 BLAST score
 E value
                    2.0e-15
 Match length
                    82
                    49
 % identity
                    (278018) predicted using Genefinder; similar to
 NCBI Description
                    serine/threonine kinase; cDNA EST yk353d10.5 comes from
                    this gene [Caenorhabditis elegans]
                    303367
 Seq. No.
 Seq. ID
                    hbs701184147.h1
 Method
                    BLASTX
 NCBI GI
                    g633040
 BLAST score
                    162
 E value
                    2.0e-11
 Match length
                    88
 % identity
                    43
                    (D37986) 130 kDa myosin-binding subunit of smooth muscle
 NCBI Description
                    myosin phophatase (M130) [Gallus gallus]
 Seq. No.
                    303368
 Seq. ID
                    hbs701184211.h1
 Method
                    BLASTX
 NCBI GI
                    g4539665
 BLAST score
                    312
 E value
                    5.0e-29
```

42870

(AF061282) polyprotein [Sorghum bicolor]



Seq. No.

303369

```
hbs701184223.hl
Seq. ID
                  BLASTX
Method
                  g4586044
NCBI GI
BLAST score
                  148
                  9.0e-10
E value
                   63
Match length
% identity
                   (AC007020) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                   303370
Seq. No.
Seq. ID
                  hbs701184240.h1
                  BLASTN
Method
                   g4206305
NCBI GI
BLAST score
                   60
                   3.0e-25
E value
                   223
Match length
                   42
% identity
                  Zea mays retrotransposon Cinful-1, complete sequence
NCBI Description
                   303371
Seq. No.
                   hbs701184295.h1
Seq. ID
                   BLASTX
Method
                   g4580389
NCBI GI
                   252
BLAST score
                   5.0e-22
E value
                   66
Match length
                   67
% identity
                   (AC007171) unknown protein [Arabidopsis thaliana]
NCBI Description
                   303372
Seq. No.
                   hbs701184360.h1
Seq. ID
                   BLASTN
Method
                   q4185305
NCBI GI
                   51
BLAST score
E value
                   6.0e-20
                   91
Match length
                   89
% identity
                   Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                   protein, polyprotein, and copia protein genes, complete
                   cds; and unknown genes
                   303373
Seq. No.
                   hbs701184364.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4164148
BLAST score
                   83
                   6.0e-39
E value
Match length
                   139
% identity
                   90
                   Oryza sativa mRNA for iron-superoxide dismutase, complete
NCBI Description
                   cds
```

42871

303374

Seq. No.

```
hbs701184370.h1
Seq. ID
                  BLASTX
Method
                  g1574938
NCBI GI
                  308
BLAST score
E value
                  1.0e-28
Match length
                  68
% identity
                 (U34726) superoxide dismutase 4 [Zea mays]
NCBI Description
                  303375
Seq. No.
Seq. ID
                  hbs701184526.h1
Method
                  BLASTX
NCBI GI
                  g4587554
BLAST score
                  339
                   3.0e-32
E value
                  86
Match length
                   67
% identity
                  (AC006577) Similar to gb_AJ005701 Na/Ca,K-exchanger from
NCBI Description
                   Caenorhabditis elegans. ESTs gb_T04173 and gb_AA585918
                   come from this gene. [Arabidopsis thaliana]
                   303376
Seq. No.
Seq. ID
                  hbs701184582.h1
Method
                  BLASTX
                  g3559814
NCBI GI
BLAST score
                   409
                   2.0e-40
E value
Match length
                  91
% identity
NCBI Description (Y15781) transketolase 1 [Capsicum annuum]
                   303377
Seq. No.
Seq. ID
                   hbs701184621.hl
                   BLASTX
Method
                   q4455276
NCBI GI
BLAST score
                   238
                   3.0e-20
E value
Match length
                   91
                   52
% identity
NCBI Description
                   (AL035527) peptide transporter-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   303378
                   hbs701184675.h1
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g1167982
BLAST score 292
E value 1.0e-26
Match length 89
% identity 62

NCBI Description (U43892) ABC transporter-7 [Mus musculus]

Seq. No. 303379

Seq. ID hbs701185116.h1

Method BLASTX NCBI GI g3776581 BLAST score 141



6.0e-09 E value 60 Match length 45 % identity (AC005388) Similar to Beta integral membrane protein NCBI Description homolog gb U43629 from A. thaliana. [Arabidopsis thaliana] 303380 Seq. No. hbs701185144.h1 Seq. ID BLASTX Method q2511578 NCBI GI 320 BLAST score 6.0e-30 E value 83 Match length 72 % identity (Y13178) multicatalytic endopeptidase [Arabidopsis NCBI Description thaliana] 303381 Seq. No. hbs701185208.h1 Seq. ID BLASTX Method g1854378 NCBI GI 208 BLAST score 8.0e-17 E value 88 Match length 53 % identity (AB001338) Sucrose-Phosphate Synthase [Saccharum NCBI Description officinarum] 303382 Seq. No. hbs701185237.h1 Seq. ID BLASTN Method NCBI GI g4185305 BLAST score 65 3.0e-28 E value 113 Match length 89 % identity Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 NCBI Description (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes 303383 Seq. No. Seq. ID hbs701185274.h1 Method BLASTX q4101591 NCBI GI BLAST score 271 3.0e-24E value 85 Match length % identity (AF005051) aspartyl aminopeptidase [Mus musculus] NCBI Description

Seq. No. 303384

Seq. ID hbs701185282.h1

Method BLASTX
NCBI GI g122099
BLAST score 144
E value 2.0e-09

E value

Match length

% identity

2.0e-16

89

45

NCBI Description Z.mays P gene



```
Match length
                  30
                  100
% identity
                  HISTONE H4 >gi_83768 pir_ S07913 histone H4 - Neurospora
NCBI Description
                  crassa >gi 3018 emb CAA25760 (X01611) histone H4
                  [Neurospora crassa]
                  303385
Seq. No.
                  hbs701185360.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4204793
                  179
BLAST score
                  2.0e-13
E value
Match length
                  51
                   69
% identity
NCBI Description (U52079) P-glycoprotein [Solanum tuberosum]
                  303386
Seq. No.
                  hbs701185419.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22459
BLAST score
                  257
E value
                  1.0e-143
                  272
Match length
                                                                     1
                   99
% identity
NCBI Description Z.mays rab28 gene
                   303387
Seq. No.
Seq. ID
                  hbs701185503.h1
                  BLASTN
Method
NCBI GI
                   g416150
                   59
BLAST score
E value
                   1.0e-24
                   106
Match length
% identity
                   89
                   Zea mays beta-8 tubulin (tub8) mRNA, complete cds
NCBI Description
                   303388
Seq. No.
Seq. ID
                   hbs701185507.h1
                   BLASTN
Method
                   q3694836
NCBI GI
                   39
BLAST score
                   9.0e-13
E value
Match length
                   54
% identity
                   95
                   Zea mays centromeric retrotransposon-like repeat CentA,
NCBI Description
                   complete sequence
                   303389
Seq. No.
Seq. ID
                   hbs701185526.h1
                   BLASTN
Method
NCBI GI
                   g22176
BLAST score
                   45
```



```
303390
Seq. No.
                  hbs701185565.h1
Seq. ID
                  BLASTX
Method
                  q3367522
NCBI GI
                  179
BLAST score
                  2.0e-13
E value
Match length
                  60
                  57
% identity
                  (ACO04392) EST gb_T04691 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                   303391
Seq. No.
                  hbs701185577.h1
Seq. ID
                  BLASTX
Method
                  g2414541
NCBI GI
                   239
BLAST score
                   2.0e-20
E value
Match length
                   68
                   56
% identity
NCBI Description (Z99263) pet112-like protein [Mycobacterium leprae]
                   303392
Seq. No.
                   hbs701185764.hl
Seq. ID
                   BLASTX
Method
                   q4406780
NCBI GI
                   328
BLAST score
                   7.0e-31
E value
                   84
Match length
                   77
% identity
                   (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                   303393
Seq. No.
                   hbs701185915.h1
Seq. ID
                   BLASTX
Method
                   g2961358
NCBI GI
                   249
BLAST score
                   1.0e-21
E value
                   73
Match length
                   67
 % identity
                   (AL022140) serine/threonine protein kinase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   303394
Seq. No.
                   hbs701185924.h1
 Seq. ID
                   BLASTN
Method
                   q5091496
NCBI GI
                   66
BLAST score
                   7.0e-29
 E value
                   102
Match length
                   91
 % identity
                   Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
 NCBI Description
                   complete sequence
```

Method BLASTX



```
g1174162
NCBI GI
BLAST score
                  255
                  1.0e-25
E value
                  58
Match length
% identity
                  (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                  thaliana] >gi 3746915 (AF091106) E2
                  ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
                  303396
Seq. No.
                  hbs701186179.h1
Seq. ID
Method
                  BLASTX
                  g3193304
NCBI GI
                  183
BLAST score
                  2.0e-22
E value
                  77
Match length
                   67
% identity
                   (AF069298) contains similarity to RNA recognition motifs
NCBI Description
                   (Pfam: rrm.hmm, score; 82.09 and 30.80); similar to
                  alternative splicing factor ASF [Arabidopsis thaliana]
                  303397
Seq. No.
Seq. ID
                  hbs701186228.h1
                  BLASTX
Method
                  q4539293
NCBI GI
                  157
BLAST score
                   8.0e-11
E value
                   56
Match length
% identity
                   52
                   (AL049480) putative membrane transporter [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   303398
                   hbs701186234.h1
Seq. ID
                   BLASTX
Method
                   q3386611
NCBI GI
BLAST score
                   149
E value
                   7.0e-10
                   89
Match length
                   37
% identity
                  (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303399
Sea. ID
                   hbs701186242.hl
Method
                   BLASTX
NCBI GI
                   q4249562
BLAST score
                   160
E value
                   3.0e-11
Match length
                   73
% identity
                   41
                   (AB003110) bete-glucosidase [Hypocrea jecorina]
NCBI Description
Seq. No.
                   303400
```

I GI g168700

BLASTN

hrx700703910.h1

NCBI GI g1 BLAST score 63

Seq. ID

Method

```
2.0e-27
E value
                  134
Match length
                  88
% identity
NCBI Description Z.mays zein mRNA, complete cds
                  303401
Seq. No.
                  hrx700703934.h1
Seq. ID
                  BLASTX
Method
                  g22122
NCBI GI
                  279
BLAST score
                  2.0e-33
E value
                  77
Match length
                   96
% identity
                   (X04050) alcohol dehydrogenase 1 [Zea mays] >gi_3420021
NCBI Description
                   (AF050457) alcohol dehydrogenase 1 [Zea mays]
                   303402
Seq. No.
                   hrx700703946.h1
Seq. ID
                   BLASTX
Method
                   g141613
NCBI GI
                   335
BLAST score
                   1.0e-31
E value
                   79
Match length
                   86
% identity
                   ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                   >qi 72305 pir ZIZM21 22K zein precursor (clone pZ22.1) -
                   maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]
                   303403
Seq. No.
                   hrx700703987.h1
Seq. ID
                   BLASTX
Method
                   g16073
NCBI GI
                   348
BLAST score
                   3.0e-33
E value
                   77
Match length
% identity
                   (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   303404
Seq. No.
                   hrx700704059.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g995778
BLAST score
                   290
                   2.0e-26
E value
                   70
Match length
 % identity
                   (U34350) cThy28kD [Gallus gallus]
NCBI Description
                   303405
 Seq. No.
                   hrx700704075.hl
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   g22528
 BLAST score
                   183
 E value
                   1.0e-98
                   266
 Match length
                   93
 % identity
 NCBI Description Zea mays mRNA encoding a zein (clone A20)
```

Seq. No.

303411

```
303406
Seq. No.
Seq. ID
                  hvj700618810.hl
                  BLASTX
Method
                  g2345154
NCBI GI
BLAST score
                  341
                  2.0e-32
E value
Match length
                  65
% identity
                  (AF015522) ribsomal protein S4 [Zea mays]
NCBI Description
                   303407
Seq. No.
                  hvj700618821.h1
Seq. ID
                  BLASTX
Method
                   g3548803
NCBI GI
                   356
BLAST score
                   4.0e-34
E value
                   90
Match length
% identity
                   (AC005313) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana] >gi 4335770 gb AAD17447 (AC006284) putative
                   SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]
                   303408
Seq. No.
                   hvj700618840.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2345154
                   324
BLAST score
                   2.0e-30
E value
                   65
Match length
% identity
                   (AF015522) ribsomal protein S4 [Zea mays]
NCBI Description
                   303409
Seq. No.
                   hvj700618867.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4587525
BLAST score
                   162
                   2.0e-11
E value
                   79
Match length
                   47
% identity
                   (AC007060) Contains the PF 00650 CRAL/TRIO
NCBI Description
                   phosphatidyl-inositol-transfer protein domain. ESTs
                   gb T76582, gb_N06574 and gb_Z25700 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   303410
Seq. ID
                   hvj700618921.h1
Method
                   BLASTN
                   g22101
NCBI GI
BLAST score
                   45
                   3.0e-16
E value
Match length
                   84
% identity
                   89
                   Maize 7SL RNA of signal recognition particle
NCBI Description
```



```
hvj700619022.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3142301
BLAST score
                  147
                  1.0e-09
E value
Match length
                  70
% identity
                  (AC002411) Contains similarity to neural cell adhesion
NCBI Description
                  molecule 2, large isoform precursor gb_M76710 from Xenopus
                  laevis, and beta transducin from S. cerevisiae gb_Q05946.
                  ESTs gb N65081 gb Z30910, gb Z34190, gb Z34611, gb R30101,
                  gb_H3630
Seq. No.
                  303412
Seq. ID
                  hvj700619145.hl
Method
                  BLASTN
                  q4490324
NCBI GI
BLAST score
                  35
E value
                   3.0e-10
Match length
                  75
                  87
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
NCBI Description
                   (ESSA project)
Seq. No.
                   303413
Seq. ID
                  hvj700619294.hl
Method
                   BLASTN
NCBI GI
                   g21800
BLAST score
                   113
                   9.0e-57
E value
                   275
Match length
% identity
                   80
NCBI Description T.aestivum L mRNA for histone H2B
                   303414
Seq. No.
                   hvj700619309.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3747046
BLAST score
                   254
                   5.0e-22
E value
                   67
Match length
                   78
% identity
                  (AF093538) voltage-dependent anion-selective channel
NCBI Description
                   protein [Zea mays]
Seq. No.
                   303415
                   hvj700619327.h1
Seq. ID
Method
                   BLASTN
                   g473186
NCBI GI
BLAST score
                   121
E value
                   1.0e-61
```

Match length 275 87 % identity

NCBI Description Z.mays (A619) PKCI mRNA for protein kinase C Inhibitor

Seq. No. 303416

hvj700619347.h1 Seq. ID

Method

NCBI GI

BLASTN

q2645878



```
BLASTX
Method
                  g2984709
NCBI GI
                  153
BLAST score
                  3.0e-10
E value
                  46
Match length
                  63
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  303417
                  hvj700619353.h1
Seq. ID
                  BLASTX
Method
                  g2190544
NCBI GI
BLAST score
                  158
                  1.0e-12
E value
                  71
Match length
                   66
% identity
                   (AC001229) Similar to Saccharomyces hypothetical protein
NCBI Description
                  P9642.2 (gb U40828). [Arabidopsis thaliana]
                   303418
Seq. No.
                  hvj700619369.h1
Seq. ID
                  BLASTX
Method
                   q2961378
NCBI GI
BLAST score
                   256
E value
                   2.0e-22
                   83
Match length
% identity
                   (AL022141) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303419
                   hvj700619481.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g533250
BLAST score
                   46
                   4.0e-17
E value
                   129
Match length
                   85
% identity
                   Zea mays (clone Sh1-BMS) MISD1 insertion sequence from
NCBI Description
                   shrunken1 allele DNA
Seq. No.
                   303420
Seq. ID
                   hvj700619567.h1
Method
                   BLASTX
NCBI GI
                   g322525
                   372
BLAST score
                   7.0e-36
E value
                   105
Match length
                   67
% identity
                   omnipotent suppressor protein SUP1 homolog (clone A18) -
NCBI Description
                   Arabidopsis thaliana (fragment) >gi 16512_emb_CAA49171
                   (X69374) similar to yeast omnipotent suppressor protein
                   SUP1 (SUP45); ORF [Arabidopsis thaliana]
Seq. No.
                   303421
Seq. ID
                   hvj700619575.hl
```

Method

NCBI GI

E value

BLAST score

BLASTX g112994

3.0e-22

254



```
BLAST score
                  2.0e-71
E value
                  181
Match length
                   94
% identity
                  Homo sapiens molybdenum cofactor biosynthesis protein A and
NCBI Description
                  molybdenum cofactor biosynthesis protein C mRNA, complete
                  cds
                  303422
Seq. No.
                  hvj700619624.hl
Seq. ID
                  BLASTX
Method
                   g1076678
NCBI GI
                   384
BLAST score
                   3.0e-37
E value
                   79
Match length
                   99
% identity
                  ubiquitin / ribosomal protein S27a - potato (fragment)
NCBI Description
                   303423
Seq. No.
                   hvj700619745.h1
Seq. ID
                   BLASTX
Method
                   g399492
NCBI GI
                   209
BLAST score
                   7.0e-28
E value
                   104
Match length
                   75
% identity
                   FIBRINOGEN BETA CHAIN PRECURSOR >gi_279672_pir__FGHUB
NCBI Description
                   fibrinogen beta chain precursor - human
                   303424
Seq. No.
                   hvj700619751.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q22292
BLAST score
                   41
                   8.0e-14
E value
                   89
Match length
% identity
                   Z.mays mRNA for glycine-rich protein
NCBI Description
                   303425
Seq. No.
                   hvj700619752.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1906603
BLAST score
                   171
                   2.0e-91
E value
                   320
Match length
 % identity
                   90
                   Zea mays ACCase gene, intron containing colonist1 and
NCBI Description
                   colonist2 retrotransposons and reverse transcriptase
                   pseudogene, complete sequence
                   303426
 Seq. No.
 Seq. ID
                   hvj700619788.h1
```

Match length % identity GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN NCBI Description >gi_82685_pir__S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564) ABA-inducible gene protein [Zea mays] >gi_226091_prf__1410284A abscisic acid inducible gene [Zea mays] 303427 Seq. No. hvj700619792.hl Seq. ID BLASTN Method NCBI GI g2245648 57 BLAST score 1.0e-23 E value 100 Match length % identity 99 Zea mays discolored-1 (mutant allele dsc1-Ref::Mul) gene, NCBI Description partial sequence 303428 Seq. No. hvj700619851.h1 Seq. ID Method BLASTX q3913804 NCBI GI 174 BLAST score 1.0e-12 E value 49 Match length 73 % identity HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone NCBI Description [Zea mays] 303429 Seq. No. Seq. ID hvj700619858.h1 BLASTN Method q2916863 NCBI GI 173 BLAST score 8.0e-93 E value Match length 197 97 % identity Human DNA sequence from PAC 417G15 on chromosome Xq25-Xq26. NCBI Description Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), pseudogene, ESTs Seq. No. 303430 hvj700619865.h1 Seq. ID BLASTX Method q4417286 NCBI GI BLAST score 157 E value 1.0e-10 Match length 43

% identity

(AC007019) putative shikimate kinase [Arabidopsis thaliana] NCBI Description

Seq. No. 303431

hvj700619867.h1 Seq. ID

BLASTX Method q3355474 NCBI GI



63

Match length % identity

```
BLAST score
                  7.0e-29
E value
Match length
                  101
% identity
                  (AC004218) unknown protein [Arabidopsis thaliana]
NCBI Description
                  303432
Seq. No.
                  hvj700619892.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729051
BLAST score
                  141
                  8.0e-09
E value
Match length
                  34
                  76
% identity
NCBI Description CALTRACTIN (CENTRIN) >gi_444342_prf__1906390A
                  caltractin-like protein [Atriplex nummularia]
Seq. No.
                   303433
                  hvj700620122.h1
Seq. ID
                  BLASTX
Method
                  g2230873
NCBI GI
BLAST score
                  155
                   7.0e-11
E value
                   62
Match length
% identity
NCBI Description
                  (X98494) M phase phosphoprotein 10 [Homo sapiens]
                   303434
Seq. No.
                   hvj700620163.h1
Seq. ID
Method
                   BLASTN
                   g4587635
NCBI GI
BLAST score
                   39
                   1.0e-12
E value
Match length
                   47
% identity
                   96
                   Homo sapiens PAC clone DJ1102A12 from 7q11.21-q11.23,
NCBI Description
                   complete sequence
                   303435
Seq. No.
                   hvj700620166.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1172836
BLAST score
                   240 -
                   5.0e-21
E value
Match length
                   65
                   83
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)
NCBI Description
                   small ras-related protein [Nicotiana tabacum]
                   303436
Seq. No.
                   hvj700620190.hl
Seq. ID
                   BLASTX
Method
                   g2708532
NCBI GI
                   294
BLAST score
                   1.0e-26
E value
```



```
(AF029351) putative RNA binding protein [Nicotiana tabacum]
NCBI Description
                  303437
Seq. No.
                  hvj700620225.h1
Seq. ID
Method
                  BLASTN
                  q4336904
NCBI GI
                  127
BLAST score
                  3.0e-65
E value
                  228
Match length
                  97
% identity
NCBI Description Zea mays Ran-related GTP binding protein mRNA, partial cds
                  303438
Seq. No.
                  hvj700620282.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2262159
BLAST score
                  320
                   9.0e-30
E value
                   82
Match length
                   70
% identity
                   (AC002329) predicted protein similar to S.pombe protein
NCBI Description
                   C5H10.03 [Arabidopsis thaliana]
                   303439
Seq. No.
                   hvj700620363.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2914695
                   248
BLAST score
                   2.0e-21
E value
Match length
                   98
% identity
                   (AC003974) putative ubiquitin specific protease
NCBI Description
                   [Arabidopsis thaliana]
                   303440
Seq. No.
                   hvj700620407.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760345
BLAST score
                   378
                   1.0e-36
E value
                   90
Match length
                   23
% identity
                   (U84967) ubiquitin [Arabidopsis thaliana]
NCBI Description
                   303441
Seq. No.
                   hvj700620440.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4185513
                   187
BLAST score
                   2.0e-19
E value
                   75
Match length
                   68
% identity
                   (AF102823) actin depolymerizing factor 5 [Arabidopsis
NCBI Description
                   thaliana] >gi_4185517 (AF102825) actin depolymerizing
```

Seq. No. 303442

factor 5 [Arabidopsis thaliana]



```
hvj700620496.hl
Seq. ID
                  BLASTN
Method
                  g21892
NCBI GI
                  91
BLAST score
                  1.0e-43
E value
                  135
Match length
                  92
% identity
                  T.aestivum (clone pTAU1.3) Ul snRNA
NCBI Description
Seq. No.
                   303443
                  hvj700620565.h1
Seq. ID
                  BLASTN
Method
                  g22151
NCBI GI
BLAST score
                   48
                   2.0e-18
E value
                   100
Match length
                   87
% identity
                  Z.mays (A188) mRNA for alpha-tubulin
NCBI Description
                   303444
Seq. No.
                   hvj700620571.h1
Seq. ID
                   BLASTX
Method
                   g134613
NCBI GI
BLAST score
                  .171
E value
                   1.0e-12
                   39
Match length
                   90
% identity
                   SUPEROXIDE DISMUTASE-2 (CU-ZN) >gi_82727_pir__A29077
NCBI Description
                   superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 2 - maize
                   >gi 168620 (M54936) superoxide dismutase 2 [Zea mays]
                   >gi 168622 (M15175) SOD2 protein [Zea mays]
Seq. No.
                   303445
Seq. ID
                   hvj700620647.h1
Method
                   BLASTN
                   g1800214
NCBI GI
                   45
BLAST score
                   1.0e-16
E value
                   97
Match length
                   87
% identity
                   Sorghum bicolor phytochrome A (PHYA) mRNA, complete cds
NCBI Description
                   303446
Seq. No.
Seq. ID
                   hvj700620775.h1
                   BLASTN
Method
                   q454880
NCBI GI
BLAST score
                   61
                   9.0e-26
E value
Match length
                   141
                   93
% identity
                   Rice mRNA for WSI724 protein induced by water stress,
NCBI Description
                   complete cds
 Seq. No.
                   303447
                   hvj700620814.h1
 Seq. ID
```

BLASTN

g21448

Method NCBI GI



BLAST score 85 E value 4.0e-40 Match length 85 % identity 100

NCBI Description S.tuberosum gene for U6 small nuclear RNA

Seq. No.

303448

Seq. ID

hvj700620815.hl

Method BLASTX
NCBI GI g4558659
BLAST score 246
E value 1.0e-38
Match length 99
% identity 70

NCBI Description (AC007063) unknown protein [Arabidopsis thaliana]

Seq. No.

303449

Seq. ID hvj700620824.h1

Method BLASTX
NCBI GI g2114207
BLAST score 179
E value 1.0e-21
Match length 72
% identity 78

NCBI Description (D86744) glutaredoxin [Oryza sativa]

Seq. No. 303450

Seq. ID hvj700620857.h1

Method BLASTN
NCBI GI 94185305
BLAST score 46
E value 4.0e-17
Match length 110
% identity 85

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 303451

Seq. ID hvj700620921.h1

Method BLASTX
NCBI GI 94587572
BLAST score 385
E value 2.0e-37
Match length 100
% identity 71

NCBI Description (AC006550) Similar to gb_U70015 lysosomal trafficking regulator from Mus musculus and contains 2 PF_00400 WD40,

regulator from Mus musculus and contains 2 Fr 00400 WD40, G-beta repeats. ESTs gb_T43386 and gb_AA395236 come from

this gene. [Arabidopsis Thaliana]

Seq. No. 303452

Seq. ID hvj700620942.h1

Method BLASTX
NCBI GI g3212863
BLAST score 257



```
2.0e-22
E value
                  76
Match length
                   63
% identity
                   (AC004005) putative translation initiation factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   303453
Seq. ID
                  hvj700621284.hl
                   BLASTX
Method
                   q4586117
NCBI GI
                   156
BLAST score
                   1.0e-10
E value
                   46
Match length
                   65
% identity
NCBI Description (AL049638) putative protein [Arabidopsis thaliana]
                   303454
Seq. No.
                   hvj700621342.h1
Seq. ID
                   BLASTN
Method
                   g499011
NCBI GI
BLAST score
                   52
                   1.0e-20
E value
                   144
Match length
                   86
% identity
                   S.vulgare SoAc1 mRNA
NCBI Description
                   303455
Seq. No.
                   hvj700621379.h1
Seq. ID
                   BLASTN
Method
                   g22503
NCBI GI
                   84
BLAST score
                   2.0e-39
E value
                   180
Match length
                   87
% identity
NCBI Description Zea mays gene for U2 small nuclear RNA (U2snRNA)
                   303456
Seq. No.
Seq. ID
                   hvj700621457.h1
                   BLASTX
Method
                   g3924603
NCBI GI
                   305
BLAST score
                   5.0e-28
E value
Match length
                   106
% identity
                   57
                   (AF069442) putative WD-repeat protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   303457
                   hvj700621540.h1
Seq. ID
                   BLASTX
Method
                   g422248
NCBI GI
BLAST score
                   200
                   3.0e-24
E value
Match length
                   64
 % identity
                   19
                   ubiquitin - basidiomycete (Phanerochaete chrysosporium)
 NCBI Description
```

>gi_395056_emb_CAA80851_ (Z24723) ubiquitin [Phanerochaete

NCBI Description



chrysosporium]

```
303458
Seq. No.
Seq. ID
                  hvj700621603.hl
Method
                  BLASTX
                  g1458245
NCBI GI
                  180
BLAST score
                  3.0e-13
E value
                  96
Match length
                  42
% identity
                  (U64834) coded for by C. elegans cDNA cm17a1; coded for by
NCBI Description
                  C. elegans cDNA cm7g1; coded for by C. elegans cDNA
                  CEMSE26F; similar to methyltransferases [Caenorhabditis
                  elegans]
                  303459
Seq. No.
Seq. ID
                  hvj700621622.hl
Method
                  BLASTX
                  q3668118
NCBI GI
                   283
BLAST score
                   2.0e-25
E value
Match length
                   77
% identity
                   (AJ224078) hypothetical protein [Brassica napus]
NCBI Description
                   303460
Seq. No.
Seq. ID
                   hvj700621627.h1
                   BLASTX
Method
                   g3549652
NCBI GI
BLAST score
                   304
                   7.0e-28
E value
                   64
Match length
% identity
                   (AJ224982) MAP3K epsilon protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   303461
Seq. No:
Seq. ID
                   hvj700621688.h1
                   BLASTX
Method
NCBI GI
                   g3851005
BLAST score
                   144
                   2.0e-09
E value
Match length
                   41
% identity
                   71
                   (AF069911) pyruvate dehydrogenase E1 alpha subunit [Zea
NCBI Description
                   mays]
                   303462
Seq. No.
Seq. ID
                   hvj700621718.h1
Method
                   BLASTN
                   g2645165
NCBI GI
BLAST score
                   69
E value
                   1.0e-30
Match length
                   85
                   95
 % identity
```

Oryza sativa mRNA, similar to ribosomal protein



Seq. No.

303463

```
hvj700621735.hl
Seq. ID
                  BLASTN
Method
                  g211907
NCBI GI
                  72
BLAST score
                  2.0e-32
E value
Match length
                  88
                   95
% identity
NCBI Description Chicken histone H4 protein gene, complete cds
                   303464
Seq. No.
                  hvj700621762.h1
Seq. ID
                  BLASTX
Method
                   g4581132
NCBI GI
                   204
BLAST score
                   4.0e-16
E value
                   69
Match length
% identity
NCBI Description (AC005825) hypothetical protein [Arabidopsis thaliana]
                   303465
Seq. No.
                   hvj700621766.h1
Seq. ID
                   BLASTX
Method
                   g2459446
NCBI GI
                   210
BLAST score
                   8.0e-17
E value
                   70
Match length
                   51
% identity
                   (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
                   303466
Seq. No.
                   hvj700621795.h1
Seq. ID
                   BLASTX
Method
                   q2130944
NCBI GI
                   302
BLAST score
                   1.0e-39
E value
                   111
Match length
                   79
% identity
                   (AB004060) sulfate transporter [Arabidopsis thaliana]
NCBI Description
                   >gi_2262137_gb_AAC78252.1_AAC78252 (AC002330) sulfate
                   transporter protein [Arabidopsis thaliana]
Seq. No.
                   303467
                   hvi700621858.h1
Seq. ID
                   BLASTX
Method
                   q4468798
NCBI GI
                   141
BLAST score
                   3.0e-09
E value
                   43
Match length
 % identity
                   (AJ010440) GST7 protein [Zea mays]
NCBI Description
                   303468
 Seq. No.
 Seq. ID
                   hvj700621992.h1
                   BLASTN
Method
                   q435312
 NCBI GI
```



```
BLAST score
                  1.0e-33
E value
                  106
Match length
                  94
% identity
NCBI Description Z.mays mRNA for beta-D-glucosidase
                   303469
Seq. No.
                  hvj700622028.hl
Seq. ID
                  BLASTX
Method
                   q4567201
NCBI GI
BLAST score
                   151
                   5.0e-10
E value
                   61
Match length
                   52
% identity
                   (AC007168) putative aspartate aminotransferase [Arabidopsis
NCBI Description
                   thaliana]
                   303470
Seq. No.
Seq. ID
                   hvj700622043.h1
                   BLASTN
Method
                   g166548
NCBI GI
                   39
BLAST score
E value
                   1.0e-12
                   69
Match length
                   92
% identity
                   Avena sativa vacuolar H+-ATPase 16 kDa proteolipid subunit
NCBI Description
                   (vatp-P1) mRNA, complete cds
                   303471
Seq. No.
Seq. ID
                   hvj700622146.hl
                   BLASTX
Method
                   q3738312
NCBI GI
BLAST score
                   407
                   5.0e-40
E value
                   108
Match length
% identity
                   68
                   (AC005309) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   303472
Seq. No.
Seq. ID
                   hvj700622190.h1
                   BLASTX
Method
                   q4191784
NCBI GI
BLAST score
                   431
E value
                   8.0e-43
                   104
Match length
                   77
% identity
                   (AC005917) putative WD-40 repeat protein [Arabidopsis
NCBI Description
                   thaliana]
                   303473
 Seq. No.
                   hvj700622196.hl
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g1168537
BLAST score
                   329
                   8.0e-31
E value
 Match length
                   70
```

89

% identity

NCBI Description



```
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732
                  aspartic proteinase (EC 3.4.23.-) - rice
                   >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase
                   [Oryza sativa]
Seq. No.
                   303474
                   hvj700622269.h1
Seq. ID
                   BLASTN
Method
                   q3342032
NCBI GI
                   60
BLAST score
                   3.0e-25
E value
Match length
                   64
% identity
                   Elegia sp. Hahn 6994 18S small subunit ribosomal RNA gene,
NCBI Description
                   complete sequence
Seq. No.
                   303475
                   hvj700622367.h1
Seq. ID
                   BLASTX
Method
                   q2244960
NCBI GI
BLAST score
                   141
                   9.0e-09
E value
                   58
Match length
% identity
                   (Z97340) similarity to copia-like retrotransposon
NCBI Description
                   [Arabidopsis thaliana]
                   303476
Seq. No.
                   hvj700622379.h1
Seq. ID
                   BLASTX
Method
                   q2335108
NCBI GI
                   248
BLAST score
E value
                   3.0e-25
                   82
Match length
% identity
                   (AC002339) putative isulinase [Arabidopsis thaliana]
NCBI Description
                   303477
Seq. No.
                   hvj700622424.h1
 Seq. ID
                   BLASTX
Method
                   g3935181
NCBI GI
 BLAST score
                   164
 E value
                   8.0e-15
Match length
                   60
 % identity
                   (AC004557) F17L21.24 [Arabidopsis thaliana]
 NCBI Description
                   303478
 Seq. No.
                   hvj700622461.h1
 Seq. ID
                   BLASTX
 Method
                   q3367520
 NCBI GI
                   231
 BLAST score
E value
                    2.0e-19
 Match length
                    74
 % identity
                    62
```

42891

(AC004392) Similar to protein kinase APK1A,

tyrosine-serine-threonine kinase gb_D12522 from A.



thaliana. [Arabidopsis thaliana]

```
303479
Seq. No.
                  hvj700622483.h1
Seq. ID
                  BLASTX
Method
                  g4455315
NCBI GI
BLAST score
                  166
E value
                  1.0e-11
                  69
Match length
                  49
% identity
                  (AL035528) RNA-binding protein like [Arabidopsis thaliana]
NCBI Description
                  303480
Seq. No.
Seq. ID
                  hvj700622512.h1
                  BLASTN
Method
NCBI GI
                   g2764801
                  230
BLAST score
E value
                   1.0e-126
                   241
Match length
                   99
% identity
NCBI Description Z.mays yptm3 mRNA
                   303481
Seq. No.
                   hvj700622957.h1
Seq. ID
                   BLASTX
Method
                   g1332579
NCBI GI
                   293
BLAST score
                   3.0e-46
E value
                   99
Match length
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                   303482
Seq. No.
                   hvj700622978.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2258468
BLAST score
                   36
                   4.0e-11
E value
Match length
                   52
% identity
                   Oryza sativa replication protein A1 (Os-RPA1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   303483
Seq. ID
                   hvj700623103.h1
                   BLASTX
Method
                   q464707
NCBI GI
                   258
BLAST score
E value
                   1.0e-22
                   82
Match length
                   57
% identity
                   40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal
NCBI Description
                   protein S18.A - Arabidopsis thaliana
                   >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
                   S18 ribosomal protein [Arabidopsis thaliana]
```

42892

>gi 434345_emb_CAA82274_ (Z28702) S18 ribosomal protein



[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

 Seq. No.
 303484

 Seq. ID
 hvj700623167.h1

 Method
 BLASTN

 NCBI GI
 g3164071

 BLAST score
 45

 E value
 3.0e-16

Match length 53 % identity 96

% identity 96
NCBI Description Human DNA sequence from PAC 389A20 on chromosome X contains
ESTs STS, CpG islands and polymorphic CA repeat

Seq. No. 303485

Seq. ID hvj700623210.h1

Method BLASTN
NCBI GI g21449
BLAST score 84
E value 2.0e-39
Match length 84
% identity 100

NCBI Description S.tuberosum DNA for U6 small nuclear RNA promoter region

Seq. No. 303486

Seq. ID hvj700623226.h1

Method BLASTN
NCBI GI g22348
BLAST score 134
E value 2.0e-69
Match length 134
% identity 100

NCBI Description Z.mays mRNA for iojap protein

Seq. No. 303487

Seq. ID hvj700623317.hl

Method BLASTX
NCBI GI g4581164
BLAST score 279
E value 6.0e-25
Match length 104
% identity 51

NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No. 303488

Seq. ID hvj700623359.h1

Method BLASTN
NCBI GI g2921303
BLAST score 188
E value 1.0e-101



```
203
Match length
                  99
% identity
                  Zea mays herbicide safener binding protein (SBP1) mRNA,
NCBI Description
                  complete cds
                  303489
Seq. No.
                  hvj700623480.h1
Seq. ID
                  BLASTX
Method
                  g1531541
NCBI GI
                  163
BLAST score
                  1.0e-11
E value
                  31
Match length
                  100
% identity
                  (D83391) uroporphyrinogen III methyltransferase [Zea mays]
NCBI Description
                   303490
Seq. No.
                  hvj700623534.h1
Seq. ID
                  BLASTN
Method
                   g5016094
NCBI GI
                   124
BLAST score
                   2.0e-63
E value
                   168
Match length
                   95
% identity
                   Zea mays lysine-ketoglutarate reductase/saccharopine
NCBI Description
                   dehydrogenase bifunctional enzyme mRNA, complete cds
                   303491
Seq. No.
                   hvj700623560.h1
Seq. ID
                   BLASTX
Method
                   g118104
NCBI GI
                   359
BLAST score
                   4.0e-38
E value
                   101
Match length
                   78
% identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi 168461 (M55021) cyclophilin [Zea mays]
                   >gi 82914\overline{8} emb CAA48638 (X68678) cyclophilin [Zea mays]
                   303492
Seq. No.
Seq. ID
                   hvj700623569.h1
                   BLASTN
Method
NCBI GI
                   g440170
BLAST score
                   76
                   1.0e-34
E value
                   309
Match length
                   97
 % identity
                   Z.mays (C6000237) trpA gene
NCBI Description
                   303493
Seq. No.
                   hvj700623579.h1
Seq. ID
                   BLASTX
```

Method BLASTX
NCBI GI g3334323
BLAST score 147
E value 1.0e-09
Match length 34



% identity GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog NCBI Description [Arabidopsis thaliana] >gi_2104532_gb AAC78700.1 (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi 2104550 (AF001535) AGAA.4 [Arabidopsis thaliana] 303494 Seq. No. hvj700623693.h1 Seq. ID BLASTX Method q3885492 NCBI GI 163 BLAST score 8.0e-12 E value 59 Match length % identity (AF063865) tapetum specific protein [Zea mays] NCBI Description 303495 Seq. No. hvj700623741.h1 Seq. ID BLASTX Method g626042 NCBI GI 152 BLAST score 4.0e-10 E value 28 Match length 100 % identity beta-glucosidase, root meristem (EC 3.2.1.-) precursor -NCBI Description maize >gi 435313 emb CAA52293 (X74217) beta-glucosidase [Zea mays] 303496 Seq. No. hvj700623780.h1 Seq. ID BLASTX Method g3004547 NCBI GI 320 BLAST score 5.0e-30 E value 83 Match length % identity (AC003673) unknown protein [Arabidopsis thaliana] NCBI Description >gi_4185150 (AC005724) unknown protein [Arabidopsis thaliana] 303497 Seq. No. hvj700623891.h1 Seq. ID BLASTX Method q1370603 NCBI GI BLAST score 477 3.0e-48E value 95 Match length % identity (X98245) annexin p35 [Zea mays] NCBI Description 303498 Seq. No.

Seq. ID hvj700623968.h1

Method BLASTN
NCBI GI g217961
BLAST score 109
E value 1.0e-54

```
185
Match length
% identity
                  90
NCBI Description Corn cystatin I mRNA, complete cds
Seq. No.
                  303499
                  hvj700624004.hl
Seq. ID
Method
                  BLASTN
                  g1235581
NCBI GI
BLAST score
                  39
                  7.0e-13
E value
Match length
                   67
                   90
% identity
NCBI Description P.sativum mRNA for elongation factor 1-alpha
                   303500
Seq. No.
Seq. ID
                   hvj700624118.h1
Method
                   BLASTN
NCBI GI
                   q313026
BLAST score
                   37
                   1.0e-11
E value
                   73
Match length
% identity
                   88
NCBI Description L.esculentum rpl38 mRNA for ribosomal protein L38
                   303501
Seq. No.
                   hvj700624129.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1430907
BLAST score
                   146
E value
                   8.0e-10
Match length
                   44
                   61
% identity
                   (Z49144) multidrug resistance-associated protein 2
NCBI Description
                   [Oryctolagus cuniculus]
                   303502
Seq. No.
Seq. ID
                   hvj700624150.hl
Method
                   BLASTX
                   g3789948
NCBI GI
BLAST score
                   157
E value
                   4.0e-11
Match length
                   32
% identity
                   94
                   (AF094773) translation initiation factor 5A [Oryza sativa]
NCBI Description
                   303503
Seq. No.
                   hvj700624312.h1
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g1546692
BLAST score 172
E value 2.0e-12
Match length 58
% identity 50

NCBI Description (X98805) peroxidase ATP19a [Arabidopsis thaliana]

Seq. No. 303504

Seq. ID hvj700624314.h1



```
BLASTX
Method
                  g1181673
NCBI GI
                  169
BLAST score
                   5.0e-21
E value
                  80
Match length
                   76
% identity
NCBI Description (U41652) heat shock protein cognate 70 [Sorghum bicolor]
                   303505
Seq. No.
                   hvj700624345.h1
Seq. ID
                   BLASTX
Method
                   g606815
NCBI GI
                   273
BLAST score
                   2.0e-24
E value
                   80
Match length
                   22
% identity
                  (U08403) carbonic anhydrase [Zea mays]
NCBI Description
                   303506
Seq. No.
                   hvj700624369.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2828297
                   141
BLAST score
                   4.0e-12
E value
                   106
Match length
                   37
% identity
                   (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   303507
Seq. No.
                   hvj700624425.h1
Seq. ID
                   BLASTN
Method
                   g2199565
NCBI GI
                   70
BLAST score
                   2.0e-31
E value
Match length
                   124
                   97
 % identity
                   Zea mays cytochrome P-450 (CYP71C1) mRNA, partial cds
NCBI Description
                   303508
 Seq. No.
 Seq. ID
                   hvj700624460.h1
                   BLASTX
Method
                   g4249391
 NCBI GI
                   158
 BLAST score
                   9.0e-11
 E value
 Match length
                   40
 % identity
                    (AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase
 NCBI Description
                    from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis
                   thaliana]
                    303509
 Seq. No.
                   hvj700624545.h1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    q100654
 BLAST score
```

42897

213 3.0e-17

E value Match length

```
% identity
                  alpha-amylase (EC 3.2.1.1) precursor (clone pOS103) - rice
NCBI Description
                  >gi 169753 (M24286) alpha-amylase (EC 3.2.1.1) [Oryza
                  303510
Seq. No.
Seq. ID
                  hvj700624582.h1
Method
                  BLASTN
NCBI GI
                  g3327233
BLAST score
                  62
E value
                  2.0e-26
Match length
                  62
% identity
                  100
NCBI Description Homo sapiens mRNA for KIAA0710 protein, complete cds
                  303511
Seq. No.
Seq. ID
                  hvj700624667.h1
Method
                  BLASTX
NCBI GI
                  g1173237
BLAST score
                  154
                  2.0e-10
E value
Match length
                  32
                  100
% identity
                  40S RIBOSOMAL PROTEIN S28 >gi 629860 pir S49035 ribosomal
NCBI Description
                  protein S28 - maize >gi 557682 emb CAA57636 (X82124) small
                  subunit ribosomal protein S28 [Zea mays]
Seq. No.
                  303512
Seq. ID
                  jfc700968540.h1
                  BLASTX
Method
NCBI GI
                  q3786005
BLAST score
                  148
                  6.0e-10
E value
Match length
                  37
% identity
                  78
NCBI Description
                  (AC005499) putative phosphoethanolamine
                  cytidylyltransferase [Arabidopsis thaliana]
                  303513
Seq. No.
                  jfc700968649.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1177368
BLAST score
                  92
E value
                  2.0e-44
Match length
                  92
% identity
                  100
NCBI Description Z.mays mRNA for ribosomal protein L39
                  303514
Seq. No.
Seq. ID
                  kem700610701.h1
                  BLASTN
Method
```

NCBI GI g22155
BLAST score 154
E value 2.0e-81
Match length 210
% identity 95

NCBI Description Z.mays mRNA for alpha-tubulin



96

% identity

NCBI Description

```
303515
Seq. No.
Seq. ID
                   kem700610759.h1
                   BLASTX
Method
                   g122022
NCBI GI
BLAST score
                   173
                   2.0e-14
E value
                   71
Match length
% identity
                   HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat
NCBI Description
                   >gi_21801_emb_C\overline{A}A42530_ (X\overline{59}873) histone H2B [Triticum
                   aestivum]
                   303516
Seq. No.
                   kem700610814.hl
Seq. ID
                   BLASTX
Method
                   g480602
NCBI GI
                   178
BLAST score
                   2.0e-13
E value
                   48
Match length
                   71
% identity
                   polyadenylate-binding protein - fern (Anemia phyllitidis)
NCBI Description
                   >gi 398327 emb CAA81127_ (Z26042) poly(A)-mRNA binding
                   protein [Anemia phyllitidis]
                   303517
Seq. No.
                   kem700610838.h1
Seq. ID
                   BLASTN
Method
                   g2832242
NCBI GI
                   45
BLAST score
                   3.0e-16
E value
                   100
Match length
                   87
% identity
                   Zea mays 22-kDa alpha zein gene cluster, complete sequence
NCBI Description
                    303518
Seq. No.
                    kem700610956.h1
Seq. ID
                    BLASTX
Method
                    g3319356
NCBI GI
                    200
BLAST score
                    6.0e-16
E value
                    81
Match length
                    49
 % identity
                    (AF077407) contains similarity glycosyl hydrolases
NCBI Description
                    [Arabidopsis thaliana]
                    303519
 Seq. No.
                    kem700611032.h1
 Seq. ID
                    BLASTN
Method
NCBI GI
                    q4416300
                    223
BLAST score
                    1.0e-122
 E value
                    267
 Match length
```

42899

region, complete sequence

Zea mays chromosome 4 22 kDa zein-associated intercluster

Method

NCBI GI BLAST score BLASTX q3550982

234

```
303520
Seq. No.
                   kem700611082.h1
Seq. ID
                   BLASTX
Method
                   g4097880
NCBI GI
                   440
BLAST score
                   5.0e-44
E value
Match length
                   89
                   94
% identity
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
                   303521
Seq. No.
                   kem700611113.h1
Seq. ID
                   {\tt BLASTX}
Method
                   g3980417
NCBI GI
                   171
BLAST score
                   1.0e-12
E value
                   39
Match length
                   85
% identity
                   (AC004561) pumilio-like protein [Arabidopsis thaliana]
NCBI Description
                   303522
Seq. No.
                   kem700611165.h1
Seq. ID
                   BLASTX
Method
                   g4539660
NCBI GI
                   257
BLAST score
                   1.0e-22
E value
                   88
Match length
                   56
% identity
                   (AF061282) polyprotein [Sorghum bicolor]
NCBI Description
                   303523
Seq. No.
                   kem700611167.h1
Seq. ID
                   BLASTX
Method
                   g2494151
NCBI GI
                   146
BLAST score
                    4.0e-12
E value
                    72
Match length
                    49
 % identity
                   DNAJ PROTEIN >gi_2119734_pir__JC4739 chaperonin dnaJ -
NCBI Description
                    Bacillus stearothermophilus >gi_1568475_emb_CAA62240_
                    (X90709) dnaJ [Bacillus stearothermophilus]
                    303524
 Seq. No.
 Seq. ID
                    kem700611222.hl
                    BLASTN
 Method
                    g22484
 NCBI GI
                    45
 BLAST score
                    2.0e-16
 E value
 Match length
                    88
                    90
 % identity
                    Z.mays RNA for superoxide dismutase Sod4A
 NCBI Description
                    303525
 Seq. No.
 Seq. ID
                    kem700611291.h1
```



```
6.0e-20
E value
Match length
                  54
% identity
                  81
                  (AB010690) mutM homologue-1 [Arabidopsis thaliana]
NCBI Description
                  303526
Seq. No.
Seq. ID
                  kem700611386.h1
Method
                  BLASTX
NCBI GI
                  q4138583
BLAST score
                  228
E value
                  3.0e-19
Match length
                  55
% identity
                  (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
NCBI Description
                  303527
Seq. No.
Seq. ID
                  kem700611434.h1
Method
                  BLASTX
NCBI GI
                  g2245000
BLAST score
                  139
E value
                  1.0e-08
Match length
                  40
% identity
                  75
                  (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  303528
Seq. No.
Seq. ID
                  kem700611442.h1
Method
                  BLASTX
NCBI GI
                  q4262233
BLAST score
                  192
E value
                  5.0e-15
Match length
                  86
% identity
                  57
                  (AC006200) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  303529
                  kem700611508.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539660
BLAST score
                  341
E value
                  2.0e-32
Match length
                  92
% identity
                  65
NCBI Description
                  (AF061282) polyprotein [Sorghum bicolor]
Seq. No.
                  303530
Seq. ID
                  kem700611548.h1
Method
                  BLASTX
NCBI GI
                  g3123270
BLAST score
                  170
```

Method BLASTX
NCBI GI g3123270
BLAST score 170
E value 1.0e-15
Match length 62
% identity 79

NCBI Description 40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)

>gi_2463335_emb_CAA75242_ (Y15009) ribosomal protein S4

[Oryza sativa]



```
303531
Seq. No.
                  kem700611563.hl
Seq. ID
                  BLASTX
Method
                  g1495251
NCBI GI
                  173
BLAST score
                  1.0e-12
E value
                  46
Match length
                  67
% identity
NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]
                   303532
Seq. No.
                  kem700611572.h1
Seq. ID
                  BLASTX
Method
                   g4337040
NCBI GI
                   311
BLAST score
                   7.0e-29
E value
                   61
Match length
% identity
                   (AF124159) molybdopterin synthase sulphurylase [Arabidopsis
NCBI Description
                   thaliana] >gi 4337042 gb AAD18051 (AF124160) molybdopterin
                   synthase sulphurylase [Arabidopsis thaliana]
                   303533
Seq. No.
                   kem700611679.h1
Seq. ID
                   BLASTN
Method
                   g168500
NCBI GI
                   93
BLAST score
                   4.0e-45
E value
                   168
Match length
                   89
% identity
NCBI Description Maize (Zea mays) histone H4 gene (H4C14), complete cds
                   303534
Seq. No.
                   kem700611874.h1
Seq. ID
                   BLASTX
Method
                   q3875246
NCBI GI
                   148
BLAST score
                   8.0e-10
E value
                   58
Match length
 % identity
                   (Z81490) similar to WD domain, G-beta repeats (2 domains);
 NCBI Description
                   cDNA EST EMBL: T00482 comes from this gene; cDNA EST
                   EMBL: T00923 comes from this gene; cDNA EST yk449d4.3 comes
                   from this gene; cDNA EST yk449d4.5 comes from this gene;
                   303535
 Seq. No.
                   kem700611879.h1
 Seq. ID
                   BLASTN
 Method
                   g168500
 NCBI GI
                   72
 BLAST score
                   2.0e-32
 E value
                   168
 Match length
                   87
 % identity
                   Maize (Zea mays) histone H4 gene (H4C14), complete cds
 NCBI Description
```

303536

kem700611908.h1

Seq. No.

Seq. ID



BLASTX Method g3122671 NCBI GI 210 BLAST score 5.0e-17 E value 58 Match length % identity 66 HYPOTHETICAL RAE1-LIKE PROTEIN >gi_2129676_pir__S71241 NCBI Description probable export protein - Arabidopsis thaliana >gi_1297188 (U53501) Theoretical protein with similarity to Swiss-Prot Accession Number P41838 poly A+ RNA export protein [Arabidopsis thaliana] 303537 Seq. No. Seq. ID kem700611910.hl BLASTN Method q1167857 NCBI GI BLAST score 33 3.0e-09 E value 77 Match length 86 % identity NCBI Description S.cereale cv. Petkus "Halo" encoding cpn60 303538 Seq. No. Seq. ID kem700611937.h1 BLASTN Method g3885883 NCBI GI 34 BLAST score 9.0e-10 E value 46 Match length 93 % identity Oryza sativa 60S ribosomal protein L21 (RPL21) mRNA, NCBI Description complete cds 303539 Seq. No. kem700611939.hl Seq. ID BLASTX Method NCBI GI g4589961 BLAST score 329 5.0e-31 E value 88 Match length % identity (AC007169) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 303540 kem700611972.h1 Seq. ID BLASTX Method g1297350 NCBI GI BLAST score 173 1.0e-12 E value 83 Match length % identity (U53668) unknown [Saccharomyces cerevisiae] NCBI Description

Seq. No. 303541

Seq. ID kem700612001.h1

Method BLASTX NCBI GI g3402673



```
317
BLAST score
                   1.0e-29
E value
                   90
Match length
% identity
                   68
                  (AC004697) unknown protein [Arabidopsis thaliana]
NCBI Description
                   303542
Seq. No.
```

Seq. ID kem700612012.h1

Method BLASTX NCBI GI g730166 297 BLAST score 3.0e-27 E value 86 Match length % identity 65

NUCLEOLAR PROTEIN NOP2 >gi 1078161 pir A55188 nucleolar NCBI Description

protein NOP2 - yeast (Saccharomyces cerevisiae)

>gi 576442 emb_CAA57979_ (X82656) Nop2p [Saccharomyces cerevisiae] >gi 1098483 (U12141) Yn12428p [Saccharomyces cerevisiae] >gi_1301934_emb_CAA95934_ (Z71337) ORF YNL061w [Saccharomyces cerevisiae] >gi_1093321_prf__2103264A

nuclear protein [Saccharomyces cerevisiae]

Seq. No. 303543

kem700612046.h1 Seq. ID

BLASTN Method q1617472 NCBI GI BLAST score 101 8.0e-50 E value Match length 189 % identity 88

Z.diploperennis DNA for Grandel-6 retrotransposon NCBI Description

Seq. No.

303544 kem700612065.h1 Seq. ID

Method BLASTX g3893081 NCBI GI BLAST score 338 E value 5.0e-32 Match length 89 % identity 64

(AJ012747) MLH1 protein [Arabidopsis thaliana] NCBI Description

Seq. No. 303545

Seq. ID kem700612074.h1

Method BLASTX g4091117 NCBI GI BLAST score 226 4.0e-19 E value Match length 84 56 % identity

(AF047428) nucleic acid binding protein [Oryza sativa] NCBI Description

303546 Seq. No.

kem700612104.h1 Seq. ID

Method BLASTN NCBI GI g1244652 BLAST score 53

```
4.0e-21
E value
                  242
Match length
                  85
% identity
                  Zea mays copia-type retroelement PREM-2 gag gene, complete
NCBI Description
                  cds
                  303547
Seq. No.
                  kem700612118.hl
Seq. ID
                  BLASTX
Method
                  g4512613
NCBI GI
                  203
BLAST score
                   3.0e-16
E value
                  60
Match length
                   68
% identity
                  (AC004793) F28K20.12 [Arabidopsis thaliana]
NCBI Description
                   303548
Seq. No.
                   kem700612126.h1
Seq. ID
Method
                   BLASTN
                   q343223
NCBI GI
                   44
BLAST score
E value
                   1.0e-15
Match length
                   44
                   100
% identity
                   Oryza sativa mitochondrial nad3 gene and rps12 gene,
NCBI Description
                   complete cds
                   303549
Seq. No.
                   kem700612141.h1
Seq. ID
                   BLASTX
Method
                   g1652164
NCBI GI
                   221
BLAST score
                   2.0e-18
E value
                   73
Match length
% identity
                   (D90903) hypothetical protein [Synechocystis sp.]
NCBI Description
                   303550
Seq. No.
                   kem700612163.h1
 Seq. ID
                   BLASTX
Method
                   g3335347
NCBI GI
                   417
 BLAST score
                   3.0e-41
 E value
 Match length
                   90
 % identity
                    (AC004512) Contains similarity to ARI, RING finger protein
 NCBI Description
                   gb_X98309 from Drosophila melanogaster. ESTs gb_T44383,
                   gb W43120, gb N65868, gb H36013, gb AA042241, gb T76869 and
                   gb_AA042359 come from this gene. [Arabidopsis thaliana]
                    303551
 Seq. No.
 Seq. ID
                    kem700612172.hl
                    BLASTX
 Method
 NCBI GI
                    q3287691
 BLAST score
                    225
```

8.0e-19

77

E value

Match length



% identity (AC003979) Contains similarity to RING zinc finger protein NCBI Description gb_X95455 from Gallus gallus. [Arabidopsis thaliana] 303552 Seq. No. kem700612186.h1 Seq. ID BLASTX Method q4587519 NCBI GI 139 BLAST score 1.0e-08 E value 36 Match length % identity (AC007060) Strong similarity to F19I3.7 gi_3033380 putative NCBI Description coatomer epsilon subunit from Arabidopsis thaliana BAC gb AC004238. ESTs gb Z17908, gb AA728673, gb N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g 303553 Seq. No. kem700612202.h1 Seq. ID BLASTX Method g2339980 NCBI GI 193 BLAST score 5.0e-15 E value 66 Match length % identity NCBI Description (Y11337) RGA2 protein [Arabidopsis thaliana] 303554 Seq. No. kem700612270.h1 Seq. ID BLASTX Method q4557060 NCBI GI BLAST score 307 2.0e-28 E value Match length 84 70 % identity (AC007154) putative chromosome-associated polypeptide, 5' NCBI Description partial [Arabidopsis thaliana] 303555 Seq. No. Seq. ID kem700612291.h1 BLASTX Method NCBI GI q2326343 BLAST score 267 E value 8.0e-24 74 Match length

69 % identity

(Y11187) G14587-5 [Arabidopsis thaliana] NCBI Description

>gi 2326350 emb_CAA72042_ (Y11155) hypothetical protein

[Arabidopsis thaliana]

303556 Seq. No.

kyv700142482.h1 Seq. ID

BLASTX Method NCBI GI g4115377 BLAST score 271 2.0e-24 E value Match length 77

% identity NCBI Description (AC005967) unknown protein [Arabidopsis thaliana] 303557 Seq. No. Seq. ID kyv700142483.h1 BLASTX Method NCBI GI q1170092 280 BLAST score 2.0e-25 E value 72 Match length % identity GLUTATHIONE S-TRANSFERASE IV (GST-IV) (GST-27) (CLASS PHI) NCBI Description >gi 1076807 pir S52037 glutathione transferase (EC 2.5.1.18) 27K chain - maize >gi_529015 (U12679) glutathione S-transferase IV [Zea mays] >gi 695789_emb_CAA56047_ (X79515) glutathione transferase [Zea mays] >gi_1094866_prf__2106424A glutathione S-transferase: ISOTYPE=IV [Zea mays] Seq. No. 303558 kyv700142485.h1 Seq. ID BLASTX Method g2190007 NCBI GI 165 BLAST score 6.0e-12 E value 76 Match length % identity 41 (AB004109) phosphatidylserine synthase II [Cricetulus NCBI Description griseus] 303559 kyv700142501.h1 Seq. ID BLASTN q22251 110

Seq. No.

Method NCBI GI BLAST score 3.0e-55 E value 126 Match length % identity 97

Z.mays mRNA that delineates a novel subset of cortical NCBI Description cells

303560 Seq. No. Seq. ID kyv700142532.hl

Method BLASTX q4490751 NCBI GI BLAST score 165 7.0e-12 E value 78 Match length % identity 47

(AL035708) proliferating-cell nucleolar antigen-like NCBI Description

protein [Arabidopsis thaliana]

Seq. No. 303561

kyv700142572.h1 Seq. ID

BLASTX Method q485518 NCBI GI BLAST score 377



```
6.0e-37
E value
                  76
Match length
                  100
% identity
                  ubiquitin / ribosomal protein CEP52 - rice
NCBI Description
                  >qi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal
                  polyprotein [Oryza sativa]
                  303562
Seq. No.
                  lhp700053328.rl
Seq. ID
Method
                  BLASTN
                  q22294
NCBI GI
                  63
BLAST score
                  2.0e-27
E value
Match length
                  102
                  100
% identity
                  Maize Gpal gene for glyceraldehyde-3-phosphate
NCBI Description
                  dehydrogenase subunit A >gi 168478 gb M18976 MZEG3PD Zea
                  mays chloroplast glyceraldehyde-3-phosphate dehydrogenase
                  gene, complete cds, clone lambda-gapA1
                   303563
Seq. No.
                   lhp700053337.r1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3914465
BLAST score
                   163
                   2.0e-25
E value
Match length
                   66
                   98
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                   >gi 2981207 (AF052076) photosystem I complex PsaH subunit
                   precursor [Zea mays]
Seq. No.
                   303564
                   lhp700053339.rl
Seq. ID
                   BLASTX
Method
                   q4490304
NCBI GI
                   341
BLAST score
                   2.0e-32
E value
                   85
Match length
% identity
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   303565
Seq. No.
Seq. ID
                   lhp700053345.rl
                   BLASTN
Method
                   q168470
NCBI GI
                   239
BLAST score
                   1.0e-132
E value
                   278
Match length
                   97
 % identity
                   Maize ferredoxin I (Fd) isoprotein mRNA, pFD1'
NCBI Description
```

Seq. No. 303566

Seq. ID lhp700053364.rl

Method BLASTX
NCBI GI q2129552

Match length

% identity

86

53



```
BLAST score
E value
                  9.0e-34
                  94
Match length
                  69
% identity
NCBI Description
                  calcium-dependent protein kinase 19 - Arabidopsis thaliana
                  (fragment)
                  303567
Seq. No.
Seq. ID
                  lhp700053427.r1
Method
                  BLASTX
NCBI GI
                  q479356
                  295
BLAST score
                  5.0e-27
E value
Match length
                  88
% identity
                  71
NCBI Description protein kinase PK1 (EC 2.7.1.-), receptor-like - maize
                  303568
Seq. No.
                  lhp700053432.rl
Seq. ID
Method
                  BLASTX
                  q1899025
NCBI GI
BLAST score
                  229
E value
                  3.0e-19
                  73
Match length
% identity
                  60
                  (U28215) hexokinase 2 [Arabidopsis thaliana] >gi 3687232
NCBI Description
                  (AC005169) hexokinase [Arabidopsis thaliana]
Seq. No.
                  303569
Seq. ID
                  lhp700053452.rl
Method
                  BLASTX
NCBI GI
                  q3789952
BLAST score
                  142
E value
                  3.0e-11
Match length
                  58
% identity
                  74
NCBI Description
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
Seq. No.
                  303570
                  ltv700479522.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4218126
BLAST score
                  179
                  2.0e-13
E value
Match length
                  94
% identity
                  40
                  (AL035353) putative protein [Arabidopsis thaliana]
NCBI Description
                  303571
Seq. No.
                  ltv700479543.h1
Seq. ID
Method
                  BLASTX
                  g419803
NCBI GI
BLAST score
                  236
E value
                  5.0e-20
```



NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea. mays]

Seq. No. 303572

Seq. ID 1tv700479650.h1
Method BLASTX
NCBI GI g1710077
BLAST score 392
E value 2.0e-38
Match length 79
% identity 90

NCBI Description PEROXIREDOXIN (REHYDRIN HOMOLOG) (B15C)

>gi 2130029 pir S60285 B15C protein - barley

>gi 471321 emb CAA54066 (X76605) HvB15C [Hordeum vulgare] >gi 1694833 emb CAA65387 (X96551) peroxiredoxin [Hordeum

vulgare]

Seq. No. 303573

Seq. ID ltv700479659.h1

Method BLASTX
NCBI GI g515377
BLAST score 244
E value 5.0e-21
Match length 50
% identity 100

NCBI Description (X79715) histone H4 [Lolium temulentum]

Seq. No. 303574

Seq. ID ltv700479671.h1

Method BLASTN
NCBI GI g687244
BLAST score 253
E value 1.0e-140
Match length 264

% identity 99

NCBI Description Zea mays oil body protein 16 kDa oleosin (ole16) gene,

complete cds

Seq. No. 303575

Seq. ID mwy700438105.h1

Method BLASTX
NCBI GI g2911067
BLAST score 387
E value 8.0e-38
Match length 86
% identity 86

NCBI Description (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis

thaliana]

Seq. No. 303576

Seq. ID mwy700438134.h1

Method BLASTX
NCBI GI g82080
BLAST score 223
E value 1.0e-18
Match length 68
% identity 66



```
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  303577
Seq. No.
                  mwy700438151.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2668742
                  285
BLAST score
                  7.0e-26
E value
                   61
Match length
                   92
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   303578
Seq. No.
                  mwy700438161.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g218227
BLAST score
                   34
                   9.0e-10
E value
                   54
Match length
                   91
% identity
                   Rice mRNA for ras-related GTP binding protein, complete cds
NCBI Description
                   303579
Seq. No.
                   mwy700438163.hl
Seq. ID
                   BLASTN
Method
                   g397395
NCBI GI
                   130
BLAST score
                   5.0e-67
E value
                   130
Match length
                   100
% identity
                   Z.mays MNBlb mRNA for DNA-binding protein
NCBI Description
                   303580
Seq. No.
Seq. ID
                   mwy700438271.h1
                   BLASTN
Method
NCBI GI
                   g1244652
BLAST score
                   46
                   4.0e-17
E value
                   46
Match length
                   50
% identity
                   Zea mays copia-type retroelement PREM-2 gag gene, complete
NCBI Description
                   303581
Seq. No.
                   mwy700438282.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1498381
BLAST score
                   86
                   5.0e-41
E value
                   153
Match length
                   93
% identity
                   Zea mays actin (Maz95) gene, partial cds
NCBI Description
```

42911

303582

mwy700438314.hl

Seq. No.

Seq. ID

```
BLASTN
Method
                  g3264604
NCBI GI
                  87
BLAST score
                  2.0e-41
E value
                  134
Match length
                  91
% identity
NCBI Description Zea mays ribosomal protein L25 mRNA, partial cds
                  303583
Seq. No.
                  mwy700438361.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3328450
                  141
BLAST score
                  7.0e-12
E value
                  53
Match length
% identity
NCBI Description (AE001280) hypothetical protein [Chlamydia trachomatis]
                   303584
Seq. No.
                  mwy700438435.h1
Seq. ID
                  BLASTX
Method
                  q1710807
NCBI GI
                  250
BLAST score
                   8.0e-22
E value
                   83
Match length
                   65
% identity
                  RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60
NCBI Description
                   KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_1185390
                   (U21105) alphacpn60 [Pisum sativum]
                   303585
Seq. No.
                   mwy700438448.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3152568
                   164
BLAST score
                   9.0e-12
E value
                   82
Match length
% identity
                   45
                   (AC002986) Similar to hypothetical protein product
NCBI Description
                   gb Z97337 from A. thaliana. EST gb_H76597 comes from this
                   gene. [Arabidopsis thaliana]
                   303586
Seq. No.
Seq. ID
                   mwy700438534.h1
                   BLASTX
Method
NCBI GI
                   q1084481
BLAST score
                   365
                   3.0e-35
E value
Match length
                   73
                   97
% identity
NCBI Description heat shock protein 70 - Maize
Seq. No.
                   303587
                   mwy700438548.h1
Seq. ID
```

42912

BLASTX

270

q546088

Method

NCBI GI

BLAST score

```
2.0e-24
E value
Match length
                  57
% identity
                   (S69272) cytoplasmic antiproteinase, CAP=38 kda
NCBI Description
                  intracellular serine proteinase inhibitor [human, placenta,
                  Peptide, 376 aa] [Homo sapiens]
                  303588
Seq. No.
Seq. ID
                  mwy700438825.hl
                  BLASTX
Method
NCBI GI
                  q1084481
                   382
BLAST score
E value
                   3.0e-37
                  73
Match length
                   100
% identity
NCBI Description
                  heat shock protein 70 - Maize
                   303589
Seq. No.
Seq. ID
                   mwy700438872.h1
                   BLASTX
Method
                   q3201627
NCBI GI
BLAST score
                   203
                   3.0e-16
E value
                   43
Match length
% identity
                   (AC004669) putative SWH1 protein [Arabidopsis thaliana]
NCBI Description
                   303590
Seq. No.
                   mwy700438877.h1
Seq. ID
Method
                   BLASTX
                   q3047085
NCBI GI
BLAST score
                   150
E value
                   3.0e-17
                   79
Match length
% identity
                   (AF058914) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303591
                   mwy700438896.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4314390
BLAST score
                   172
E value
                   1.0e-12
                   87
Match length
% identity
                   45
                   (AC006232) putative calcium binding protein [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 303592

Seq. ID mwy700438932.h1

Method BLASTN
NCBI GI g4507310
BLAST score 57
E value 7.0e-24
Match length 73
% identity 95

NCBI Description Homo sapiens suppressor of Ty (S.cerevisiae) 4 homolog 1



(SUPT4H1) mRNA >gi_1297309_gb_U43923_HSU43923 Human transcription factor SUPT4H mRNA, complete cds

303593 Seq. No. Seq. ID mwy700438986.h1 Method BLASTX g3128199 NCBI GI 165 BLAST score 5.0e-12 E value 42 Match length % identity (AC004521) putative proteinase [Arabidopsis thaliana] NCBI Description 303594 Seq. No. mwy700439012.hl Seq. ID BLASTX Method NCBI GI g4006893 202 BLAST score 2.0e-17 E value 75 Match length % identity (Z99708) aminopeptidase-like protein [Arabidopsis thaliana] NCBI Description 303595 Seq. No. mwy700439035.h1 Seq. ID BLASTN Method g178522 NCBI GI BLAST score 191 1.0e-103 E value 258 Match length 95 % identity Human S-adenosylmethionine decarboxylase (AMD1) gene, exons NCBI Description 303596 Seq. No. mwy700439053.h1 Seq. ID BLASTX Method g2088658 NCBI GI BLAST score 292 1.0e-26 E value 76 Match length % identity (AF002109) unknown protein [Arabidopsis thaliana] NCBI Description 303597 Seq. No. Seq. ID mwy700439054.h1 BLASTX Method NCBI GI g1362008 BLAST score 393 1.0e-38 E value

% identity
NCBI Description

Match length

Seq. No. 303598

Seq. ID mwy700439116.h1

86 20

Method BLASTN

42914

ubiquitin-like protein 12 - Arabidopsis thaliana



```
q3882170
NCBI GI
                  149
BLAST score
                  1.0e-78
E value
                  157
Match length
                  99
% identity
NCBI Description Homo sapiens mRNA for KIAA0725 protein, partial cds
                  303599
Seq. No.
Seq. ID
                  mwy700439118.h1
                  BLASTX
Method
NCBI GI
                  q4558549
                  233
BLAST score
                  8.0e-31
E value
                  87
Match length
% identity
                   (AC007138) putative SecA-type chloroplast protein transport
NCBI Description
                  factor [Arabidopsis thaliana]
                   303600
Seq. No.
                  mwy700439136.h1
Seq. ID
                  BLASTX
Method
                   q2494892
NCBI GI
BLAST score
                   383
                   2.0e-37
E value
                   86
Match length
                   87
% identity
                   HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA
NCBI Description
                   BINDING PROTEIN P46) (RETINOBLASTOMA-BINDING PROTEIN 7)
                   >gi 2137733 pir I49367 retinoblastoma-binding protein
                   mRbAp46 - mouse >gi 1016277 (U35142) retinoblastoma-binding
                   protein mRbAp46 [Mus musculus] >gi_1585657_prf__2201425B
                   retinoblastoma-binding protein [Mus musculus]
                   303601
Seq. No.
                   mwy700439146.h1
Seq. ID
                   BLASTN
Method
                   q4038570
NCBI GI
BLAST score
                   49
                   3.0e-19
E value
                   73
Match length
                   92
% identity
                   Human DNA sequence from clone 51J12 on chromosome 6q26-27.
NCBI Description
                   Contains the 3' part of the alternatively spliced gene for
                   the human orthologs of mouse QKI-7 and QKI-7B (KH Domain
                   RNA Binding proteins) and zebrafish ZKQ-1 (Qu
                   303602
 Seq. No.
```

 Seq. No.
 303602

 Seq. ID
 mwy700439155.h1

 Method
 BLASTX

 NCBI GI
 g2833282

 BLAST score
 268

 E value
 1.0e-33

Match length 85 % identity 90

NCBI Description DEOXYGUANOSINE KINASE PRECURSOR (DGUOK) >gi_1477482

(U41668) deoxyguanosine kinase [Homo sapiens]



```
303603
Seq. No.
                  mwy700439213.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1869775
BLAST score
                  129
E value
                  2.0e-66
                  161
Match length
                  95
% identity
                  Human DNA sequence from cosmid 313D11 from a contig on the
NCBI Description
                  short arm of chromosome 16. Contains ESTs, STS and CpG
                  islands
                  303604
Seq. No.
Seq. ID
                  mwy700439254.h1
Method
                  BLASTN
NCBI GI
                  g2981206
BLAST score
                  220
E value
                  1.0e-121
                  235
Match length
                  99
% identity
                  Zea mays photosystem I complex PsaH subunit precursor
NCBI Description
                   (psaH) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  303605
Seq. No.
                  mwy700439262.h1
Seq. ID
Method
                  BLASTN
                  g4504160
NCBI GI
BLAST score
                   196
E value
                   1.0e-106
                   267
Match length
                   94
% identity
                   Homo sapiens G-rich RNA sequence binding factor 1 (GRSF1)
NCBI Description
                  mRNA >gi 517195_gb_U07231_HSU07231 Homo sapiens G-rich
                   sequence factor-1 (GRSF-1) mRNA, complete cds
Seq. No.
                   303606
                   mwy700439289.h1
Seq. ID
Method
                   BLASTN
                   g4500264
NCBI GI
BLAST score
                   240
                   1.0e-132
E value
Match length
                   268
                   98
% identity
                   Homo sapiens mRNA; cDNA DKFZp586L012 (from clone
NCBI Description
                   DKFZp586L012)
Seq. No.
                   303607
                   mwy700439372.h1
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g119143
BLAST score 294
E value 2.0e-28
Match length 74
% identity 87

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1

alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_(X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_(X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_(X16431) elongation factor 1-alpha [Arabidopsis thaliana]

>gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]

Seq. No. 303608 Seq. ID mwy700439379.h1

Method BLASTX
NCBI GI g2924776
BLAST score 349
E value 2.0e-33
Match length 86
% identity 77

NCBI Description (AC002334) hypothetical protein [Arabidopsis thaliana]

Seq. No. 303609

Seq. ID mwy700439449.h1 Method BLASTN

NCBI GI g1491773
BLAST score 75
E value 2.0e-34
Match length 181
% identity 91

NCBI Description Z.mays mRNA for cysteine proteinase, Seel

Seq. No. 303610

Seq. ID mwy700439569.h1

Method BLASTX
NCBI GI g4006921
BLAST score 380
E value 6.0e-37
Match length 89
% identity 79

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 303611

Seq. ID mwy700439643.h1

Method BLASTX
NCBI GI g66009
BLAST score 314
E value 3.0e-29
Match length 69
% identity 90

NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,

cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH

(AA 1-337) [Zea mays]

Seq. No. 303612

Seq. ID mwy700439729.h1

Method BLASTN
NCBI GI g4508152
BLAST score 120
E value 2.0e-61



120 Match length 100 % identity

NCBI Description Homo sapiens clone DJ0568B10, complete sequence

303613 Seq. No.

mwy700439733.h1 Seq. ID

BLASTN Method q496977 NCBI GI 94 BLAST score 5.0e-46 E value 98 Match length 99 % identity

Human a6(IV) collagen (COL4A6) mRNA, complete cds NCBI Description

Seq. No. 303614

mwy700439791.h1 Seq. ID

Method BLASTX g4504023 NCBI GI BLAST score 363 5.0e-35 E value Match length 83 86 % identity

glycine receptor, beta >gi_1346173_sp_P48167_GRB_HUMAN NCBI Description

GLYCINE RECEPTOR BETA CHAIN PRECURSOR >gi_992687 (U33267) glycine receptor beta subunit [Homo sapiens] >gi_3834635 (AF094754) glycine receptor beta subunit precursor [Homo sapiens] >gi_3834637 (AF094755) glycine receptor beta subunit precursor [Homo sapiens] >gi_1589657_prf__2211391A

Gly receptor: SUBUNIT=beta [Homo sapiens]

303615 Seq. No.

mwy700439833.h1 Seq. ID

BLASTX Method g2833482 NCBI GI 296 BLAST score 2.0e-27 E value Match length 67 84 % identity

HYPOTHETICAL PROTEIN HI0895 >gi_1073812_pir__H64100 NCBI Description

acriflavine resistance protein (acrB) homolog - Haemophilus

influenzae (strain Rd KW20) >gi_1573914 (U32771) acriflavine resistance protein (acrB) [Haemophilus

influenzae Rd]

303616 Seq. No.

mwy700439836.h1 Seq. ID

BLASTX Method g825671 NCBI GI 322 BLAST score 3.0e-30 E value 86 Match length % identity 77

(X16934) B23 nucleophosmin (280 AA) [Homo sapiens] NCBI Description

303617 Seq. No.

mwy700439837.h1 Seq. ID

BLASTX Method

```
NCBI GI
                  g3929772
                  139
BLAST score
                   6.0e-09
E value
                  29
Match length
                  97
% identity
                  (AJ009853) elongation factor-1 alpha [Isotoma klovstadi]
NCBI Description
Seq. No.
                  303618
                  mwy700439871.h1
Seq. ID
                  BLASTX
Method
                   g3702327
NCBI GI
BLAST score
                   185
                   4.0e-14
E value
                   52
Match length
% identity
                   58
                   (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                   303619
Seq. No.
                   mwy700439905.h1
Seq. ID
                   BLASTN
Method
                   g4506732
NCBI GI
BLAST score
                   154
                   2.0e-81
E value
                   217
Match length
                   94
% identity
                   Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide
NCBI Description
                   1 (RPS6KA1) mRNA >gi 292456 gb L07597 HUMS6KINA Homo
                   sapiens ribosomal protein S6 kinase 1 (RPS6KA1) mRNA,
                   complete cds
                   303620
Seq. No.
                   mwy700440009.h1
Seq. ID
                   BLASTX
Method
                   g3775997
NCBI GI
BLAST score
                   180
                   2.0e-13
E value
                   75
Match length
                   48
% identity
                  (AJ010462) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   303621
Seq. No.
                   mwy700440030.h1
Seq. ID
                   BLASTX
Method
                   g585328
NCBI GI
                   303
BLAST score
                   6.0e-28
E value
                   58
Match length
                   90
% identity
                   INTESTINAL TREFOIL FACTOR PRECURSOR (HP1.B)
NCBI Description
                   >gi_539652_pir__A48284 intestinal trefoil factor 3
                   precursor - human >gi_402483 (L15203) secretory protein
                   [Homo sapiens] >gi_940946 (U25657) intestinal trefoil
                   factor [Homo sapiens]
```

Seq. No. 303622

Seq. ID mwy700440044.h1

Method BLASTX

E value

Match length

NCBI Description

% identity

4.0e-11

59 51



```
NCBI GI
                  g125088
BLAST score
                  210
                  4.0e-17
E value
                  84
Match length
                  43
% identity
                  KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK
NCBI Description
                  19) >gi_90421_pir__JQ0028 cytokeratin 19 - mouse >gi_387393
                   (M36120) keratin 19 [Mus musculus] >gi_623168 (M28698)
                  cytokeratin [Mus musculus]
                  303623
Seq. No.
                  mwy700440048.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3913437
BLAST score
                  266
                  1.0e-23
E value
                  86
Match length
                   65
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                   HELICASE >gi 1402875 emb CAA66825 (X98130) RNA helicase
                   [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)
                   RNA helicase [Arabidopsis thaliana]
                   303624
Seq. No.
                  mwy700440092.h1
Seq. ID
Method
                  BLASTX
                   g1707015
NCBI GI
BLAST score
                   302
                   7.0e-28
E value
                   85
Match length
                   67
% identity
                   (U78721) protein phosphatase 2C isolog [Arabidopsis
NCBI Description
                   thaliana]
                   303625
Seq. No.
                   mwy700440291.h1
Seq. ID
                   BLASTX
Method
                   g4507731
NCBI GI
                   205
BLAST score
                   1.0e-16
E value
                   44
Match length
                   93
% identity
                   tubulin, gamma polypeptide >gi_135505_sp_P23258_TBG_HUMAN
NCBI Description
                   TUBULIN GAMMA CHAIN >gi 71594 pir UBHUG tubulin gamma
                   chain - human >gi 183703 (M61764) gamma-tubulin [Homo
                   sapiens]
                   303626
Seq. No.
                   mwy700440322.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4587589
BLAST score
                   157
```

(AC007232) hypothetical protein [Arabidopsis thaliana]



```
303627
Seq. No.
                  mwy700440417.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4049345
BLAST score
                  212
E value
                   3.0e-17
Match length
                   93
% identity
                   43
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303628
                  mwy700440439.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3327049
BLAST score
                   155
E value
                   4.0e-82
Match length
                   183
% identity
                   96
NCBI Description Homo sapiens mRNA for KIAA0618 protein, complete cds
                   303629
Seq. No.
Seq. ID
                   mwy700440453.h1
Method
                   BLASTN
NCBI GI
                   g4210725
BLAST score
                   94
                   8.0e-46
E value
Match length
                   145
                   92
% identity
                   Homo sapiens mRNA for puromycin sensitive aminopeptidase,
NCBI Description
                   partial
Seq. No.
                   303630
                   mwy700440490.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3850561
BLAST score
                   167
E value
                   3.0e-89
                   219
Match length
                   94
% identity
                   Homo sapiens chromosome 19, cosmid F23613, complete
NCBI Description
                   sequence [Homo sapiens]
                   303631
Seq. No.
                   mwy700440508.h1
Seq. ID
                   BLASTX
Method
                   g2780196
NCBI GI
BLAST score
                   398
                   4.0e-39
E value
                   88
Match length
                   91
% identity
                   (AJ223083) retinoic acid X receptor gamma-1 [Rattus
NCBI Description
                   norvegicus]
                   303632
Seq. No.
```

Seq. ID

mwy700440518.hl

Method BLASTN NCBI GI g1255992



```
235
BLAST score
                   1.0e-129
E value
                   267
Match length
                   97
% identity
                  Human dystrobrevin-gamma mRNA, complete cds
NCBI Description
                   303633
Seq. No.
Seq. ID
                   mwy700440525.h1
Method
                   BLASTN
NCBI GI
                   g2463543
BLAST score
                   208
                   1.0e-113
E value
                   259
Match length
% identity
                   96
                   Homo sapiens mRNA for CAB1, complete cds
NCBI Description
Seq. No.
                   303634
Seq. ID
                   mwy700440549.h1
                   BLASTN
Method
                   q1710211
NCBI GI
                   189
BLAST score
E value
                   1.0e-102
                   240
Match length
                   95
% identity
NCBI Description Human clone 23732 mRNA, partial cds
                   303635
Seq. No.
                   mwy700440682.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3355474
BLAST score
                   208
                   7.0e-17
E value
Match length
                   62
                   58
% identity
                   (AC004218) unknown protein [Arabidopsis thaliana]
NCBI Description
                   303636
Seq. No.
                   mwy700440705.h1
Seq. ID
                   BLASTX
Method
                   g733456
NCBI GI
                   195
BLAST score
                   3.0e-15
E value
Match length
                   55
                   80
 % identity
                   (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                   303637
 Seq. No.
                   mwy700440751.h1
 Seq. ID
                   BLASTX
 Method
                   g1706453
 NCBI GI
 BLAST score
                   256
                   2.0e-22
 E value
                   81
 Match length
                   65
 % identity
                   DMR-N9 PROTEIN (PROTEIN 59) >gi_1082161_pir__A49364 59
 NCBI Description
```

protein, brain - human (fragment) > gi_306712 (L19267)



putative [Homo sapiens]

```
Seq. No.
                   303638
                   mwy700440792.h1
Seq. ID
Method
                   BLASTX
                   g230638
NCBI GI
BLAST score
                   154
                   1.0e-10
E value
Match length
                   33
% identity
                   94
```

NCBI Description Myoglobin Mutant With Lys 45 Replaced By Arg And Cys 110 Replaced By Ala (K45r, C110a Mutant)

 Seq. No.
 303639

 Seq. ID
 mwy700440855.h1

 Method
 BLASTN

 NCBI GI
 g2554603

 BLAST score
 125

BLAST score 125 E value 4.0e-64 Match length 191 % identity 100

NCBI Description Homo sapiens mRNA for ISLR, complete cds

Seq. No. 303640

Seq. ID mwy700440930.h1

Method BLASTX
NCBI GI g115771
BLAST score 212
E value 2.0e-17
Match length 43
% identity 95

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll

a/b-binding protein precursor - maize

>gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 303641

Seq. ID mwy700440988.h1

Method BLASTX
NCBI GI g3150410
BLAST score 231
E value 1.0e-19
Match length 76
% identity 55

NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]

Seq. No. 303642

Seq. ID mwy700441021.h1

Method BLASTX
NCBI GI g1077569
BLAST score 151
E value 4.0e-10
Match length 77
% identity 42

NCBI Description probable membrane protein YDR109c - yeast (Saccharomyces cerevisiae) >gi 747884 emb CAA88663 (Z48758) unknown

BLAST score

% identity

E value Match length 214 9.0e-18

47

89



[Saccharomyces cerevisiae]

```
303643
Seq. No.
                  mwy700441063.h1
Seq. ID
                  BLASTN
Method
                  g2981206
NCBI GI
                  173
BLAST score
                  1.0e-92
E value
Match length **
                  180
                   99
% identity
                  Zea mays photosystem I complex PsaH subunit precursor
NCBI Description
                   (psaH) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
Seq. No.
                   303644
                  mwy700441071.h1
Seq. ID
                  BLASTN
Method
                   q2981206
NCBI GI
                   175
BLAST score
                   7.0e-94
E value
                   182
Match length
                   99
% identity
                   Zea mays photosystem I complex PsaH subunit precursor
NCBI Description
                   (psaH) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                   303645
Seq. No.
                   mwy700441158.h1
Seq. ID
                   BLASTX
Method
                   g1706260
NCBI GI
                   286
BLAST score
                   5.0e-26
E value
                   73
Match length
                   77
% identity
                   CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131_pir__ S59597
NCBI Description
                   cysteine proteinase 1 precursor - maize
                   >gi 643597 dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                   mays]
                   303646
Seq. No.
                   mwy700441185.h1
Seq. ID
                   BLASTX
Method
                   g2766452
NCBI GI
                   146
BLAST score
E value
                   1.0e-09
                   82
Match length
% identity
                   40
                   (AF029858) cytochrome P450 CYP71E1 [Sorghum bicolor]
NCBI Description
                   303647
Seq. No.
Seq. ID
                   mwy700441217.h1
Method
                   BLASTX
NCBI GI
                   q166655
```

Seq. No.

Seq. ID

303653

mwy700441847.hl



```
(M73712) calmodulin-3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  303648
Seq. ID
                  mwy700441229.hl
Method
                  BLASTN
                  g1805253
NCBI GI
                  33
BLAST score
                  4.0e-09
E value
Match length
                  61
% identity
                  89
                  Cucumis sativus monogalactosyldiacylglycerol synthase mRNA,
NCBI Description
                  complete cds
                  303649
Seq. No.
Seq. ID
                  mwy700441259.h1
Method
                  BLASTX
                  g4115377
NCBI GI
BLAST score
                  224
E value
                   1.0e-18
Match length
                  83
% identity
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   303650
Seq. No.
                  mwy700441547.hl
Seq. ID
Method
                  BLASTX
                   g4584521
NCBI GI
BLAST score
                   148
E value
                   5.0e-10
Match length
                   39
                   72
% identity
                   (AL049607) putative protein [Arabidopsis thaliana]
NCBI Description
                   303651
Seq. No.
                   mwy700441579.h1
Seq. ID
Method
                   BLASTX
                   g3617837
NCBI GI
BLAST score
                   176
                   7.0e-21
E value
Match length
                   58
                   91
% identity
                   (AF035820) gibberellin action negative regulator SPY
NCBI Description
                   [Hordeum vulgare]
                   303652
Seq. No.
                   mwy700441654.hl
Seq. ID
                   BLASTX
Method
                   g247308
NCBI GI
BLAST score
                   169
E value
                   9.0e-22
Match length
                   75
% identity
                   74
                   ubiquitin [Chlamydomonas reinhardtii, CW-15, Peptide, 76
NCBI Description
```

```
BLASTX
Method
                  g3080438
NCBI GI
                  184
BLAST score
                  5.0e-14
E value
Match length
                  58
% identity
                   64
                   (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                   303654
Seq. No.
                  mwy700441926.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g585204
BLAST score
                   188
                   2.0e-14
E value
                   36
Match length
% identity
                   97
                   GLUTAMINE SYNTHETASE ROOT ISOZYME 4 (GLUTAMATE--AMMONIA
NCBI Description
                   LIGASE) (GS107) >gi_481809_pir__S39480 glutamate--ammonia
                   ligase (EC 6.3.1.2) 1-4, cytosolic - maize
                   >gi_434330_emb_CAA46722_ (X65929) glutamine synthetase [Zea
                   mays]
                   303655
Seq. No.
                   mwy700441991.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2852449
BLAST score
                   357
                   3.0e-34
E value
                   76
Match length
% identity
                   89
                   (D88207) protein kinase [Arabidopsis thaliana] >gi_2947061
NCBI Description
                   (AC002521) putative protein kinase [Arabidopsis thaliana]
                   303656
Seq. No.
                   mwy700442017.h1
Seq. ID
                   BLASTX
Method
                   q112994
NCBI GI
BLAST score
                   242
                   7.0e-21
E value
                   55
Match length
% identity
                   87
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >gi_82685_pir__S04536 embryonic abundant protein,
                   glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >gi 226091_prf__1410284A abscisic acid inducible gene [Zea
                   mays]
                   303657
Seq. No.
                   mwy700442067.hl
Seq. ID
                   BLASTN
Method
                   g4239886
NCBI GI
                   43
BLAST score
                   3.0e-15
E value
                   58
Match length
```

42926

NCBI Description Zea mays mRNA for MAP kinase 4, complete cds

95

% identity.

Method

NCBI GI

BLASTX

g168586

```
303658
Seq. No.
                  mwy700442078.hl
Seq. ID
Method
                  BLASTX
                  g2980761
NCBI GI
                  205
BLAST score
                  1.0e-16
E value
                  51
Match length
                  73
% identity
                  (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                  303659
Seq. No.
                  mwy700442119.hl
Seq. ID
                  BLASTX
Method
                  g550436
NCBI GI
                   348
BLAST score
                   3.0e-33
E value
                   71
Match length
                   94
% identity
                   (X81827) cytochrome P450 [Zea mays]
NCBI Description
                   303660
Seq. No.
                   mwy700442376.h1
Seq. ID
                   BLASTX
Method
                   g1076583
NCBI GI
BLAST score
                   271
                   3.0e-24
E value
Match length
                   53
% identity
                   100
                  histone H3 variant H3.3 - tomato (fragment)
NCBI Description
                   303661
Seq. No.
                   mwy700442405.h1
Seq. ID
                   BLASTN
Method
                   g3337311
NCBI GI
BLAST score
                   257
                   1.0e-143
E value
                   269
Match length
                   99
% identity
                   Homo sapiens chromosome 17, clone hRPK.597_M_12, complete
NCBI Description
                   sequence [Homo sapiens]
                   303662
Seq. No.
                   mwy700442462.h1
Seq. ID
                   BLASTN
Method
                   g3702356
NCBI GI
BLAST score
                   218
                   1.0e-119
E value
                   246
Match length
                   97
% identity
                   Homo sapiens chromosome 3, clone hRPK.165 I 16, complete
NCBI Description
                   sequence [Homo sapiens]
                   303663
Seq. No.
Seq. ID
                   mwy700442486.h1
```

NCBI GI

E value

BLAST score

g169818

2.0e-44

92

```
BLAST score
                  206
                                                                     ·..
E value
                  1.0e-16
Match length
                  73
                  60
% identity
                  (M58656) pyruvate, orthophosphate dikinase [Zea mays]
NCBI Description
                  303664
Seq. No.
                  mwy700442544.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4455245
BLAST score
                  175
                   6.0e-13
E value
Match length
                  75
% identity
                  41
                  (AL035523) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  303665
Seq. No.
                  mwy700442722.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1778093
BLAST score
                   205
E value
                   2.0e-16
                  80
Match length
                  51
% identity
NCBI Description
                   (U64902) putative sugar transporter; member of major
                   facilitative superfamily; integral membrane protein [Beta
                  vulgaris]
Seq. No.
                   303666
                  mwy700442854.h1
Seq. ID
Method
                  BLASTX
                   g3834314
NCBI GI
BLAST score
                   268
E value
                   6.0e-24
Match length
                   83
                   69
% identity
NCBI Description
                   (AC005679) Similar to gene pi010 glycosyltransferase
                   gi_2257490 from S. pombe clone 1750 gb_AB004534. ESTs
                   gb_T46079 and gb_AA394466 come from this gene. [Arabidopsis
                   thaliana]
                   303667
Seq. No.
                  mwy700442917.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1362008
BLAST score
                   154
E value
                   1.0e-10
Match length
                   47
% identity
NCBI Description
                  ubiquitin-like protein 12 - Arabidopsis thaliana
Seq. No.
                   303668
                  mwy700442947.hl
Seq. ID
Method
                   BLASTN
```

```
Match length
                  144
% identity
                   91
                  Rice 25S ribosomal RNA gene
NCBI Description
                  303669
Seq. No.
                  mwy700442982.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q475252
BLAST score
                  236
E value
                   1.0e-130
Match length
                   277
% identity
                   97
NCBI Description Z.mays MPI gene
Seq. No.
                   303670
Seq. ID
                  mwy700443219.h2
Method
                  BLASTX
                   g4417279
NCBI GI
BLAST score
                   240
E value
                   1.0e-20
Match Tength
                   64
% identity
                   64
                   (AC007019) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303671
Seq. ID
                   nbm700464572.h1
Method
                   BLASTX
NCBI GI
                   g1495251
BLAST score
                   186
                   2.0e-14
E value
Match length
                   49
% identity
                   69
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   303672
Seq. No.
                   nbm700464617.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076746
BLAST score
                   354
                   3.0e - 34
E value
Match length
                   69
                   99
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                   [Oryza sativa]
                   303673
Seq. No.
                   nbm700464657.h1
Seq. ID
Method
                   BLASTX
```

NCBI GI g1841864
BLAST score 161
E value 3.0e-11
Match length 52
% identity 28

NCBI Description (U87108) nucleic acid binding protein [Trypanosoma

equiperdum]

```
303674
Seq. No.
Seq. ID
                  nbm700464693.h1
Method
                  BLASTN
                  q2582382
NCBI GI
BLAST score
                  46
                  2.0e-17
E value
Match length
                  86
% identity
                  88
NCBI Description Mus musculus Dgcr6 protein (Dgcr6) mRNA, partial cds
                  303675
Seq. No.
Seq. ID
                  nbm700464704.h1
Method
                  BLASTN
NCBI GI
                   g206246
BLAST score
                  175
E value
                   5.0e-94
Match length
                   203
                   97
% identity
                  Rat brain myelin proteolipid protein (PLP) mRNA, complete
NCBI Description
                   303676
Seq. No.
                  nbm700464720.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2352919
BLAST score
                   206
                   8.0e-17
E value
Match length
                   47
                   89
% identity
NCBI Description
                   (AF012861) plastidic glucose-6-phosphate dehydrogenase
                   [Petroselinum crispum]
                   303677
Seq. No.
Seq. ID
                   nbm700464728.h1
Method
                   BLASTX
NCBI GI
                   q2827141
BLAST score
                   199
E value
                   8.0e-16
Match length
                   46
% identity
                   72
                   (AF027173) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   303678
Seq. No.
Seq. ID
                   nbm700464736.h1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g1419090
BLAST score 168
E value 3.0e-19
Match length 61
% identity 68

NCBI Description (X94968) 37kDa chloroplast inner envelope membrane

polypeptide precursor [Nicotiana tabacum]

Seq. No. 303679

Seq. ID nbm700464885.h1

Method BLASTX

```
g2853081
NCBI GI
                                                                    - 47.
                  186
BLAST score
                  5.0e-21
E value
Match length
                  80
% identity
                  (AL021768) ATP binding protein-like [Arabidopsis thaliana]
NCBI Description
                  303680
Seq. No.
                  nbm700464940.h1
Seq. ID
                  BLASTX
Method
                  q3292826
NCBI GI
BLAST score
                  426
                  2.0e-42
E value
Match length
                  94
% identity
                  79
                  (AL031018) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   303681
Seq. No.
                  nbm700464948.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3176669
BLAST score
                   445
                   2.0e-44
E value
Match length
                   95
                   79
% identity
                  (AC004393) End is cut off. [Arabidopsis thaliana]
NCBI Description
                   303682
Seq. No.
                   nbm700464955.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3063465
                   171
BLAST score
                   2.0e-12
E value
                   38
Match length
                   89
% identity
                  (AC003981) F22013.27 [Arabidopsis thaliana]
NCBI Description
                   303683
Seq. No.
                   nbm700465064.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4510339
                   337
BLAST score
E value
                   7.0e-32
                   93
Match length
                   69
% identity
                   (AC006921) putative ABC transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   303684
Seq. No.
                   nbm700465071.h1
Seq. ID
Method
                   BLASTX
                   q3273243
NCBI GI
                   247
BLAST score
                   2.0e-23
E value
Match length
                   85
% identity
                   75
NCBI Description (AB004660) NLS receptor [Oryza sativa]
```

NCBI Description



```
303685
Seq. No.
Seq. ID
                  nbm700465111.h1
Method
                  BLASTX
                  q4558557
NCBI GI
                  143
BLAST score
                   4.0e-09
E value
                  75
Match length
% identity
                   44
                   (AC007138) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   303686
Seq. No.
Seq. ID
                   nbm700465148.h1
Method
                   BLASTN
NCBI GI
                   g168436
                   63
BLAST score
                   4.0e-27
E value
                   139
Match length
                   86
% identity
                  Zea mays catalase (Cat3) gene, complete cds
NCBI Description
                   303687
Seq. No.
                   nbm700465149.h1
Seq. ID
Method
                   BLASTN
                   q3452304
NCBI GI
                   143
BLAST score
E value
                   1.0e-74
                   288
Match length
                   92
% identity
NCBI Description Zea mays retrotransposon Opie-1 5' LTR, partial sequence
                   303688
Seq. No.
                   nbm700465152.h1
Seq. ID
                   BLASTX
Method
                   g3875246
NCBI GI
BLAST score
                   218
                   6.0e-18
E value
Match length
                   78
% identity
                   56
                   (Z81490) similar to WD domain, G-beta repeats (2 domains);
NCBI Description
                   cDNA EST EMBL: T00482 comes from this gene; cDNA EST
                   EMBL: T00923 comes from this gene; cDNA EST yk449d4.3 comes
                   from this gene; cDNA EST yk449d4.5 comes from this gene;
Seq. No.
                   303689
                   nbm700465160.h1
Seq. ID
                   BLASTX
Method
                   g136063
NCBI GI
BLAST score
                   288
E value
                   4.0e-26
Match length
                   72
                   78
% identity
```

>gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza

>gi 68426 pir ISZMT triose-phosphate isomerase (EC

TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

5.3.1.1) - maize >gi_168647 (L00371) triosephosphate isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012) triosephosphate isomerase [Zea mays]

Seq. No. 303690

Seq. ID nbm700465195.h1

Method BLASTN
NCBI GI g452047
BLAST score 140
E value 3.0e-73
Match length 144
% identity 99

NCBI Description Homo sapiens HnRNP F protein mRNA, complete cds

Seq. No. 303691

Seq. ID nbm700465225.h1

Method BLASTX
NCBI GI g2589162
BLAST score 379
E value 8.0e-37
Match length 89
% identity 82

NCBI Description (D88451) aldehyde oxidase [Zea mays]

Seq. No. 303692

Seq. ID nbm700465264.h1

Method BLASTX
NCBI GI g3694807
BLAST score 301
E value 1.0e-27
Match length 93
% identity 72

NCBI Description (AF055898) alanine aminotransferase [Zea mays]

Seq. No. 303693

Seq. ID nbm700465407.h1

Method BLASTX
NCBI GI g3033400
BLAST score 202
E value 1.0e-19
Match length 86
% identity 56

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 303694

Seq. ID nbm700465445.h1

Method BLASTN
NCBI GI g22263
BLAST score 61
E value 2.0e-26
Match length 101
% identity 91

NCBI Description Z.mays Ds insertion element

Seq. No. 303695

Seq. ID nbm700465852.h1

```
Method
                  BLASTN
                  g4503452
NCBI GI
BLAST score
                  113
                  4.0e-57
E value
                  173
Match length
                  91
% identity
                  Homo sapiens endothelial differentiation-related factor 1
NCBI Description
                   (EDF1) mRNA >gi 3043444 emb AJ005259 HSAJ5259 Homo sapiens
                  mRNA for EDF-1 protein
                  303696
Seq. No.
                  nbm700465870.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4503452
BLAST score
                  71
                  3.0e-32
E value
Match length
                  123
                  89
% identity
                  Homo sapiens endothelial differentiation-related factor 1
NCBI Description
                   (EDF1) mRNA >gi 3043444 emb AJ005259 HSAJ5259 Homo sapiens
                  mRNA for EDF-1 protein
                  303697
Seq. No.
                  nbm700465891.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1841894
BLAST score
                  147
                  7.0e-10
E value
                  35
Match length
                  74
% identity
                  (D78136) Glutathione Reductase [Oryza sativa]
NCBI Description
                   303698
Seq. No.
                  nbm700465988.h1
Seq. ID
Method
                  BLASTX
                   g421929
NCBI GI
BLAST score
                   191
E value
                   2.0e-26
Match length
                   75
                   14
% identity
                  ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156)
NCBI Description
                   ubiquitin [Lycopersicon esculentum]
                   303699
Seq. No.
Seq. ID
                   nbm700466123.h1
Method
                   BLASTX
NCBI GI
                   g282900
BLAST score
                   372
```

E value 6.0e-36 Match length 92 % identity 76

maturation-associated protein MAT1 - soybean >gi 170020 NCBI Description (L00921) maturation protein [Glycine max] >gi_170022

(M93568) maturation-associated protein [Glycine max]

303700 Seq. No.

nbm700466147.h1 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g3176726
BLAST score
                  176
                  5.0e-13
E value
                  63
Match length
                  57
% identity
                   (AC002392) putative serine proteinase [Arabidopsis
NCBI Description
                  thaliana]
                  303701
Seq. No.
                  nbm700466159.h1
Seq. ID
Method
                  BLASTX
                  g3152566
NCBI GI
BLAST score
                  168
                   4.0e-12
E value
                  82
Match length
                   44
% identity
                   (AC002986) Similar to hypothetical protein YLR002c,
NCBI Description
                  qb Z7314 from S. cerevisiae. [Arabidopsis thaliana]
                   303702
Seq. No.
                  nbm700466254.h1
Seq. ID
Method
                  BLASTX
                   g4206640
NCBI GI
BLAST score
                   253
                   5.0e-22
E value
Match length
                   56
                   91
% identity
                  (AF072858) zinc transporter ZAT [Arabidopsis thaliana]
NCBI Description
                   303703
Seq. No.
                  nbm700466268.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4585271
BLAST score
                   429
                   1.0e-42
E value
Match length
                   89
                   97
% identity
                   (AF115314) seed maturation protein PM22; late embryogenesis
NCBI Description
                   abundant protein; LEA protein [Glycine max]
                   303704
Seq. No.
                   nbm700466288.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3819215
                   39
BLAST score
                   1.0e-12
E value
                   107
Match length
% identity
NCBI Description
                  Hordeum vulgare partial mRNA; clone cMWG0706
                   303705
Seq. No.
```

Seq. ID nbm700466311.h1

Method BLASTX
NCBI GI g2119719
BLAST score 220
E value 3.0e-23



```
Match length
                   65
                   89
% identity
                   heat-shock cognate protein 70-3 - tomato >gi 762844
NCBI Description
                   (L41253) Hsc70 [Lycopersicon esculentum]
                   303706
Seq. No.
                   nbm700466320.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g123613
BLAST score
                   160
                   2.0e-11
E value
Match length
                   31
                   94
% identity
NCBI Description
                   HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 100222 pir $14949
                   heat shock cognate protein 70 - tomato
                   >gi 19256 emb CAA37970 (X54029) heat shock protein cognate
                   70 [Lycopersicon esculentum]
                   303707
Seq. No.
Seq. ID
                   nbm700466353.h1
Method
                   BLASTX
NCBI GI
                   g2738750
.BLAST score
                   325
E value
                   2.0e-30
Match length
                   78
                   82
% identity
NCBI Description
                  (AF016305) ATP sulfurylase [Zea mays]
                   303708
Seq. No.
Seq. ID
                   nbm700466512.h1
Method
                   BLASTX
NCBI GI
                   g2244771
BLAST score
                   189
E value
                   2.0e-14
Match length
                   95
                   63
% identity
NCBI Description
                  (Z97335) kinesin homolog [Arabidopsis thaliana]
                   303709
Seq. No.
Seq. ID
                   nbm700466531.hl
Method
                   BLASTX
NCBI GI
                   g3025299
BLAST score
                   368
E value
                   2.0e-35
Match length
                   98
                   71
% identity
NCBI Description
                   HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi 2088660
                   (AF002109) ABC1 isolog [Arabidopsis thaliana]
```

Seq. ID nbm700466533.h1

303710

Method BLASTX NCBI GI g2853084 BLAST score 209 E value 6.0e-17 Match length 66 % identity 61

Seq. No.



```
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]
                  303711
Seq. No.
Seq. ID
                  nbm700466554.h1
                  BLASTX
Method
                  g541546
NCBI GI
BLAST score
                  274
E value
                  2.0e-24
Match length
                  81 .
                  15
% identity
                  ubiquitin precursor - Volvox carteri
NCBI Description
                  >gi_395295_emb_CAA52290_ (X74214) polyubiquitin [Volvox
                  carteri]
Seq. No.
                   303712
Seq. ID
                  nbm700466559.h1
Method
                  BLASTX
NCBI GI
                   q4204265
BLAST score
                   285
                   8.0e-26
E value
Match length
                   68
                  75
% identity
                  (AC005223) 45643 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303713
                  nbm700466572.h1
Seq. ID
Method
                  BLASTX
                   g3093294
NCBI GI
                   196
BLAST score
                   4.0e-24
E value
                   92
Match length
                   62
% identity
                  (Y12782) putative villin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303714
                   nbm700466588.h1
Seq. ID
Method
                   BLASTX
                   g4580990
NCBI GI
BLAST score
                   186
E value
                   3.0e-14
                   93
Match length
                   40
% identity
                   (AF120335) putative transposase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303715
                   nbm700466589.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539351
BLAST score
                   195
                   3.0e-15
E value
Match length
                   92
                   48
% identity
NCBI Description
                   (AL035539) putative protein [Arabidopsis thaliana]
```

Seq. ID nbm700466783.h1

Method BLASTN

BLAST score

E value

```
g1930069
NCBI GI
BLAST score
                  41
                  3.0e-14
E value
                  61
Match length
% identity
NCBI Description Oryza sativa proteasome alpha subunit mRNA, complete cds
                  303717
Seq. No.
                  nbm700466822.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1709970
BLAST score
                  178
                  1.0e-13
E value
                  47
Match length
% identity
                  74
NCBI Description 60S RIBOSOMAL PROTEIN L10A
                  303718
Seq. No.
                  nbm700466824.hl
Seq. ID
                  BLASTN
Method
                  q736271
NCBI GI
BLAST score
                  47
                  8.0e-18
E value
Match length
                  85
% identity
NCBI Description O.sativa hsp70 gene for heat shock protein
                   303719
Seq. No.
                  nbm700466862.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4510345
BLAST score
                   137
E value
                   9.0e-09
Match length
                   37
% identity
                   65
                   (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   303720
Seq. No.
                   nbm700466917.h1
Seq. ID
                   BLASTN
Method
                   g2984708
NCBI GI
BLAST score
                   67
                   1.0e-29
E value
                   114
Match length
                   100
% identity
                   Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
NCBI Description
                   cds
                   303721
Seq. No.
                   nbm700466943.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2443321
```

Match length 49
% identity 92
NCBI Description Oryza australiensis retrotransposon RIRE1, LTR sequence

33 4.0e-09

BLAST score

156

```
Seq. No.
                  303722
                  nbm700466976.h1
Seq. ID
                  BLASTX
Method
                  g4150963
NCBI GI
                  142
BLAST score
                  2.0e-09
E value
Match length
                  59
                  51
% identity
NCBI Description (Y18620) DsPTP1 protein [Arabidopsis thaliana]
Seq. No.
                  303723
Seq. ID
                  nbm700466989.h1
Method
                  BLASTX
                  g3152731
NCBI GI
BLAST score
                  229
                  2.0e-19
E value
Match length
                  46
                  93
% identity
                  (AF056325) myo-inositol 1-phosphate synthase; INO1 [Hordeum
NCBI Description
                  vulgare]
                  303724
Seq. No.
Seq. ID
                  nbm700466990.h1
Method
                  BLASTX
NCBI GI
                   g3540198
BLAST score
                   226
                   6.0e-19
E value
                   68
Match length
% identity
                   59
NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]
                   303725
Seq. No.
Seq. ID
                   nbm700467020.h1
Method
                   BLASTX
                   g2244865
NCBI GI
BLAST score
                   142
                   5.0e-09
E value
                   73
Match length
                   34
% identity
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                   303726
Seq. No.
Seq. ID
                   nbm700467049.h1
Method
                   BLASTN
NCBI GI
                   q435172
BLAST score
                   36
E value
                   3.0e-11
Match length
                   48
                   94
% identity
NCBI Description A.sativa (Pewi) ASTCP-K19 mRNA for t complex polypeptide
                   303727
Seq. No.
                   nbm700467179.h1
Seq. ID
Method
                   BLASTX
                   g4581164
NCBI GI
```



```
1.0e-10
E value
                                                 ج
Match length
                  82
% identity
                  46
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
NCBI Description
                  303728
Seq. No.
                  nbm700467311.hl
Seq. ID
                  BLASTX
Method
                  g4191784
NCBI GI
BLAST score
                  169
                  2.0e-12
E value
Match length
                  52
% identity
                  63
                  (AC005917) putative WD-40 repeat protein [Arabidopsis
NCBI Description
                  thaliana]
                  303729
Seq. No.
                  nbm700467357.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g113217
BLAST score
                  229
                  3.0e-25
E value
Match length
                  61
                  100
% identity
NCBI Description ACTIN 1 >gi 100149 pir S07002 actin 1 - carrot
                   303730
Seq. No.
Seq. ID
                  nbm700467387.h1
Method
                  BLASTN
                   q3399678
NCBI GI
BLAST score
                   37
                   7.0e-12
E value
Match length
                   85
                   86
% identity
                  Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   303731
Seq. No.
Seq. ID
                   nbm700467388.h1
Method
                   BLASTN
                   g168436
NCBI GI
                   79
BLAST score
                   7.0e-37
E value
Match length
                   111
                   93
% identity
NCBI Description
                  Zea mays catalase (Cat3) gene, complete cds
Seq. No.
                   303732
                   nbm700467571.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2335106
                   330
BLAST score
                   4.0e-31
E value
                   77
Match length
                   75
% identity
NCBI Description
                   (AC002339) salt inducible protein-like [Arabidopsis
```

42940

thaliana]

303738

```
Seq. No.
                   303733
                   nbm700467733.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g553073
BLAST score
                   238
                   2.0e-23
E value
                   59
Match length
% identity
                   95
NCBI Description
                   (M94481) reverse transcriptase [Zea mays]
Seq. No.
                   303734
                   nbm700467853.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2130149
BLAST score
                   485
                   3.0e-49
E value
Match length
                   92
% identity
                   100
                   translation elongation factor eEF-1 alpha chain - maize
NCBI Description
                   (fragment)
Seq. No.
                   303735
                   nbm700467885.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g6598458
BLAST score
                   40
E value
                   3.0e-13
Match length
                   96
                   85
% identity
                   Arabidopsis thaliana chromosome II BAC T16F16 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   303736
Seq. No.
                   nbm700467909.h1
Seq. ID
Method
                   BLASTX
                   g4206209
NCBI GI
BLAST score
                   155
                   2.0e-19
E value
                   99
Match length
                   54
% identity
NCBI Description
                   (AF071527) putative glucan synthase component [Arabidopsis
                   thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative
                   glucan synthase component [Arabidopsis thaliana]
Seq. No.
                   303737
Seq. ID
                   nbm700467938.h1
Method
                   BLASTX
NCBI GI
                   g2244913
BLAST score
                   328
E value
                   8.0e-31
Match length
                   98
% identity
                   62
NCBI Description
                   (Z97339) similar to SEN1 protein - yeast [Arabidopsis
                   thaliana]
```



```
Seq. ID
                  nbm700467939.h1
                  BLASTX
Method
NCBI GI
                  g452519
BLAST score
                  180
                  2.0e-13
E value
                  69
Match length
                  51
% identity
                  (D26362) similar to Human homolog of Drosophila female
NCBI Description
                  sterile homeotic mRNA ( HUMFSHG) [Homo sapiens]
                  303739
Seq. No.
                  nbm700467941.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3522948
BLAST score
                  181
                  1.0e-13
E value
                  79
Match length
% identity
                  44
                  (AC004411) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  303740
                  nbm700467948.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3757521
BLAST score
                  205
E value
                  2.0e-16
Match length
                  95
% identity
                  51
NCBI Description
                  (AC005167) unknown protein [Arabidopsis thaliana]
                  303741
Seq. No.
Seq. ID
                  nbm700467952.h1
Method
                  BLASTX
NCBI GI
                  g3335349
BLAST score
                  193
E value
                  3.0e-15
Match length
                  76
                  47
% identity
NCBI Description
                  (AC004512) Similar to gb_U46691 putative chromatin
                  structure regulator (SUPT6H) from Homo sapiens. ESTs
                  gb_T42908, gb_AA586170 and gb_AA395125 come from this gene.
                   [Arabidopsis thaliana]
                  303742
Seq. No.
Seq. ID
                  nbm700468004.h1
Method
                  BLASTX
NCBI GI
                  g1657621
BLAST score
                  388
E value
                  8.0e-38
Match length
                  99
% identity
                  74
```

(U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236) NCBI Description

putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Seq. No.

303743

Seq. ID nbm700468044.h1

Method BLASTX

```
g585771
NCBI GI
BLAST score
                  286
E value
                  3.0e - 26
Match length
                  60
                  92
% identity
                  MEIOTIC RECOMBINATION PROTEIN DMC1 HOMOLOG
NCBI Description
                  >gi 629874 pir JC2214 hypothetical 38.3K protein, LIM15 -
                  Trumpet lily >gi 431168 dbj BAA04845 (D21821) RAD51-like
                  protein [Lilium longiflorum]
Seq. No.
                  303744
Seq. ID
                  nbm700468170.h1
Method
                  BLASTX
NCBI GI
                  g3702343
BLAST score
                  366
                  3.0e-35
E value
Match length
                  91
                  74
% identity
                  (AC005397) putative homeotic gene regulator [Arabidopsis
NCBI Description
                  thalianal
                  303745
Seq. No.
Seq. ID
                  nbm700468322.h1
```

Method BLASTX NCBI GI g2290528 BLAST score 147 E value 7.0e-10 Match length 32 88

% identity

NCBI Description (U94746) ATAN11 [Arabidopsis thaliana]

Seq. No. 303746

nbm700468344.h1 Seq. ID

Method BLASTX NCBI GI g4325344 BLAST score 180 E value 2.0e-13 Match length 44 % identity 84

NCBI Description (AF128393) similar to beta-transducins (Pfam: PF00400,

Score=71.7, E=1.5e-17, N=6) [Arabidopsis thaliana]

Seq. No. 303747

Seq. ID nbm700468358.h1

Method BLASTX NCBI GI g135398 BLAST score 249 E value 3.0e-25 Match length 58 100 % identity

TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1 NCBI Description

chain - maize >gi_22147_emb_CAA33734_ (X15704)

alpha1-tubulin [Zea mays]

Seq. No. 303748

Seq. ID nbm700468370.h1

Method BLASTX

E value

Match length

6.0e-14

85

```
g4539440
NCBI GI
BLAST score
                   184
                   2.0e-30
E value
Match length ,
                   92
                   61
% identity
                   (AL049523) putative protein [Arabidopsis thaliana]
NCBI Description
                   303749
Seq. No.
                   nbm700468384.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4185311
BLAST score
                   258
E value
                   1.0e-22
Match length
                   92
                   59
% identity
NCBI Description (AF090446) polyprotein [Zea mays]
                   303750
Seq. No.
                   nbm700468418.h1
Seq. ID
Method
                   BLASTX
                   g3024018
NCBI GI
BLAST score
                   354
                   6.0e-34
E value
Match length
                   68
% identity
                   97
                   INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_1546919_emb_CAA69225_ (Y07920) translation initiation
                   factor 5A [\overline{\text{Zea mays}}] >gi\overline{\text{2}}2668738 (AF034943) translation
                   initiation factor 5A [Zea mays]
                   303751
Seq. No.
                   nbm700468454.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076678
BLAST score
                   189
                   1.0e-14
E value
Match length
                   41
% identity
                   95
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.
                   303752
                   nbm700468460.h1
Seq. ID
                   BLASTX
Method
                   g2444178
NCBI GI
BLAST score
                   268
                   8.0e-24
E value
                   86
Match length
% identity
                   64
NCBI Description
                   (U94784) unconventional myosin [Helianthus annuus]
Seq. No.
                   303753
Seq. ID
                   nbm700468478.h1
Method
                   BLASTX
NCBI GI
                   g2829910
BLAST score
                   184
```



% identity NCBI Description (AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana] 303754 Seq. No. nbm700468489.h1 Seq. ID Method BLASTX NCBI GI g2149640 BLAST score 177 2.0e-13 E value Match length 46 74 % identity NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana] 303755 Seq. No. Seq. ID nbm700468496.h1 Method BLASTX NCBI GI g3337367 BLAST score 203 E value 3.0e-16 Match length 66 58 % identity NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana] Seq. No. 303756 nbm700468530.h1 Seq. ID Method BLASTX g3600038 NCBI GI BLAST score 280 2.0e-25 E value Match length 54 91 % identity (AF080119) similar to Saccharomyces cerevisiae NCBI Description . transcription regulator SPO8 (SW:P41833) [Arabidopsis thaliana] Seq. No. 303757 Seq. ID nbm700468590.h1 Method BLASTX NCBI GI q1076746 BLAST score 344 E value 1.0e-40 Match length 101 88 % identity NCBI Description heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa] Seq. No. 303758 Seq. ID nbm700468724.h1 Method BLASTX NCBI GI q4309736

-

NCBI GI g430973 BLAST score 233 E value 1.0e-19 Match length 96 % identity 53

NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]

NCBI Description

[Zea mays]



```
303759
Seq. No.
                  nbm700468742.h1
Seq. ID
                  BLASTX
Method
                  g3176874
NCBI GI
                  174
BLAST score
                  9.0e-13
E value
Match length
                  57
                  61 -
% identity
                  (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                  thaliana]
                  303760
Seq. No.
                  nbm700468789.h1
Seq. ID
Method
                  BLASTX
                  g1710401
NCBI GI
BLAST score
                  192
                  5.0e-24
E value
Match length
                  79
                  78
% identity
                  RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN
NCBI Description
                   (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)
                  >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase
                  R2 [Nicotiana tabacum]
                  303761
Seq. No.
                  nbm700468794.h1
Seq. ID
                  BLASTX
Method
                  g2288985
NCBI GI
BLAST score
                  195
                  3.0e-15
E value
Match length
                  52
                  77
% identity
                  (AC002335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  303762
Seq. No.
                  nbm700468802.h1
Seq. ID
Method
                  BLASTX
                  g2104683
NCBI GI
BLAST score
                  166
E value
                   9.0e-12
Match length
                   62
                   42
% identity
NCBI Description (X97908) transcription factor [Vicia faba]
Seq. No.
                  303763
                  nbm700468914.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q629843
BLAST score
                   429
E value
                   2.0e-46
                   99
Match length
                   100
% identity
```

heat shock protein hsp70-4 - maize (fragment)

>gi_498773_emb_CAA55183_ (X78414) heat shock protein 70 kDa

Method

NCBI GI

BLAST score

BLASTX

179

g3033384



```
303764
Seq. No.
Seq. ID
                  nbm700468930.h1
Method
                  BLASTX
                  q3386604
NCBI GI
                   179
BLAST score
                   3.0e-13
E value
Match length
                  80
% identity
                   42
                  (AC004665) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   303765
Seq. No.
Seq. ID
                  nbm700469004.h1
Method
                  BLASTX
NCBI GI
                   g2145356
BLAST score
                   215
E value
                   2.0e-17
Match length
                   49
                   78
% identity
                  (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474
NCBI Description
                   (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]
                   303766
Seq. No.
                   nbm700469063.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4586242
BLAST score
                   154
                   1.0e-10
E value
Match length
                   53
                   49
% identity
NCBI Description
                   (AL049640) putative protein (fragment) [Arabidopsis
                   thaliana]
                   303767
Seq. No.
Seq. ID
                   nbm700469179.h1
Method
                   BLASTX
NCBI GI
                   g2943792
BLAST score
                   311
E value
                   6.0e-29
Match length
                   62
% identity
                   81
NCBI Description
                  (AB006809) PV72 [Cucurbita sp.]
                   303768
Seq. No.
Seq. ID
                   nbm700469191.h1
Method
                   BLASTX
NCBI GI
                   g2282584
BLAST score
                   300
E value
                   1.0e-27
Match length
                   63
% identity
                   92
NCBI Description
                  (U76259) elongation factor 1-alpha [Zea mays]
                   303769
Seq. No.
Seq. ID
                   nbm700469258.h1
```



```
3.0e-16
E value
Match length
                  83
% identity
                  58
                  (AC004238) putative CTP synthase [Arabidopsis thaliana]
NCBI Description
                  303770
Seq. No.
                  nbm700469274.h1
Seq. ID
                  BLASTX
Method
                  g1568480
NCBI GI
BLAST score
                  199
                  5.0e-34
E value
                  80
Match length
% identity
                  95
NCBI Description
                  (Z71703) cdc2-like protein kinase [Beta vulgaris]
                  303771
Seq. No.
                  nbm700469432.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4467111
BLAST score
                  228
                  2.0e-19
E value
Match length
                  55
% identity
                   64
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                  303772
Seq. No.
                  nbm700469433.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4454012
BLAST score
                   180
                   9.0e-14
E value
                   49
Match length
                   57
% identity
NCBI Description
                   (AL035396) Pollen-specific protein precursor like
                   [Arabidopsis thaliana]
Seq. No.
                   303773
                   nbm700469507.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4582786
BLAST score
                   36
                   6.0e-11
E value
                   48
Match length
% identity
                   94
NCBI Description Zea mays mRNA for adenosine kinase, putative
Seq. No.
                   303774
                   nbm700469525.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2078350
BLAST score
                   273
E value
                   2.0e-24
Match length
                   76
% identity
                   67
NCBI Description
                  (U95923) transaldolase [Solanum tuberosum]
```

```
Seq. ID
                   nbm700469530.h1
Method
                   BLASTX
NCBI GI
                   q3163946
BLAST score
                   316
E value
                   2.0e-29
Match length
                   59
% identity
                   98
NCBI Description
                   (AJ005599) alpha-tubulin 1 [Eleusine indica]
                   303776
Seq. No.
Seq. ID
                   nbm700469546.hl
Method
                   BLASTX
NCBI GI
                   q1084481
BLAST score
                   363
                   6.0e-35
E value
Match length
                   93
% identity
                   80
NCBI Description heat shock protein 70 - Maize
                   303777
Seq. No.
                   nbm700469586.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g248336
BLAST score
                   67
                   1.0e-29
E value
Match length
                   143
% identity
                   29
NCBI Description
                   polyubiquitin [maize, Genomic, 3841 nt]
                   303778
Seq. No.
Seq. ID
                   nbm700469752.h1
Method
                   BLASTX
NCBI GI
                   g3850573
BLAST score
                   301
E value
                   1.0e-27
Match length
                   91
% identity
                   65
NCBI Description
                   (AC005278) Similar to gi 1652733 glycogen operon protein
                   GlgX from Synechocystis sp. genome gb D90908. ESTs
                   gb_H36690, gb_AA712462, gb_AA651230 and gb_N95932 come from
                   this gene. [Arabidopsis thaliana]
                   303779
Seq. No.
Seq. ID
                   nbm700469757.h1
Method
                   BLASTX
NCBI GI
                   g224970
BLAST score
                   449
                   4.0e-45
E value
Match length
                   88
% identity
                   100
NCBI Description heat shock protein hsp70 [Zea mays]
```

Seq. ID nbm700469758.h1

Method BLASTX g2388578 NCBI GI BLAST score 307

```
2.0e-28
74
77
```

E value Match length % identity (AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs NCBI Description gb T75785,gb R30580,gb T04698 come from this gene. [Arabidopsis thaliana] Seq. No. 303781 nbm700469852.h1 Seq. ID Method BLASTX NCBI GI g1651689 BLAST score 182 E value 9.0e-14 Match length 76 47 % identity NCBI Description (D90899) hypothetical protein [Synechocystis sp.] 303782 Seq. No. Seq. ID nbm700469944.h1 Method BLASTX g3935147 NCBI GI BLAST score 327 9.0e-31 E value Match length 87 % identity 69 NCBI Description (AC005106) T25N20.11 [Arabidopsis thaliana] Seq. No. 303783 nbm700470059.h1 Seq. ID Method BLASTX NCBI GI q4249382 BLAST score 197 1.0e-15 E value Match length 50 % identity 76 NCBI Description (AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana] Seq. No. 303784 Seq. ID nbm700470105.h1 Method BLASTN NCBI GI q3108052 BLAST score 42 E value 1.0e-14 Match length 66 91 % identity NCBI Description Zea mays myo-inositol 1-phosphate synthase mRNA, complete Seq. No. 303785 nbm700470304.h1 Seq. ID Method BLASTX

NCBI GI g115795 BLAST score 246 3.0e-21 E value 96 Match length



% identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-C) (LHCP) >gi_72735_pir__CDNTCC chlorophyll a/b-binding protein type I precursor (cab-C) - curled-leaved tobacco >gi_170210 (M21397) chlorophyll a/b-binding protein-C [Nicotiana plumbaginifolia] 303786 Seq. No. nbm700470317.h1 Seq. ID Method BLASTX NCBI GI q1076678 BLAST score 375 E value 3.0e-36 Match length 77 99 % identity NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment) 303787 Seq. No. nbm700470322.h1 Seq. ID Method BLASTX NCBI GI g131770 BLAST score 232 E value 1.0e-19 Match length 61 % identity 70 NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024 ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi 7353 emb CAA29844 (X06636) rp1024 protein [Dictyostelium discoideum] 303788 Seq. No. nbm700470450.h1 Seq. ID Method BLASTX g2495365 NCBI GI BLAST score 315 E value 2.0e-29 Match length 62 98 % identity NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf 1908431B heat shock protein HSP81-2 [Arabidopsis thaliana] 303789 Seq. No. Seq. ID nbm700470520.h1 Method BLASTX NCBI GI g1800215 BLAST score 249 E value 4.0e-44Match length 89

89 % identity

NCBI Description (U56729) phytochrome A [Sorghum bicolor]

303790 Seq. No.

nbm700470582.h1 Seq. ID

Method BLASTX g2130149 NCBI GI BLAST score 361

% identity

NCBI Description

57

```
E value
                   9.0e-35
Match length
                   88
                   80
% identity
                  translation elongation factor eEF-1 alpha chain - maize
NCBI Description
                   (fragment)
                   303791
Seq. No.
                   nbm700470655.h1
Seq. ID
                   BLASTN
Method ·
NCBI GI
                   g312178
BLAST score
                   47
                   2.0e-17
E value
Match length
                   71
% identity
                   92
                  Z.mays GapC2 gene
NCBI Description
                   303792
Seq. No.
                   nbm700470723.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3935168
BLAST score
                   172
                   2.0e-12
E value
                   69
Match length
                   49
% identity
                  (AC004557) F17L21.11 [Arabidopsis thaliana]
NCBI Description
                   303793
Seq. No.
                   nbm700470739.h1
Seq. ID
Method
                   BLASTX
                   q4455188
NCBI GI
BLAST score
                   215
                   1.0e-17
E value
                   77
Match length
                   55
% identity
                  (AL035521) putative protein [Arabidopsis thaliana]
NCBI Description
                   303794
Seq. No.
                   nbm700470825.h1
Seq. ID
                   BLASTX
Method
                   q1076746
NCBI GI
BLAST score
                   410
                   2.0e-40
E value
                   91
Match length
                   88
% identity
                   heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   303795
Seq. No.
Seq. ID
                   nbm700470880.h1
Method
                   BLASTX
                   q3860886
NCBI GI
BLAST score
                   230
E value
                   2.0e-19
                   84
Match length
```

42952

(AJ235271) DNA TOPOISOMERASE I (topA) [Rickettsia

Match length

NCBI Description

% identity

195

partial cds

92



prowazekii]

303796 Seq. No. nbm700470918.h1 Seq. ID Method BLASTN g4160401 NCBI GI BLAST score 34 E value 1.0e-09 Match length 66 88 % identity NCBI Description Zea mays eIF-5 gene, exons 1-2 303797 Seq. No. Seq. ID nbm700471060.hl Method BLASTX g3193291 NCBI GI BLAST score 261 5.0e-23 E value Match length 64 % identity 75 (AF069298) Similar to DNA mismatch repair protein; T14P8.6 NCBI Description [Arabidopsis thaliana] 303798 Seq. No. Seq. ID nbm700471069.h1 Method BLASTX NCBI GI g2565010 BLAST score 261 8.0e-26 E value Match length 86 % identity 74 (AC002983) putative microfibril-associated protein NCBI Description [Arabidopsis thaliana] >gi_3377811 (AF076275) contains similarity to ATP synthase B/B' (Pfam: ATP-synt_B.hmm, score: 11.71) [Arabidopsis thaliana] Seq. No. 303799 Seq. ID nbm700471314.h1 Method BLASTX g3688328 NCBI GI BLAST score 167 E value 2.0e-22 Match length 94 60 % identity NCBI Description (AJ228325) reverse transcriptase [Ginkgo biloba] 303800 Seq. No. Seq. ID nbm700471375.h1 Method BLASTN NCBI GI g1181672 BLAST score 124 E value 2.0e-63

42953

Sorghum bicolor heat shock protein 70 cognate (hsc70) mRNA,



```
303801
Seq. No.
                nbm700471380.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1658192
BLAST score
                  53
                  4.0e-21
E value
                  142
Match length
% identity
                  84
                  Sorghum bicolor obtusifoliol 14-alpha demethylase CYP51
NCBI Description
                  (CYP51) mRNA, complete cds
                  303802
Seq. No.
                  nbm700471391.h1
Seq. ID
Method
                  BLASTX
                  g3426038
NCBI GI
                  250
BLAST score
                  1.0e-21
E value
Match length
                  88
                  53
% identity
                  (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
                  303803
Seq. No.
                  nbm700471461.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4455176
BLAST score
                  181
                   1.0e-13
E value
                  94
Match length
                   47
% identity
                  (AL035521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   303804
Seq. No.
                  nbm700471463.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4501867
BLAST score
                   477
E value
                   3.0e-48
Match length
                   95
% identity
                   95
NCBI Description
                  aconitase 2, mitochondrial >gi 3366620 (U87939) aconitate
                  hydratase [Homo sapiens]
                   303805
Seq. No.
                   nbm700471524.h1
Seq. ID
Method
                   BLASTX
                   g4539452
NCBI GI
BLAST score
                   252
                   4.0e-22
E value
Match length
                   70
% identity
                   70
                   (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. ID nbm700471660.h1

Method BLASTX NCBI GI g2829910

```
BLAST score
                  427
                  2.0e-42
E value
                  94
Match length
                  79
% identity
                  (AC002291) Unknown protein, contains regulator of
NCBI Description
                  chromosome condensation motifs [Arabidopsis thaliana]
                  303807
Seq. No.
                  nbm700471674.hl
Seq. ID
                  BLASTX
Method
                  g1800217
NCBI GI
BLAST score
                  464
                  8.0e-47
E value
                  92
Match length
% identity
                  98
                  (U56730) Phytochrome B [Sorghum bicolor]
NCBI Description
                  303808
Seq. No.
                  nbm700471693.hl
Seq. ID
                  BLASTX
Method
                  g4204312
NCBI GI
                  414
BLAST score
                  6.0e-41
E value
                  93
Match length
                  84
% identity
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  303809
Seq. No.
                  nbm700471777.h1
Seq. ID
Method
                  BLASTX
                   q4337040
NCBI GI
BLAST score
                  145
                  1.0e-17
E value
                  85
Match length
% identity
                   62
                   (AF124159) molybdopterin synthase sulphurylase [Arabidopsis
NCBI Description
                   thaliana] >gi_4337042_gb_AAD18051_ (AF124160) molybdopterin
                   synthase sulphurylase [Arabidopsis thaliana]
                   303810
Seq. No.
Seq. ID
                  nbm700471781.hl
                   BLASTX
Method
NCBI GI
                   g1589778
BLAST score
                   161
```

E value 2.0e-11 33 Match length 85 % identity

(U62135) SPINDLY [Arabidopsis thaliana] NCBI Description

Seq. No. 303811 nbm700471850.h1 Seq. ID Method

BLASTX g584741 NCBI GI BLAST score 140 E value 4.0e-09

Match length 43



% identity NCBI Description ANKYRIN REPEAT PROTEIN (AKRP) >gi_322461_pir__JQ1729 ankyrin-repeat protein - Arabidopsis thaliana >gi_166744 (M82883) ankyrin repeat-containing protein [Arabidopsis thaliana] 303812 Seq. No. nbm700471933.h1 Seq. ID BLASTX Method g3461813 NCBI GI 233 BLAST score 1.0e-19 E value 100 Match length % identity

(AC004138) putative sucrose/H+ symporter [Arabidopsis NCBI Description

thaliana]

303813 Seq. No.

nbm700471937.hl Seq. ID

Method BLASTX NCBI GI q3080740 BLAST score 237 2.0e-20 E value Match length 58 % identity

(U77366) pasticcino 1-D [Arabidopsis thaliana] NCBI Description

303814 Seq. No.

nbm700472115.h1 Seq. ID

BLASTX Method q2499087 NCBI GI BLAST score 443 3.0e-44 E value 103 Match length 74 % identity

UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR NCBI Description

(DUGT) >gi_1085170_pir__S54723 UDP-glucose--glycoprotein glucosyltransferase - fruit fly (Drosophila sp.) >gi_790585

(U20554) UDP-glucose:glycoprotein glucosyltransferase

precursor [Drosophila melanogaster]

Seq. No. 303815

nbm700472170.h1 Seq. ID

BLASTX Method g1931640 NCBI GI BLAST score 212 4.0e-17 E value 95 Match length % identity

(U95973) Serine carboxypeptidase isolog [Arabidopsis NCBI Description

thaliana]

303816 Seq. No.

nbm700472290.h1 Seq. ID

BLASTX Method NCBI GI q4249390 BLAST score 189



```
2.0e-14
E value
Match length
                  91
% identity
                  36
                  (AC005966) Similar to gb AF039182 probable aldo-keto
NCBI Description
                  reductase from Fragaria x ananassa. This gene may be cut
                  off. EST gb_U74151 comes from this gene. [Arabidopsis
                  thaliana]
                  303817
Seq. No.
                  nbm700472389.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2792295
BLAST score
                  182
                  9.0e-14
E value
Match length
                  66
% identity
                  52
                  (AF039182) unknown [Fragaria x ananassa]
NCBI Description
                  303818
Seq. No.
                  nbm700472522.h1
Seg. ID
Method
                  BLASTX
                  g170354
NCBI GI
BLAST score
                  249
                  2.0e-21
E value
Match length
                  81
% identity
                  14
                  (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
NCBI Description
Seq. No.
                  303819
                  nbm700472525.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213632
BLAST score
                  145
                  2.0e-09
E value
Match length
                   43
% identity
                   65
                  (AC000103) F21J9.24 [Arabidopsis thaliana]
NCBI Description
                  303820
Seq. No.
                  nbm700472530.h1
Seq. ID
Method
                  BLASTX
                  g121349
NCBI GI
BLAST score
                   149
E value
                   5.0e-10
Match length
                   68
```

% identity 46

GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA NCBI Description

LIGASE) (CLONE LAMBDA-GS28) >gi_20368_emb_CAA32461

(X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza

sativa]

Seq. No. 303821 :

nbm700472543.h1 Seq. ID

Method BLASTX NCBI GI q3962377 BLAST score 268 E value 7.0e-24

```
Match length
                   88
% identity
                   (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303822
                  nbm700472633.h1
Seq. ID
                  BLASTX
Method
                  q3176714
NCBI GI
                   244
BLAST score
                   4.0e-32
E value
Match length
                   96
                   77
% identity
                   (AC002392) putative tRNA-splicing endonuclease positive
NCBI Description
                   effector [Arabidopsis thaliana]
Seq. No.
                   303823
                   nbm700472651.h1
Seq. ID
                   BLASTX
Method
                   g2668744
NCBI GI
BLAST score
                   285
E value
                   9.0e-26
Match length
                   53
% identity
                   98
                   (AF034946) ubiquitin conjugating enzyme [Zea mays]
NCBI Description
Seq. No.
                   303824
                   nbm700472656.h1
Seq. ID
Method
                   BLASTN
                   g435174
NCBI GI
BLAST score
                   44
                   1.0e-15
E value
Match length
                   84
                   88
% identity
                   A.sativa (Pewi) ASTCP-K36 mRNA for t complex polypeptide
NCBI Description
Seq. No.
                   303825
                   nbm700472728.h1
Seq. ID
Method
                   BLASTX
                   g3249064
NCBI GI
                   183
BLAST score
E value
                   4.0e-14
Match length
                   51
                   57
% identity
                   (AC004473) Strong similarity to trehalose-6-phosphate
NCBI Description
                   synthase homolog gb 2245136 from A. thaliana chromosome 4
                   contig gb_Z97344. [Arabidopsis thaliana]
```

Seq. ID nbm700472733.h1

Method BLASTX
NCBI GI g3820614
BLAST score 164
E value 1.0e-11
Match length 97
% identity 40

NCBI Description (AF094516) E1-like protein [Homo sapiens]



```
303827
Seq. No.
                  nbm700472818.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4506221
BLAST score
                   163
                   2.0e-11
E value
Match length
                   66
% identity
                   47
                  proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
NCBI Description
                   >gi 1945611_dbj_BAA19749_ (AB003103) 26S proteasome subunit
                   p55 [Homo sapiens]
Seq. No.
                   303828
                   nbm700472831.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2865393
BLAST score
                   42
E value
                   2.0e-14
                   86
Match length
                   87
% identity
                   Zea mays basic leucine zipper protein (liguleless2) mRNA,
NCBI Description
                   complete cds
                   303829
Seq. No.
                   nbm700472844.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3776011
BLAST score
                   289
E value
                   3.0e-26
Match length
                   91
% identity
                   (AJ010469) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   303830
Seq. No.
                   nbm700472871.h1
Seq. ID
                   BLASTX
Method
                   g3249109
NCBI GI
BLAST score
                   210
                   5.0e-17
E value
                   46
Match length
% identity
                   83
                   (AC003114) Contains similarity to pre-mRNA splicing factor
NCBI Description
                   (SF2), P33 subunit gb M72709 from Homo sapiens. ESTs
                   gb_{142588} and gb_{165514} come from this gene. [Arabidopsis
                   thaliana]
                   303831
Seq. No.
                   nbm700472874.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3668092
BLAST score
                   310
                   1.0e-28
E value
                   71
Match length
% identity
```

NCBI Description

(AC004667) unknown protein [Arabidopsis thaliana]



```
nbm700472952.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100440
BLAST score
                  204
E value
                  1.0e-16
Match length
                  39
                  95
% identity
                  heat shock protein 70 (clone D7) - potato (fragment)
NCBI Description
                  >gi 100441 pir_S21363 heat shock protein 70 (clone D3) -
                  potato (fragment) >gi_21477_emb_CAA78036_ (Z11984) 70-kD
                  heat shock protein [Solanum tuberosum]
                   303833
Seq. No.
                  nbm700472961.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2791834
BLAST score
                   217
E value
                   4.0e-18
                   42
Match length
                   100
% identity
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
NCBI Description
                   303834
Seq. No.
                   nbm700472970.h1
Seq. ID
                   BLASTX
Method
                   q4558549
NCBI GI
BLAST score
                   364
                   3.0e-35
E value
                   82
Match length
% identity
                   88
                   (AC007138) putative SecA-type chloroplast protein transport
NCBI Description
                   factor [Arabidopsis thaliana]
                   303835
Seq. No.
                   nbm700473003.h1
Seq. ID
                   BLASTX
Method
                   g3024657
NCBI GI
                   246
BLAST score
                   5.0e-23
E value
                   70
Match length
                   86
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi 2668740 (AF034944) translation initiation factor; GOS2
                   [Zea mays]
                   303836
Seq. No.
                   nbm700473036.h1
Seq. ID
                   BLASTX
Method
                   g1762130
NCBI GI
BLAST score
                   227
                   6.0e-19
E value
```

Match length 77 % identity 70

NCBI Description (U46136) chaperonin-60 beta subunit [Solanum tuberosum]

Seq. No.

303837

Seq. ID

nbm700473041.h1

BLAST score

E value

340 3.0e-32

```
BLASTX
Method
NCBI GI
                  q4587584
BLAST score
                  251
                  9.0e-22
E value
Match length
                  98
% identity
                  (AC007232) unknown protein [Arabidopsis thaliana]
NCBI Description
                  303838
Seq. No.
                  nbm700473042.h1
Seq. ID
Method
                  BLASTX
                  g2920587
NCBI GI
BLAST score
                  271
                   4.0e-24
E value
                   95
Match length
% identity
                  (AF038362) TBP-associated factor 172 [Homo sapiens]
NCBI Description
                  >gi_2995136_emb_CAA04475_ (AJ001017) TAFII170 [Homo
                   sapiens]
                   303839
Seq. No.
Seq. ID
                   nbm700473054.h1
                   BLASTX
Method
                   g286122
NCBI GI
                   219
BLAST score
                   6.0e-36
E value
Match length
                   77
                   93
% identity
                  (D14576) glutamine synthetase [Zea mays]
NCBI Description
                   303840
Seq. No.
Seq. ID
                   nbm700473113.h1
Method
                   BLASTX
                   g4512667
NCBI GI
                   179
BLAST score
                   1.0e-13
E value
Match length
                   40
                   85
% identity
                  (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
                   303841
Seq. No.
                   nbm700473245.h1
Seq. ID
                   BLASTX
Method
                   g2191150
NCBI GI
                   144
BLAST score
                   3.0e-09
E value
                   94
Match length
                   40
% identity
                   (AF007269) similar to mitochondrial carrier family
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   303842
                   nbm700473253.h1
Seq. ID
Method
                   BLASTX
                   g3228517
NCBI GI
```

```
76
Match length
                   83
% identity
                   (AF007788) ETTIN [Arabidopsis thaliana]
NCBI Description
                   303843
Seq. No.
                   nbm700473276.h1
Seq. ID
                   BLASTN
Method
                   q293888
NCBI GI
                   180
BLAST score
E value
                   6.0e-97
Match length
                   191
                   99
 % identity
                   Zea mays, glyceraldehyde-3-phosphate dehydrogenase mRNA, 3'
NCBI Description
                   end (clone GAPC2)
 Seq. No.
                   303844
                   nbm700473315.h1
 Seq. ID
Method
                   BLASTN
                   q4206305
 NCBI GI
 BLAST score
                   43
                   5.0e-15
 E value
 Match length
                   199
                   80
 % identity
                   Zea mays retrotransposon Cinful-1, complete sequence
 NCBI Description
                   303845
 Seq. No.
                   nbm700473376.h1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q1076746
 BLAST score
                   205
                    2.0e-29
 E value
 Match length
                    92
 % identity
                    80
                   heat shock protein 70 - rice (fragment)
 NCBI Description
                    >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                    [Oryza sativa]
                    303846
 Seq. No.
                    nbm700473459.h1
 Seq. ID
                   BLASTX
 Method
                    g3800878
 NCBI GI
 BLAST score
                    334
                    2.0e-31
 E value
                    82
 Match length
                    79
 % identity
                    (AF096281) threonine dehydratase/deaminase [Arabidopsis
 NCBI Description
                    thaliana]
```

nbm700473523.h1 Seq. ID

Method BLASTX g3337352 NCBI GI BLAST score 215 2.0e-17 E value Match length 66 67 % identity

(AC004481) putative chromatin structural protein Supt5hp NCBI Description



[Arabidopsis thaliana]

```
Seq. No.
                  303848
Seq. ID
                  nbm700473524.hl
Method
                  BLASTX
                  q225587
NCBI GI
BLAST score
                  284
                  9.0e-37
E value
                  91
Match length
% identity
NCBI Description tubulin alpha [Physarum sp.]
                   303849
Seq. No.
                  nbm700473563.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2583129
BLAST score
                   162
E value
                   2.0e-21
Match length
                   59
                   93
% identity
                  (AC002387) putative methionine aminopeptidase [Arabidopsis
NCBI Description
                   thaliana]
                   303850
Seq. No.
                   nbm700473580.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3860277
BLAST score
                   142
E value
                   3.0e-09
Match length
                   35
% identity
                   77
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi 4314394 gb_AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                   303851
                   nbm700473589.h1
Seq. ID
                   BLASTX
Method
                   g2914706
NCBI GI
BLAST score
                   219
                   4.0e-18
E value
Match length
                   61
                   59
% identity
                   (AC003974) putative homeobox protein [Arabidopsis thaliana]
NCBI Description
                   303852
Seq. No.
                   nbm700473737.h1
Seq. ID
                   BLASTX
Method
                   g2492526
NCBI GI
BLAST score
                   272
E value
                   3.0e-24
Match length
                   84
                   32
% identity
                   HYPOTHETICAL 93.1 KD PROTEIN YLL034C
NCBI Description
                   >gi_2131732_pir__S64785 hypothetical protein YLL034c -
                   yeast (Saccharomyces cerevisiae) >gi 1360222 emb CAA97483
```

(Z73139) ORF YLL034c [Saccharomyces cerevisiae]

```
303853
Seq. No.
                  nbm700473744.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4581164
BLAST score
                  151
                  5.0e-10
E value
                  64
Match length
% identity
NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]
                  303854
Seq. No.
Seq. ID
                  nbm700473775.h1
                  BLASTN
Method
                  g168456
NCBI GI
BLAST score
                  127
E value
                  2.0e-65
                  164
Match length
                  95
% identity
NCBI Description Z.mays cell wall protein mRNA, 3' end
                  303855
Seq. No.
Seq. ID
                  nbm700473780.hl
                  BLASTX
Method
                  g3776025
NCBI GI
                   292
BLAST score
                   1.0e-26
E value
                   71
Match length
% identity
NCBI Description (AJ010474) RNA helicase [Arabidopsis thaliana]
                   303856
Seq. No.
                   nbm700473794.hl
Seq. ID
                   BLASTX
Method
                   g130186
NCBI GI
BLAST score
                   387
                   6.0e-39
E value
Match length
                   95
% identity
                   PHYTOCHROME A >gi_82715_pir__JQ0382 phytochrome A - maize
NCBI Description
                   303857
Seq. No.
                   nbm700473847.h1
Seq. ID
                   BLASTX
Method
                   q1839188
NCBI GI
                   215
BLAST score
                   7.0e-18
E value
                   59
Match length
                   66
% identity
                   (U86081) root hair defective 3 [Arabidopsis thaliana]
NCBI Description
                   303858
Seq. No.
                   nbm700473907.h1
Seq. ID
                   BLASTX
Method
                   g3319340
NCBI GI
```

42964

189

2.0e-14

BLAST score E value



```
63
Match length
                   60
% identity
                   (AF077407) contains similarity to E. coli cation transport
NCBI Description
                   protein ChaC (GB:D90756) [Arabidopsis thaliana]
                   303859
Seq. No.
                   nbm700473979.hl
Seq. ID
                   BLASTX
Method
                   g1175470
NCBI GI
BLAST score
                   142
                   5.0e-09
E value
Match length
                   46
                   54
% identity
                   HYPOTHETICAL 37.3 KD PROTEIN C22G7.10 IN CHROMOSOME I
NCBI Description
                   >gi 2130331 pir S62454 hypothetical protein SPAC22G7.10 -
                   fission yeast (Schizosaccharomyces pombe)
                   >gi_1009460_emb_CAA91134.1_ (Z54328) hypothetical protein
                   [Schizosaccharomyces pombe]
Seq. No.
                   303860
                   nbm700473991.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4185740
BLAST score
                   274
                   2.0e-24
E value
Match length
                   73
% identity
                    (AF079999) putative glutamate receptor [Arabidopsis
NCBI Description
                   thaliana]
                   303861
Seq. No.
                   nbm700474023.h1
Seq. ID
                   BLASTX
Method
                   g1706473
NCBI GI
                    191
BLAST score
                    5.0e-15
E value
Match length
                    36
                    100
% identity
                   DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40)
NCBI Description
                    (HSP40) >gi 542840 pir__JN0912 heat-shock protein hsp40 -
                    human >gi_575891_dbj_BAA08495_ (D49547) HSP40 [Homo sapiens] >gi_1816452_dbj_BAA12819_ (D85429) heat shock
                    protein 40 [Homo sapiens]
                    303862
Seq. No.
                    nbm700474077.h1
Seq. ID
Method
                    BLASTN
```

Method BLASTN
NCBI GI g1143704
BLAST score 46
E value 2.0e-17
Match length 82
% identity 95

NCBI Description Z.mays mRNA for homeobox 2a protein

Seq. No. 303863

Seq. ID nbm700474104.h1

Method BLASTX



```
q113621
NCBI GI
                  166
BLAST score
                  4.0e-12
E value
Match length
                  33
% identity
                  97
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                  >gi 68196_pir__ADZM fructose-bisphosphate aldolase (EC
                  4.1.2.13), cytosolic - maize >gi 168420 (M16220) aldolase
                  [Zea mays] >qi 295850 emb CAA31366 (X12872) fructose
                  bisphosphate aldolase [Zea mays] >gi_225624 prf__1307278A
                  cytoplasmic aldolase [Zea mays]
Seq. No.
                  303864
                  nbm700474207.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2317902
BLAST score
                  212
E value
                  1.0e-17
Match length
                  64
% identity
                  (U89959) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  303865
Seq. ID
                  nbm700474287.h1
Method
                  BLASTX
NCBI GI
                  g4567095
BLAST score
                  144
E value
                  1.0e-09
Match length
                  55
% identity
                   (AF129516) fertilization-independent endosperm protein
NCBI Description
                   [Arabidopsis thaliana]
                  303866
Seq. No.
                  nbm700474296.h1
Seq. ID
                  BLASTX
Method
                  g4006926
NCBI GI
BLAST score
                  155
                  7.0e-11
E value
Match length
                  36
% identity
                   69
                  (Z99708) putative protein (fragment) [Arabidopsis thaliana]
NCBI Description
                  303867
Seq. No.
                  nbm700474475.h1
Seq. ID
                  BLASTN
Method
                  g4519189
NCBI GI
BLAST score
                   42
                  1.0e-14
E value
Match length
                  70
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
```

NCBI Description

Seq. No. 303868

Seq. ID nbm700474509.h1

Method BLASTX

42966

K5A21, complete sequence

% identity

48



```
g4567283
NCBI GI
                  152
BLAST score
E value
                   2.0e-10
Match length
                   33
% identity
                   79
                  (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303869
                  nbm700474581.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3650465
BLAST score
                   160
                   7.0e-85
E value
                   263
Match length
                   97
% identity
                   Zea mays histone deacetylase HD2-p39 (HD2) gene, complete
NCBI Description
                   303870
Seq. No.
Seq. ID
                   nbm700474862.h1
Method
                   BLASTX
NCBI GI
                   q4115377
BLAST score
                   226
                   7.0e-19
E value
                   70
Match length
                   67
% identity
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   303871
Seq. No.
                   nbm700474941.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2827514
BLAST score
                   336
                   8.0e-32
E value
Match length
                   91
% identity
                   69
                   (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                   303872
Seq. No.
                   nbm700474976.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4582435
BLAST score
                   145
                   1.0e-09
E value
                   39
Match length
                   64
% identity
                   (AC007196) putative selenium-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   303873
Seq. No.
                   nbm700474991.h1
Seq. ID
                   BLASTX
Method
                   g4586105
NCBI GI
                   152
BLAST score
                   7.0e-18
E value
                   88
Match length
```



```
(AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
                  303874
Seq. No.
                  nbm700474995.h1
Seq. ID
Method
                  BLASTX
                  q1703115
NCBI GI
                  170
BLAST score
                  2.0e-12
E value
Match length
                  32
% identity
                  100
                  ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis
NCBI Description
                  thaliana >gi_1145695 (U\overline{39}480) actin [Arabidopsis thaliana]
                  >gi 3236244 (AC004684) actin 3 protein (Arabidopsis
                  thaliana]
Seq. No.
                  303875
Seq. ID
                  nbm700475096.hl
Method
                  BLASTX
                  q100489
NCBI GI
BLAST score
                  142
E value
                  5.0e-09
Match length
                  96
% identity
                  29
                  transposase Tam3 - garden snapdragon transposon Tam3
NCBI Description
                  >gi 16064 emb CAA38906 (X55078) Tam3-transposase
                  [Antirrhinum majus] >gi 3219237 dbj BAA28817.1_ (AB013982)
                  transposase [Antirrhinum majus] >gi_3219239_dbj_BAA28818.1_
                  (AB013983) transposase [Antirrhinum majus]
                  >gi_3219241_dbj_BAA28819.1_ (AB013984) transposase
                  [Antirrhinum majus] >gi 3219244 dbj_BAA28820.1_ (AB013986)
                  transposase [Antirrhinum majus] >gi_3219249_dbj_BAA28821.1_
                  (AB013990) transposase [Antirrhinum majus]
                  >qi 3219251 dbj BAA28822.1 (AB013991) transposase
                  [Antirrhinum majus] >gi 3219256_dbj_BAA28823.1_ (AB013995)
                  transposase [Antirrhinum majus] > gi_3219259_dbj_BAA28824.1_
                  (AB013997) transposase [Antirrhinum majus]
                  303876
Seq. No.
                  nbm700475208.h1
Seq. ID
Method
                  BLASTX
                  g553073
NCBI GI
BLAST score
                  364
                  5.0e-35
E value
Match length
                  90
                  83
% identity
NCBI Description
                  (M94481) reverse transcriptase [Zea mays]
                  303877
Seq. No.
                  nbm700475328.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  180
                  2.0e-13
E value
```

36 Match length 100 % identity

GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN NCBI Description

>gi 82685 pir S04536 embryonic abundant protein,

Seq. ID Method

NCBI GI

E value

Seq. No.

Seq. ID Method

NCBI GI

E value

BLAST score

Match length

% identity

Seq. No.

Seq. ID Method

NCBI GI

E value Match length

BLAST score

% identity

Seq. No.

Seq. ID

Method

NCBI GI BLAST score

E value Match length

% identity

BLAST score

Match length

% identity



```
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
                  303878
                  nbm700475374.h1
                  BLASTX
                  q3738339
                  176
                  5.0e-13
                  55
                  71
                  (AC005170) putative kinase [Arabidopsis thaliana]
NCBI Description
                  303879
                  nbm700475383.h1
                  BLASTN
                  q602252
                  71
                  3.0e - 32
                  111
                  92
                  Zea mays enolase (eno2) mRNA, complete cds
NCBI Description
                  303880
                  nbm700475429.h1
                  BLASTX
                  g4581164
                  165
                  1.0e-11
                  62
                  50
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
NCBI Description
                  303881
                  nbm700475439.h1
                  BLASTN
                  g3687405
                  42
                  1.0e-14
                  54
                  94
NCBI Description Lycopersicon esculentum mRNA for hypothetical protein
                   303882
                  nbm700475440.h1
                  BLASTX
                   g1076634
                   314
```

Seq. No.

Seq. ID

Method NCBI GI BLAST score E value 3.0e-29 Match length 76 80 % identity

protein-serine/threonine kinase NPK15 - common tobacco NCBI Description >qi 505146 dbj BAA06538 (D31737) protein-serine/threonine

kinase [Nicotiana tabacum]



```
nbm700475549.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829910
BLAST score
                  146
                  2.0e-09
E value
Match length
                  51
% identity
                  ,53
                  (ACO02291) Unknown protein, contains regulator of
NCBI Description
                  chromosome condensation motifs [Arabidopsis thaliana]
                   303884
Seq. No.
                  nbm700475670.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760844
BLAST score
                   281
E value
                   3.0e-25
Match length
                   102
% identity
                   (AC003105) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303885
                   nbm700475674.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3776029
BLAST score
                   254
E value
                   4.0e-22
Match length
                   58
% identity
                   (AJ010476) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303886
                   nbm700475846.h1
Seq. ID
                   BLASTX
Method
                   g1709129
NCBI GI
BLAST score
                   387
                   1.0e-37
E value
                   96
Match length
                   74
% identity
                   GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3
NCBI Description
                   >gi_481018_pir__S37642 protein kinase MSK-3 (EC 2.7.1.-) -
                   alfalfa >gi_313148_emb_CAA48472_ (X68409) protein kinase
                   [Medicago sativa]
                   303887
Seq. No.
                   nbm700475866.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4415929
BLAST score
                   231
E value
                   2.0e-19
Match length
                   97
% identity
                   45
                   (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303888
Seq. ID
                   nbm700475904.h1
Method
                   BLASTX
```

```
g4502325
NCBI GI
                  257
BLAST score
                  2.0e-22
E value
                  84
Match length
                  63
% identity
                  ataxia telangiectasia and Rad3 related
NCBI Description
                  >gi 1653996 emb CAA70298 (Y09077) atr [Homo sapiens]
                  >qi 1666240 (U76308) protein kinase ATR [Homo sapiens]
                   303889
Seq. No.
Seq. ID
                  nbm700475913.h1
Method
                  BLASTX
                  g3982634
NCBI GI
                  454
BLAST score
                   1.0e-45
E value
                  88
Match length
                   100
% identity
NCBI Description (AF056161) disease resistance gene analog PIC21 [Zea mays]
                   303890
Seq. No.
                  nbm700475925.h1
Seq. ID
                   BLASTX
Method
                   g2213643
NCBI GI
                   155
BLAST score
                   8.0e-11
E value
                   38
Match length
                   84
% identity
NCBI Description (U57338) glossyl homolog [Oryza sativa]
                   303891
Seq. No.
                   nbm700475984.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q113334
                   250
BLAST score
                   9.0e-22
E value
                   83
Match length
% identity
                   ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2
NCBI Description
                   ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A)
                   (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT)
                   >gi 90291_pir__A30111 alpha-adaptin A - mouse
                   >qi 49878 emb CAA33096 (X14971) alpha-adaptin (A) (AA
                   1-977) [Mus musculus]
                   303892
Seq. No.
                   nbm700476035.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3402697
                   309
BLAST score
                   1.0e-28
E value
                   88
Match length
                   69
% identity
                   (AC004261) putative phosphatidylinositol-4-phosphate
NCBI Description
```

5-kinase [Arabidopsis thaliana]

303893

nbm700476038.h1

Seq. No.

Seq. ID

```
BLASTN
Method
                  ·g474009
NCBI GI
                  70
BLAST score
                  3.0e - 31
E value
                  98
Match length
                  93
% identity
                  Rice mRNA, partial homologous to ribosomal protein S19 gene
NCBI Description
Seq. No.
                  303894
                  nbm700476093.h1
Seq. ID
                  BLASTX
Method
                  g4138131
NCBI GI
                  173
BLAST score
                   1.0e-12
E value
Match length
                  72
% identity
                  50
                  (AJ011828) NDX1 homeobox protein [Lotus japonicus]
NCBI Description
                   303895
Seq. No.
                   nbm700476111.hl
Seq. ID
Method
                   BLASTX
                   q3043415
NCBI GI
BLAST score
                   391
                   4.0e-38
E value
Match length
                   76
% identity
                   97
                   (Y17053) At-hsc70-3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303896
                   nbm700476125.h1
Seq. ID
Method
                   BLASTX
                   q1871195
NCBI GI
BLAST score
                   334
                   2.0e-31
E value
                   100
Match length
% identity
                   60
                   (U90439) Ca++ dependent protein kinase isolog [Arabidopsis
NCBI Description
                   thaliana] >gi 2335093 (AC002339) putative calcium-dependent
                   protein kinase [Arabidopsis thaliana]
                   303897
Seq. No.
                   nbm700476233.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3152572
BLAST score
                   183
                   4.0e-14
E value
Match length
                   53
                   75
% identity
                   (AC002986) Contains homology to DNAJ heatshock protein
NCBI Description
                   gb U32803 from Haemophilus influenzae. [Arabidopsis
                   thaliana]
```

Seq. ID nbm700476288.h1

Method BLASTX
NCBI GI g3193224
BLAST score 158



```
7.0e-11
E value
Match length
                   55
% identity
                   60
                  (AF068271) mutL homolog PMS2 [Drosophila melanogaster]
NCBI Description
                  303899
Seq. No.
                  nbm700476350.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4105131
BLAST score
                   194
                   4.0e-15
E value
                   45
Match length
                   82
% identity
NCBI Description
                  (AF043539) ClpC protease [Spinacia oleracea]
                   303900
Seq. No.
                   nbm700476390.h1
Seq. ID
                   BLASTN
Method
                   g349717
NCBI GI
                   75
BLAST score
                   1.0e-34
E value
                   79
Match length
                   99
% identity
                   Zea mays cytochrome P-450 (cyp78) mRNA, complete cds
NCBI Description
                   303901
Seq. No.
                   nbm700476588.h1
Seq. ID
                   BLASTX
Method
                   q4580395
NCBI GI
BLAST score
                   189
                   1.0e-14
E value
Match length
                   47
                   72
% identity
                   (AC007171) putative kinesin-related protein [Arabidopsis
NCBI Description
                   thaliana]
                   303902
Seq. No.
                   nbm700476624.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2462744
BLAST score
                   215
                   1.0e-17
E value
                   95
Match length
                   43
% identity
                  (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   303903
Seq. No.
                   nbm700476671.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3152595
BLAST score
                   304
                   5.0e-28
E value
                   91
Match length
% identity
                   64
                   (AC002986) Similar to D. melanogaster sno gene gb_U95760.
NCBI Description
```

[Arabidopsis thaliana]

EST gb N97148 and gb Z26221 come from this gene.

Seq. ID nbm700476677.h1

Method BLASTX
NCBI GI g1698582
BLAST score 289
E value 3.0e-26
Match length 73
% identity 81

NCBI Description (U60767) integral membrane protein OsNramp3 [Oryza sativa]

Seq. No. 303905

Seq. ID nbm700476693.h1

Method BLASTX
NCBI GI g3915519
BLAST score 400
E value 3.0e-39
Match length 92
% identity 83

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE CO4H5.6

>gi_3873886_emb_CAB03819_ (Z81457) similar to Helicases conserved C-terminal domain; cDNA EST yk272f1.3 comes from this gene; cDNA EST yk410g7.3 comes from this gene; cDNA EST yk410g7.5 comes from this gene; cDNA EST yk316b6.3 comes from this gene; cDNA... >gi_3873945_emb_CAB03845_ (Z81462) similar to Helicases conserved C-terminal domain; cDNA EST yk272f1.3 comes from this gene; cDNA EST yk410g7.3 comes from this gene; cDNA EST yk410g7.3

gene; cDNA EST yk316b6.3 comes from this gene; cDNA

Seq. No. 303906

Seq. ID nbm700476718.h1

Method BLASTN
NCBI GI g4160401
BLAST score 45

E value 3.0e-16
Match length 61
% identity 93

NCBI Description Zea mays eIF-5 gene, exons 1-2

303907

Seq. No.

Seq. ID nbm700476753.h1

Method BLASTX
NCBI GI g2529678
BLAST score 212
E value 2.0e-17
Match length 68
% identity 65

NCBI Description (AC002535) unknown protein [Arabidopsis thaliana]

Seq. No. 303908

Seq. ID nbm700476781.h1

Method BLASTX
NCBI GI g3413719
BLAST score 180
E value 2.0e-13
Match length 53

```
% identity
                   (AC004747) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 3643592 (AC005395) unknown protein [Arabidopsis
                  thaliana]
                  303909
Seq. No.
                  nbm700476822.h1
Seq. ID
                  BLASTX
Method
                  g1353239
NCBI GI
BLAST score
                  192
                  3.0e-15
E value
Match length
                  56
% identity
                   61
                  (U10245) putative RNA helicase A [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303910
                  nbm700476828.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4539470
BLAST score
                   179
E value
                   2.0e-13
Match length
                   73
% identity
                   49
                  (AL049500) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303911
                   nbm700476837.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g551444
BLAST score
                   392
                   3.0e-38
E value
Match length
                   97
                   75
% identity
                  (X79365) protein MFP-b [Cucumis sativus]
NCBI Description
                   303912
Seq. No.
                   nbm700477049.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3420753
                   299
BLAST score
                   2.0e-27
E value
Match length
                   95
                   60
% identity
                   (AF079449) TBP-associated factor A [Dictyostelium
NCBI Description
                   discoideum]
                   303913
Seq. No.
                   nbm700477113.h1
Seq. ID
Method
                   BLASTX
```

NCBI GI g1421730
BLAST score 173
E value 6.0e-13
Match length 40
% identity 75

NCBI Description (U43082) RF2 [Zea mays]

Seq. No. 303914

BLAST score

E value Match length 215 1.0e-17

93



```
nbm700477150.h1
Seq. ID
                  BLASTX
Method
                  g4090259
NCBI GI
                  296
BLAST score
                  5.0e-27
E value
Match length
                  100
% identity
                  (AJ131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga
NCBI Description
                  menziesii]
                  303915
Seq. No.
                  nbm700477184.h1
Seq. ID
                  BLASTN
Method
                  g168480
NCBI GI
BLAST score
                  145
                   4.0e-76
E value
Match length
                  169
                   76
% identity
NCBI Description Maize embryo globulin S allele (7S-like) mRNA, complete cds
                   303916
Seq. No.
Seq. ID
                   nbm700477280.h1
                   BLASTX
Method
                   g2589164
NCBI GI
                   187
BLAST score
                   1.0e-14
E value
Match length
                   39
                   97
% identity
                  (D88452) aldehyde oxidase-2 [Zea mays]
NCBI Description
Seq. No.
                   303917
Seq. ID
                   nbm700477309.h1
Method
                   BLASTX
                   q729671
NCBI GI
BLAST score
                   193
E value
                   2.0e-25
Match length
                   98
% identity
                   60
                  HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]
NCBI Description
                   303918
Seq. No.
                   nbm700477435.h1
Seq. ID
                   BLASTX
Method
                   g4580397
NCBI GI
                   195
BLAST score
                   3.0e-15
E value
Match length
                   51
                   71
% identity
                   (AC007171) putative RNA helicase [Arabidopsis thaliana]
NCBI Description
                   303919
Seq. No.
                   nbm700477580.h1
Seq. ID
                   BLASTX
Method
                   g4585981
NCBI GI
```

```
% identity
                   (AC005287) similar to Na+/H+-exchanging proteins
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  303920
                  nbm700477672.h1
Seq. ID
                  BLASTX
Method
                  g3169835
NCBI GI
BLAST score
                  159
E value
                   4.0e-11
Match length
                  35
                  89
% identity
                  (AF031353) heat shock protein 70 [Euplotes aediculatus]
NCBI Description
Seq. No.
                   303921
                  nbm700477745.h1
Seq. ID
Method
                  BLASTX
                   q4008159
NCBI GI
BLAST score
                   185
E value
                   4.0e-14
Match length
                   40
% identity
                   90
                  (AB015601) DnaJ homolog [Salix gilgiana]
NCBI Description
                   303922
Seq. No.
Seq. ID
                   nbm700477842.h1
Method
                   BLASTX
NCBI GI
                   g3885341
BLAST score
                   238
                   3.0e-20
E value
                   87
Match length
                   49
% identity
                  (AC005623) unknown protein [Arabidopsis thaliana]
NCBI Description
                   303923
Seq. No.
                   nbm700477929.h1
Seq. ID
                   BLASTX
Method
                   g21479
NCBI GI
BLAST score
                   317
E value
                   1.0e-29
Match length
                   60
                   98
% identity
                  (Z11985) 70-Kd heat shock protein [Solanum tuberosum]
NCBI Description
                   303924
Seq. No.
                   nbm700477946.h1
Seq. ID
                   BLASTX
Method
                   g4469009
NCBI GI
BLAST score
                   295
                   6.0e-27
E value
Match length
                   71
                   77
% identity
                   (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. ID nbm700478010.h1

Method BLASTX

```
g4587553
NCBI GI
                  148
BLAST score
                  2.0e-11
E value
Match length
                  84
% identity
                  54
                  (AC006577) F15I1.20 [Arabidopsis thaliana]
NCBI Description
                  303926
Seq. No.
                  nbm700478035.h1
Seq. ID
                  BLASTX
Method
                  g1709619
NCBI GI
                   227
BLAST score
                   6.0e-24
E value
                   87
Match length
% identity
                   63
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
NCBI Description
                   DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
                   (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
                   >gi 2146814_pir__S69181 protein disulfide isomerase (EC
                   5.3.4.1) precursor - maize >gi 625148 (L39014) protein
                   disulfide isomerase [Zea mays]
                   303927
Seq. No.
                   nbm700478058.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g296593
BLAST score
                   55
                   3.0e-22
E value
Match length
                   75
                   93
% identity
NCBI Description H. vulgare pZE40 gene
                   303928
Seq. No.
                   ntr700071604.h1
Seq. ID
                   BLASTX
Method
                   g2660670
NCBI GI
                   304
BLAST score
                   5.0e-28
E value
Match length
                   84
                   39
% identity
                   (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
NCBI Description
                   thaliana]
                   303929
Seq. No.
                   ntr700071690.h1
Seq. ID
                   BLASTN
Method
```

Method BLASTN
NCBI GI g2894376
BLAST score 63
E value 5.0e-27
Match length 207
% identity 83

NCBI Description Hordeum vulgare DNA for chromosome 4H

Seq. No. 303930

Seq. ID ntr700071723.h1

Method BLASTX NCBI GI g2244749



```
273
BLAST score
                  2.0e-24
E value
                  55
Match length
                  93
% identity
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
                  303931
Seq. No.
                  ntr700071849.h1
Seq. ID
                  BLASTX
Method
                  g2495171
NCBI GI
                  185
BLAST score
                   4.0e-14
E value
                   57
Match length
                   70
% identity
                  DELTA-AMINOLEVULINIC ACID DEHYDRATASE PRECURSOR
NCBI Description
                   (PORPHOBILINOGEN SYNTHASE) (ALADH)
                   >gi_1041423_emb_CAA63139_ (X92402) aminolevulinate
                   dehydratase [Hordeum vulgare]
                   303932
Seq. No.
                   ntr700071887.h1
Seq. ID
                   BLASTN
Method
                   g440170
NCBI GI
BLAST score
                   189
                   1.0e-102
E value
                   197
Match length
                   99
% identity
                   Z.mays (C6000237) trpA gene
NCBI Description
                   303933
Seq. No.
Seq. ID
                   ntr700071955.h1
                   BLASTX
Method
                   q3122753
NCBI GI
                   254
BLAST score
                   2.0e-22
E value
                   56
Match length
                   80
% identity
                   60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_
NCBI Description
                   (Z97336) ribosomal protein [Arabidopsis thaliana]
                   303934
Seq. No.
                   ntr700072044.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4115373
BLAST score
                   243
                   7.0e-21
E value
Match length
                   91
 % identity
                   (AC005967) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   303935
 Seq. No.
                   ntr700072052.h1
 Seq. ID
                   BLASTX
 Method
                   g66615
 NCBI GI
```

253

3.0e-22

BLAST score

E value

```
48
Match length
                  100
% identity
                  glutathione transferase (EC 2.5.1.18) I - maize
NCBI Description
Seq. No.
                  303936
                  ntr700072125.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1518673
BLAST score
                   54
                   1.0e-21
E value
Match length
                  70
                   94
% identity
                   Zea mays beta-D-glucosidase (glu1) gene, intron 4
NCBI Description
                   transposon 1, complete sequence
Seq. No.
                   303937
Seq. ID
                   ntr700072142.hl
Method
                   BLASTN
                   q451192
NCBI GI
                   45
BLAST score
                   3.0e-16
E value
Match length
                   103
% identity
                   88
                   Triticum aestivum (wali7) mRNA, 3' end, partial cds
NCBI Description
                   303938
Seq. No.
                   ntr700072148.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4335756
BLAST score
                   228
E value
                   4.0e-19
Match length
                   78
% identity
                   58
                   (AC006284) putative ankyrin [Arabidopsis thaliana]
NCBI Description
                   303939
Seq. No.
                   ntr700072242.h1
Seq. ID
                   BLASTX
Method
                   g3395440
NCBI GI
BLAST score
                   218
                   6.0e-18
E value
                   91
Match length
                   51
% identity
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   303940
Seq. No.
                   ntr700072255.h1
Seq. ID
                   BLASTX
Method
                   g3341679
NCBI GI
BLAST score
                   207
E value
                   1.0e-16
Match length
                   58
% identity
                   62
                   (AC003672) dynamin-like protein phragmoplastin 12
NCBI Description
                   [Arabidopsis thaliana]
```

```
ntr700072261.h1
Seq. ID
Method
                  BLASTX
                  g4263722
NCBI GI
BLAST score
                  291
                  2.0e-36
E value
                  93
Match length
                  80
% identity
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  303942
                  ntr700072265.h1
Seq. ID
                  BLASTX
Method
                  g1170373
NCBI GI
BLAST score
                  207
E value
                   6.0e-17
Match length
                   42
% identity
                  100
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir S46302
NCBI Description
                  heat shock cognate protein 70-1 - Arabidopsis thaliana
                  >gi 397482 emb CAA52684_ (X74604) heat shock protein 70
                  cognate [Arabidopsis thaliana]
                   303943
Seq. No.
Seq. ID
                  ntr700072303.h2
Method
                  BLASTX
NCBI GI
                   g2921304
BLAST score
                   171
E value
                   2.0e-12
Match length
                   55
% identity
                   64
                   (AF033496) herbicide safener binding protein [Zea mays]
NCBI Description
                   303944
Seq. No.
                   ntr700072312.h2
Seq. ID
                   BLASTN
Method
                   g1256711
NCBI GI
BLAST score
                   78
                   5.0e-36
E value
                   195
Match length
                   87
% identity
                  Zea mays O-methyltransferase (OMT) gene, complete cds
NCBI Description
                   303945
Seq. No.
                   ntr700072316.h2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1184775
                   108
BLAST score
                   5.0e-54
E value
                   158
Match length
                   95
% identity
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4
NCBI Description
                   (gpc4) mRNA, complete cds
```

Seq. ID ntr700072326.h2

Method BLASTX NCBI GI g3264596

```
BLAST score
                   2.0e-10
E value
                   58
Match length
                   59
% identity
                  (AF057183) putative tonoplast aquaporin [Zea mays]
NCBI Description
                   303947
Seq. No.
                   ntr700072383.h1
Seq. ID
                   BLASTX
Method
                   g3510251
NCBI GI
BLAST score
                   285
                   9.0e-26
E value
                   97
Match length
% identity
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303948
Seq. ID
                   ntr700072486.h1
                   BLASTX
Method
                   g729135
NCBI GI
                   207
BLAST score
E value
                   1.0e-16
Match length
                   69
                   65
% identity
                   CAFFEIC ACID 3-O-METHYLTRANSFERASE
NCBI Description
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi 283034_pir___$28612
                   catechol O-methyltransferase (EC \overline{2}.1.1.6) - maize
                   >gi 168532 (M73235) O-methyltransferase [Zea mays]
                   303949
Seq. No.
Seq. ID
                   ntr700072490.h1
Method
                   BLASTX
NCBI GI
                   q3242717
BLAST score
                   179
                   2.0e-13
E value
                   70
Match length
% identity
                   50
                   (AC003040) putative APG protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   303950
                   ntr700072496.hl
Seq. ID
Method
                   BLASTN
                   q3821780
NCBI GI
                   35
BLAST score
                   2.0e-10
E value
                   35
Match length
                   100
% identity
                   Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   303951
Seq. No.
```

 Seq. ID
 ntr700072555.h1

 Method
 BLASTN

 NCBI GI
 g4007864

 BLAST score
 256

 E value
 1.0e-142

Match length 284

```
% identity
NCBI Description
                  Zea mays HRGP gene, AC1503 line
                  303952
Seq. No.
Seq. ID
                  ntr700072563.h1
Method
                  BLASTX
NCBI GI
                  g465012
                  169
BLAST score
                   5.0e-12
E value
                   48
Match length
% identity
                   URICASE II CLONE PCCLNUO-02 (URATE OXIDASE)
NCBI Description
                   >gi 1086285 pir S38910 uricase - Canavalia lineata
                   >gi_432631_emb_CAA53905_ (X76287) uricase [Canavalia
                   lineata]
Seq. No.
                   303953
Seq. ID
                   ntr700072595.h1
                   BLASTX
Method
NCBI GI
                   g2388580
BLAST score
                   489
E value
                   1.0e-49
                   97 1
Match length
                   85
% identity
NCBI Description (AC000098) Similar to Sequence 10 from patent 5477002
                   (gb_1253956). [Arabidopsis thaliana]
                   303954
Seq. No.
                   ntr700072614.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4376203
BLAST score
                   272
                   3.0e-24
E value
Match length
                   82
% identity
                   63
                   (U35226) putative cytochrome P-450 [Nicotiana
NCBI Description
                   plumbaginifolia]
                   303955
Seq. No.
                   ntr700072650.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2632105
                   415
```

BLAST score 6.0e-41 E value 103 Match length 75 % identity

(Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana] NCBI Description >gi 4539426 emb CAB38959.1_ (AL049171) arginyl-tRNA

synthetase [Arabidopsis thaliana]

303956 Seq. No. Seq. ID ntr700072660.h1 Method BLASTX g4006861 NCBI GI BLAST score 161 E value 3.0e-11 Match length 101

```
% identity
                  (Z99707) tubulin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  303957
                  ntr700072702.h1
Seq. ID
                  BLASTX
Method
                  q3056725
NCBI GI
                  257
BLAST score
                  2.0e-22
E value
Match length
                  115
% identity
                  43
                  (AF034774) ent-kaurene synthase [Arabidopsis thaliana]
NCBI Description
                  303958
Seq. No.
Seq. ID
                  ntr700072713.h1
Method
                  BLASTX
NCBI GI
                  g4455287
BLAST score
                  241
                  2.0e-20
E value
Match length
                  89
% identity
                  56
NCBI Description (AL035527) putative protein [Arabidopsis thaliana]
                  303959
Seq. No.
                  ntr700072718.h1
Seq. ID
Method
                  BLASTX
                  g130186
NCBI GI
BLAST score
                  225
E value
                  1.0e-18
                  45
Match length
                  100
% identity
                  PHYTOCHROME A >gi_82715_pir__JQ0382 phytochrome A - maize
NCBI Description
                  303960
Seq. No.
                  ntr700072744.h1
Seq. ID
Method
                  BLASTX
                  g2589164
NCBI GI
BLAST score
                  281
                  2.0e-28
E value
                  107
Match length
% identity
                  58
                  (D88452) aldehyde oxidase-2 [Zea mays]
NCBI Description
```

Seq. ID ntr700072748.h1

303961

Method BLASTX
NCBI GI g1354849
BLAST score 259
E value 1.0e-22
Match length 74
% identity 62

NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No. 303962

Seq. ID ntr700072753.h1

Method BLASTX NCBI GI g113217

```
BLAST score
                  333
                  3.0e-31
E value
Match length
                  63
                  100
% identity
NCBI Description ACTIN 1 >gi_100149_pir S07002 actin 1 - carrot
                  303963
Seq. No.
                  ntr700072755.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4098238
BLAST score
                  184
                   6.0e-14
E value
                  59
Match length
% identity
                  (U76384) o-methyltransferase [Triticum aestivum]
NCBI Description
                   303964
Seq. No.
Seq. ID
                  ntr700072794.hl
                  BLASTN
Method
                   g3043528
NCBI GI
BLAST score
                   189
E value
                   1.0e-102
                   280
Match length
                   96
% identity
                  Zea mays mRNA for flavin containing polyamine oxidase (PAO)
NCBI Description
Seq. No.
                   303965
                   ntr700072802.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q629641
BLAST score
                   226
                   8.0e-19
E value
Match length
                   53
% identity
                   PsHSC71.0 protein - garden pea >gi_1076530_pir__S53500
NCBI Description
                   HSC71.0 protein - garden pea >gi_473217_emb_CAA83548_
                   (Z32537) PsHSC71.0 [Pisum sativum]
                   303966
Seq. No.
                   ntr700072840.hl
Seq. ID
Method
                   BLASTX
                   g2129636
NCBI GI
BLAST score
                   140
                   4.0e-12
E value
                   80
Match length
                   40
% identity
                   lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase
NCBI Description
                   [Arabidopsis thaliana]
                   303967
Seq. No.
                   ntr700072861.h1
Seq. ID
                   BLASTX
Method
                   g4558552
NCBI GI
                   306
BLAST score
                   3.0e-28
E value
```

100

28

Match length % identity



```
(AC007138) putative P-glycoprotein-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  303968
Seq. No.
Seq. ID
                  ntr700072875.hl
Method
                  BLASTX
                  g2462826
NCBI GI
                  151
BLAST score
                  5.0e-10
E value
                  72
Match length
                  47
% identity
NCBI Description (AF000657) unknown protein [Arabidopsis thaliana]
                  303969
Seq. No.
                  ntr700072876.h1
Seq. ID
                  BLASTX
Method
                  g4588001
NCBI GI
                  261
BLAST score
                   6.0e-23
E value
                  76
Match length
                   70
% identity
                  (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   303970
Seq. No.
                  ntr700072922.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4079809
                   149
BLAST score
                   8.0e-10
E value
                   60
Match length
% identity
                   43
NCBI Description (AF071172) HERC2 [Homo sapiens]
                   303971
Seq. No.
                   ntr700072993.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4454471
                   426
BLAST score
                   3.0e-42
E value
                   104
Match length
% identity
                   74
                   (ACO06234) putative G protein coupled receptor [Arabidopsis
NCBI Description
                   thaliana]
                   303972
Seq. No.
                   ntr700073057.hl
Seq. ID
                   BLASTX
Method
                   g1707364
NCBI GI
BLAST score
                   316
                   3.0e-29
E value
Match length
                   76
 % identity
                   76
                   (X94626) AATP2 [Arabidopsis thaliana]
NCBI Description
```

303973

ntr700073062.h1

Seq. No.

Seq. ID

```
BLASTX
Method
                  g3834316
NCBI GI
                  209
BLAST score
E value
                   2.0e-28
Match length
                  89
% identity
                   65
                   (AC005679) Similar to gb X16648 pathogenesis related
NCBI Description
                  protein from Hordeum vulgare. EST gb_Z18206 comes from
                   this gene. [Arabidopsis thaliana]
                   303974
Seq. No.
                   ntr700073089.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4006918
BLAST score
                   317
E value
                   2.0e-29
Match length
                   105
% identity
                   (Z99708) peroxidase like protein [Arabidopsis thaliana]
NCBI Description
                   303975
Seq. No.
                   ntr700073167.hl
Seq. ID
                   BLASTX
Method
                   q4220480
NCBI GI
BLAST score
                   206
                   2.0e-16
E value
Match length
                   93
% identity
                   47
                   (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   303976
Seq. No.
Seq. ID
                   ntr700073177.h1
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   35
E value
                   1.0e-10
Match length
                   35
                   100
% identity
                   Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                   303977
Seq. ID
                   ntr700073207.h1
Method
                   BLASTX
                   g2984709
NCBI GI
                   289
BLAST score
                   3.0e-26
E value
Match length
                   98
% identity
                   63
                   (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                   303978
Seq. No.
                   ntr700073213.h1
 Seq. ID
                   BLASTX
Method
                   g3953479
NCBI GI
                   371
BLAST score
```

7.0e-36

93

E value Match length

```
75
% identity
NCBI Description (AC002328) F2202.24 [Arabidopsis thaliana]
                  303979
Seq. No.
                  ntr700073217.hl
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
                  34
BLAST score
                  1.0e-09
E value
                  34
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  303980
Seq. No.
                  ntr700073232.h1
Seq. ID
                  BLASTX
Method
                  g112947
NCBI GI
                  203
BLAST score
                  4.0e-16
E value
                  96
Match length
                  42
% identity
                  AAC-RICH MRNA CLONE AAC3 PROTEIN >gi_84121_pir__S05357
NCBI Description
                  hypothetical protein (clone AAC3) - slime mold
                   (Dictyostelium discoideum) (fragment)
                  >gi 7176_emb_CAA34531_ (X16524) coding region (AA 1 - 437)
                   [Dictyostelium discoideum]
                  303981
Seq. No.
                  ntr700073272.h1
Seq. ID
                  BLASTX
Method
                  g4115377
NCBI GI
                   256
BLAST score
                   2.0e-24
E value
                   70
Match length
                   84
% identity
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   303982
Seq. No.
                   ntr700073281.h1
Seq. ID
                   BLASTX
Method
                   g1346512
NCBI GI
                   147
BLAST score
                   1.0e-09
E value
                   91
Match length
                   31
% identity
                  ATP-DEPENDENT PERMEASE MDL1 >gi_1078101_pir__S51433 MDL1
NCBI Description
                   protein - yeast (Saccharomyces cerevisiae) >gi_577195
                   (U17246) Mdllp [Saccharomyces cerevisiae]
```

Seq. ID ntr700073309.h1

Method BLASTX
NCBI GI g4455284
BLAST score 304
E value 5.0e-28
Match length 95
% identity 54

```
(AL035527) beta-glucosidase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  303984
Seq. No.
                  ntr700073324.h1
Seq. ID
                  BLASTX
Method
                  g2190547
NCBI GI
                  405
BLAST score
                  7.0e-40
E value
                  97
Match length
                  76
% identity
                  (AC001229) ESTs
NCBI Description
                  gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb_AA404382 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                   303985
                  ntr700073329.h1
Seq. ID
                  BLASTN
Method
                  q22144
NCBI GI
BLAST score
                   165
                   7.0e-88
E value
                  283
Match length
                   90
% identity
                  Maize anaerobically regulated gene for fructose
NCBI Description
                   bisphosphate aldolase (EC 4.1.2.13)
                   303986
Seq. No.
Seq. ID
                   ntr700073333.h1
Method
                   BLASTX
                   g4056568
NCBI GI
                   272
BLAST score
                   3.0e-24
E value
                   57
Match length
                   95
% identity
                  (U90944) PDI-like protein [Zea mays]
NCBI Description
                   303987
Seq. No.
                   ntr700073372.h1
Seq. ID
                   BLASTX
Method
                   g4490706
NCBI GI
                   191
BLAST score
                   1.0e-14
E value
Match length
                   55
                   64
% identity
                  (AL035680) putative protein [Arabidopsis thaliana]
NCBI Description
                   303988
Seq. No.
                   ntr700073403.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q122007
BLAST score
                   199
                   1.0e-15
E value
                   42
Match length
                   95
% identity
                   HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
NCBI Description
                   >gi 20448 emb CAA37828 (X53831) H2A histone protein (AA 1
```

- 149) [Petroselinum crispum]

```
303989
Seq. No.
                  ntr700073422.h1
Seq. ID
                  BLASTN
Method
                  g1917018
NCBI GI
                  63
BLAST score
                  5.0e-27
E value
                  79
Match length
                  95
% identity
                  Zea mays ribosomal protein S6 RPS6-1 (rps6-1) mRNA,
NCBI Description
                  complete cds
                  303990
Seq. No.
                  ntr700073479.h1
Seq. ID
Method
                  BLASTX
                  g3785989
NCBI GI
                  242
BLAST score
                   5.0e-21
E value
Match length
                   60
                   72
% identity
                  (AC005560) unknown protein [Arabidopsis thaliana]
NCBI Description
                ~~303991
Seq. No.
                   ntr700073547.hl
Seq. ID
                   BLASTX
Method
                   g2293566
NCBI GI
BLAST score
                   207
                   3.0e-27
E value
Match length
                   79
                   86
% identity
                  (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
NCBI Description
                   303992
Seq. No.
                   ntr700073548.h1
Seq. ID
                   BLASTN
Method
                   g22312
NCBI GI
BLAST score
                   145
                   3.0e-76
E value
                   161
Match length
                   98
% identity
                   Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
                   303993
Seq. No.
                   ntr700073549.h1
Seq. ID
                   BLASTX
Method
                   g3004950
NCBI GI
                   376
BLAST score
                   2.0e-36
E value
                   68
Match length
                   100
 % identity
                   (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
NCBI Description
                   303994
 Seq. No.
                   ntr700073569.h1
 Seq. ID
                   BLASTN
 Method
NCBI GI
                   g168462
```



```
BLAST score
                  1.0e-153
E value
                  282
Match length
                  99
% identity
                  Zea mays defective suppressor-mutator from the
NCBI Description
                  brittle-1-mutable allele
                  303995
Seq. No.
                  ntr700073650.hl
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2199565
                  112
BLAST score
                  1.0e-56
E value
                  112
Match length
                  100
% identity
NCBI Description Zea mays cytochrome P-450 (CYP71C1) mRNA, partial cds
                   303996
Seq. No.
                  ntr700073688.h1
Seq. ID
                  BLASTX
Method
                  q1172836
NCBI GI
BLAST score
                   407
                   5.0e-40
E value
                   78
Match length
                   96
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)
NCBI Description
                   small ras-related protein [Nicotiana tabacum]
                   303997
Seq. No.
Seq. ID
                   ntr700073709.hl
                   BLASTN
Method
NCBI GI
                   q1008878
BLAST score
                   203
                   1.0e-110
E value
                   270
Match length
                   99
% identity
NCBI Description Zea mays RS1 mRNA, complete cds
                   303998
Seq. No.
                   ntr700073719.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3929108
BLAST score
                   149
                   9.0e-10
E value
Match length
                   83
% identity
                   45
NCBI Description (AF067179) kinesin heavy chain [Mus musculus]
                   303999
Seq. No.
                   ntr700073814.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2459426
                   185
BLAST score
                   5.0e-14
E value
                   49
Match length
                   76
 % identity
NCBI Description (AC002332) putative splicing factor U2AF large chain
```

Seq. ID



[Arabidopsis thaliana]

```
304000
Seq. No.
                  ntr700073821.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4581108
                  280
BLAST score
                  4.0e-25
E value
                  102
Match length
                  48
% identity
                   (AC005825) putative chloroplast outer membrane protein
NCBI Description
                   86, also very similar to GTP-inding protein from pea
                   (GB:L36857) [Arabidopsis thaliana]
                   304001
Seq. No.
Seq. ID
                   ntr700073824.h1
                   BLASTX
Method
NCBI GI
                   q4582459
                   381
BLAST score
                   5.0e-37
E value
                   97
Match length
                   71
% identity
                   (AC007071) putative RanBP7/importin protein [Arabidopsis
NCBI Description
                   thaliana]
                   304002
Seq. No.
Seq. ID
                   ntr700073867.h1
                   BLASTX
Method
                   q1076687
NCBI GI
BLAST score
                   184
                   7.0e-14
E value
                   77
Match length
% identity
                   49
                   integral membrane protein - garden snapdragon
NCBI Description
                   304003
Seq. No.
                   ntr700073872.h1
 Seq. ID
Method
                   BLASTX
                   g4204265
NCBI GI
 BLAST score
                   159
                   6.0e-11
 E value
Match length
                   50
 % identity
                   60
                   (AC005223) 45643 [Arabidopsis thaliana]
 NCBI Description
                   304004
 Seq. No.
                   ntr700073878.h1
 Seq. ID
                   BLASTX
 Method
                   g3983665
 NCBI GI
                    340
 BLAST score
                    3.0e-32
 E value
                    80
 Match length
 % identity
                    88
                   (AB011271) importin-beta2 [Oryza sativa]
 NCBI Description
                    304005
```

42992

ntr700073891.h1

```
BLASTN
Method
                  g3821780
NCBI GI
                  36
BLAST score
                  7.0e-11
E value
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  304006
Seq. No.
Seq. ID
                  ntr700073895.hl
                  BLASTX
Method
NCBI GI
                   g1731426
                   328
BLAST score
                   9.0e-31
E value
                   89
Match length
                   72
% identity
NCBI Description ZEAMATIN PRECURSOR >gi_459170 (U06831) unnamed protein
                   product [Zea mays]
                   304007
Seq. No.
                   ntr700073924.hl
Seq. ID
                   BLASTX
Method
                   q3935147
NCBI GI
                   326
BLAST score
                   1.0e-30
E value
                   88
Match length
                   66
% identity
NCBI Description (AC005106) T25N20.11 [Arabidopsis thaliana]
                   304008
Seq. No.
                   ntr700073930.hl
Seq. ID
                   BLASTX
Method
                   q1172836
NCBI GI
                   379
BLAST score
                   8.0e-37
E value
                   72
Match length
 % identity
                   96
                   GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)
 NCBI Description
                   small ras-related protein [Nicotiana tabacum]
                   304009
 Seq. No.
 Seq. ID
                   ntr700073951.h1
 Method
                   BLASTX
                    g3819164
 NCBI GI
 BLAST score
                    170
                    2.0e-12
 E value
                    53
 Match length
                    66
 % identity
                   (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
 NCBI Description
```

Seq. ID ntr700073967.h1

Method BLASTX
NCBI GI g3914423
BLAST score 156
E value 4.0e-20

Method

NCBI GI

BLAST score E value

Match length



```
Match length
                  80
% identity
                  PROFILIN 4 >gi 2642324 (AF032370) profilin [Zea mays]
NCBI Description
                  304011
Seq. No.
                  ntr700073968.hl
Seq. ID
Method
                  BLASTX
                  g4587990
NCBI GI
BLAST score
                  210
E value
                  7.0e-17
Match length
                  98
                  44
% identity
NCBI Description (AF085279) hypothetical protein [Arabidopsis thaliana]
                  304012
Seq. No.
Seq. ID
                  ntr700073984.h1
Method
                  BLASTX
NCBI GI
                  q3080389
BLAST score
                  165
                  1.0e-11
E value
                   34
Match length
% identity
                   91
                   (AL022603) putative membrane associated protein
NCBI Description
                   [Arabidopsis thaliana]
                   304013
Seq. No.
                   ntr700074060.hl
Seq. ID
Method
                   BLASTX
                   g730558
NCBI GI
BLAST score
                   159
                   5.0e-11
E value
Match length
                   46
                   70
% identity
                   60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir__S48027 ribosomal
NCBI Description
                   protein L34 - common tobacco >gi_2129964_pir__S48028
                   ribosomal protein L34.e, cytosolic - common tobacco
                   >gi_436030 (L27089) 60S ribosomal protein L34 [Nicotiana
                   tabacum] >gi_436032 (L27107) 60S ribosomal protein L34
                   [Nicotiana tabacum]
                   304014
Seq. No.
                   ntr700074081.h1
Seq. ID
Method
                   BLASTX
                   g2078350
NCBI GI
                   217
BLAST score
                   7.0e-18
E value
                   89
Match length
                   54
% identity
                  (U95923) transaldolase [Solanum tuberosum]
NCBI Description
Seq. No.
                   304015
                   ntr700074123.h1
Seq. ID
```

42994

BLASTN

52

148

q2239259

2.0e-20

E value

Match length

```
% identity
NCBI Description Zea mays mRNA for cinnamoyl CoA reductase
                  304016
Seq. No.
                  ntr700074131.h1
Seq. ID
Method
                  BLASTX
                  q82696
NCBI GI
                  221
BLAST score
```

% identity 69 glycine-rich protein - maize >gi_22293_emb_CAA43431_ NCBI Description (X61121) glycine-rich protein [Zea mays]

Seq. No. ntr700074139.h1 Seq. ID Method BLASTX g4539351 NCBI GI BLAST score 361 1.0e-34 E value Match length 98

3.0e-18

304017

65

% identity 61 (AL035539) putative protein [Arabidopsis thaliana] NCBI Description

304018 Seq. No. ntr700074193.h1 Seq. ID Method BLASTX g2160189 NCBI GI BLAST score 169 3.0e-12 E value

Match length 87 43 % identity

(AC000132) Similar to A. thaliana receptor-like protein NCBI Description kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come

from this gene. [Arabidopsis thaliana]

304019 Seq. No. ntr700074211.h1 Seq. ID BLASTX Method g4218010 NCBI GI

155 BLAST score 2.0e-10 E value Match length 56 55 % identity

(AC006135) putative sugar transporter [Arabidopsis NCBI Description thaliana] >gi_4309720_gb_AAD15490_ (AC006439) putative

sugar transporter [Arabidopsis thaliana]

304020 Seq. No.

ntr700074240.hl Seq. ID

BLASTN Method g433043 NCBI GI 54 BLAST score 1.0e-21 E value 106 Match length 89 % identity

NCBI Description Zea mays W-22 clone PREM-1E retroelement PREM-1, partial



sequence

105

52

Match length

NCBI Description

% identity

304021 Seq. No. Seq. ID ntr700074274.h1 Method BLASTX NCBI GI g2244786 176 BLAST score 5.0e-13 E value 47 Match length % identity (Z97335) ribonucleoprotein homolog [Arabidopsis thaliana] NCBI Description 304022 Seq. No. ntr700074293.h1 Seq. ID BLASTX Method NCBI GI q4582468 BLAST score 181 2.0e-21 E value Match length 60 97 % identity (AC007071) putative 40S ribosomal protein; contains NCBI Description C-terminal domain [Arabidopsis thaliana] 304023 Seq. No. ntr700074528.h1 Seq. ID BLASTX Method NCBI GI g122022 474 BLAST score 6.0e-48 E value 99 Match length % identity 98 HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat NCBI Description >gi_21801_emb[CAA42530_ (X $\overline{59}873$) histone H2B [Triticum aestivum] 304024 Seq. No. ntr700074531.h1 Seq. ID BLASTX Method g3176686 NCBI GI 299 BLAST score 2.0e-27 E value 90 Match length % identity 60 (AC003671) Similar to high affinity potassium transporter, NCBI Description HAK1 protein gb_U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana] 304025 Seq. No. ntr700074619.h1 Seq. ID BLASTX Method g4432857 NCBI GI 293 BLAST score 1.0e-26 E value

(AC006300) hypothetical protein [Arabidopsis thaliana]



```
304026
Seq. No.
                  ntr700074631.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4580472
BLAST score
                  297
                  4.0e-27
E value
                  101
Match length
                  56
% identity
                  (AC006081) DNA binding protein; similar to CDC27 and nuclear
NCBI Description
                  scaffold proteins [Arabidopsis thaliana]
                  304027
Seq. No.
                  ntr700074655.hl
Seq. ID
                  BLASTX
Method
                  q2827536
NCBI GI
BLAST score
                  322
E value
                   4.0e-30
Match length
                   96
% identity
NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]
                   304028
Seq. No.
                  ntr700074674.h1
Seq. ID
                   BLASTX
Method
                   g4581164
NCBI GI
                   238
BLAST score
E value
                   2.0e-20
                   73
Match length
% identity
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
NCBI Description
                   304029
Seq. No.
                   ntr700074722.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3461846
BLAST score
                   267
E value
                   1.0e-23
                   105
Match length
% identity
                   25
                   (AC005315) putative zinc-finger protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   304030
                   ntr700074745.h1
Seq. ID
                   BLASTX
Method
                   g2062169
NCBI GI
                   404
BLAST score
                   1.0e-39
E value
                   101
Match length
                   85
% identity
                   (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                   thaliana]
                   304031
Seq. No.
                   ntr700074808.hl
Seq. ID
```

BLASTX

g541824

Method

NCBI GI



```
333
BLAST score
                  2.0e-31
E value
                  81
Match length
                  78
% identity
NCBI Description protein kinase - spinach >gi_457709_emb_CAA82991_ (Z30330)
                  protein kinase [Spinacia oleracea]
                  304032
Seq. No.
                  ntr700074809.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3193303
                  167
BLAST score
                   6.0e-12
E value
                   56
Match length
% identity
                   (AF069298) similar to several proteins containing a tandem
NCBI Description
                   repeat region such as Plasmodium falciparum GGM tandem
                   repeat protein (GB:U27807); partial CDS [Arabidopsis
                   thaliana]
                   304033
Seq. No.
                   ntr700074871.h1
Seq. ID
                   BLASTX
Method
                   g2462825
NCBI GI
                   260
BLAST score
                   8.0e-23
E value
                   61
Match length
                   74
% identity
                  (AF000657) contains Procite 'RNP1' putative RNA-binding
NCBI Description
                   region [Arabidopsis thaliana]
                   304034
Seq. No.
                   ntr700074872.h1
Seq. ID
                   BLASTX
Method
                   g4185507
NCBI GI
BLAST score
                   226
                   8.0e-19
E value
Match length
                   96
                   52
 % identity
                   (AF100163) EZA1 [Arabidopsis thaliana]
NCBI Description
                   304035
 Seq. No.
                   ntr700074923.hl
 Seq. ID
                                                                      40
                   BLASTX
 Method
                   q3560166
 NCBI GI
                   155
 BLAST score
                   3.0e-10
 E value
 Match length
                   105
 % identity
                   35
                    (AL031525) ubiquitin carboxyl-terminal hydrolase
 NCBI Description
                    [Schizosaccharomyces pombe]
                   304036
```

ntr700074937.h1 Seq. ID

BLASTX Method q4467124 NCBI GI 211 BLAST score

```
8.0e-17
E value
                  146
Match length
% identity
                  (AL035538) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  304037
Seq. No.
                  ntr700074961.h1
Seq. ID
                  BLASTX
Method
                  g728938
NCBI GI
BLAST score
                  151
                   5.0e-10
E value
                   69
Match length
% identity
```

PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP NCBI Description (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)

(H+-PPASE) >gi_322841_pir__JC1466 inorganic pyrophosphatase

(EC 3.6.1.1) - barley >gi_285638_dbj_BAA02717_ (D13472)

inorganic pyrophosphatse ase' [Hordeum vulgare]

```
304038
Seq. No.
                  ntr700074968.hl
Seq. ID
Method
                  BLASTX
                  g1345644
NCBI GI
                  162
BLAST score
                  3.0e-11
E value
                  45
Match length
% identity
                  CYTOCHROME P450 86A1 (CYPLXXXVI) >gi_940446_emb_CAA62082_
NCBI Description
                  (X90458) cytochrome p450 [Arabidopsis thaliana]
```

304039 Seq. No. Seq. ID ntr700074996.h1 Method BLASTX q3395938 NCBI GI BLAST score 414 6.0e-41 E value

100 Match length % identity 80

(AF076924) polypyrimidine tract-binding protein homolog NCBI Description [Arabidopsis thaliana]

304040 Seq. No. ntr700075079.h1 Seq. ID BLASTX Method

q2244876 NCBI GI 189 BLAST score 2.0e-14 E value Match length 60 57 % identity

E value

(Z97338) hypothetical protein [Arabidopsis thaliana] NCBI Description

304041 Seq. No. ntr700075114.h1 Seq. ID BLASTX Method q1345587 NCBI GI 411 BLAST score 2.0e-40

```
96
Match length
                  88
% identity
                  14-3-3-LIKE PROTEIN GF14-6 >gi 998430_bbs_164522 (S77133)
NCBI Description
                  GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261
                  aa] [Zea mays]
                  304042
Seq. No.
                  ntr700075146.h1
Seq. ID
                  BLASTX
Method
                  g119355
NCBI GI
BLAST score
                  217
                   9.0e-18
E value
                  73
Match length
% identity
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                   >gi 100869 pir__S16257 phosphopyruvate hydratase (EC
                   4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
                   [Zea mays]
                   304043
Seq. No.
                   ntr700075159.h1
Seq. ID
                   BLASTX
Method
                   g1431870
NCBI GI
                   221
BLAST score
                   3.0e-18
E value
Match length
                   95
% identity
                   48
                   (U43904) ent-kaurene synthase B [Cucurbita maxima]
NCBI Description
                   304044
Seq. No.
                   ntr700075162.h1
Seq. ID
                   BLASTX
Method
                   g2738248
NCBI GI
                   195
BLAST score
                   2.0e-15
E value
Match length
                   39
                   92
% identity
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                   304045
 Seq. No.
                   ntr700075195.hl
 Seq. ID
                   BLASTX
 Method
                   g1352427
 NCBI GI
                   234
 BLAST score
                   8.0e-20
 E value
 Match length
                   45
                   96
 % identity
                   EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
 NCBI Description
                    (EIF-4C)
                    304046
```

 Seq. No.
 304046

 Seq. ID
 ntr700075294.h1

 Method
 BLASTX

 NCBI GI
 g4582459

BLAST score 181



```
9.0e-25
E value
                  79
Match length
                  71
% identity
                  (AC007071) putative RanBP7/importin protein [Arabidopsis
NCBI Description
                  thaliana]
                  304047
Seq. No.
                  ntr700075336.hl
Seq. ID
                  BLASTN
Method
                  g2653557
NCBI GI
                  185
BLAST score
```

1.0e-100 E value 295 Match length 92 % identity Zea mays mRNA for ferredoxin-sulfite reductase precursor, NCBI Description

complete cds

304048 Seq. No.

ntr700075359.h1 Seq. ID

BLASTX Method g1709970 NCBI GI BLAST score 366 2.0e-35 E value Match length 85 82 % identity

60S RIBOSOMAL PROTEIN L10A NCBI Description

304049 Seq. No.

ntr700075406.h1 Seq. ID

BLASTX Method q520570 NCBI GI BLAST score 422 8.0e-42 E value 102 Match length % identity 82

(U12315) peroxidase [Cenchrus ciliaris] NCBI Description

304050 Seq. No.

ntr700075466.h1 Seq. ID

BLASTX Method g2529677 NCBI GI 397 BLAST score 7.0e-39 E value 89 Match length 88 % identity

(AC002535) kinesin-like protein, heavy chain [Arabidopsis NCBI Description

thaliana]

304051 Seq. No.

ntr700075469.h1 Seq. ID

BLASTN Method NCBI GI g3135542 88 BLAST score 6.0e-42 E value 156 Match length 90 % identity

NCBI Description Oryza sativa aquaporin (PIP2a) mRNA, complete cds



```
304052
Seq. No.
                  ntr700075520.h1
Seq. ID
                  BLASTX
Method
                  g2281705
NCBI GI
                  152
BLAST score
                  2.0e-10
E value
Match length
                  34
                  85
% identity
                  (AF013979) ethylene responsive factor [Oryza sativa]
NCBI Description
                  304053
Seq. No.
                  ntr700075548.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                   g218179
BLAST score
                   224
                   1.0e-24
E value
                   90
Match length
                   71
% identity
                   (D10207) H-ATPase [Oryza sativa] >gi_444339_prf__1906387A H
NCBI Description
                  ATPase [Oryza sativa]
                   304054
Seq. No.
                   ntr700075549.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4263787
                   228
BLAST score
E value
                   4.0e-19
Match length
                   52
                   79
% identity
                  (AC006068) unknown protein [Arabidopsis thaliana]
NCBI Description
                   304055
Seq. No.
                   ntr700075584.h1
Seq. ID
                   BLASTX
Method
                   g2494034
NCBI GI
BLAST score
                   216
                   5.0e-35
E value
Match length
                   93
                   70
% identity
                   DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG
NCBI Description
                   KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase ~
                   Arabidopsis thaliana >gi 1374772 dbj_BAA09856_ (D63787)
                   diacylglycerol kinase [Arabidopsis thaliana]
                   304056
Seq. No.
                   ntr700075588.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3927831
BLAST score
                   276
```

E value 9.0e-25 Match length 81 % identity

(AC005727) similar to mouse ankyrin 3 [Arabidopsis NCBI Description

thaliana]

304057 Seq. No.

43002

```
ntr700075606.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2425065
BLAST score
                   89
                   2.0e-42
E value
                   143
Match length
% identity
                   93
NCBI Description Zea mays cysteine proteinase Mir3 (mir3) mRNA, complete cds
                   304058
Seq. No.
Seq. ID
                  ntr700075624.h1
Method
                  BLASTN
NCBI GI
                   g22245
BLAST score
                   33
E value
                   4.0e-09
Match length
                   41
% identity
                   95
NCBI Description
                  Zea mays DNA for cin4 element (showing homology to reverse
                   transcriptase)
                   304059
Seq. No.
Seq. ID
                   ntr700075694.h1
Method
                   BLASTN
NCBI GI
                   g1321660
BLAST score
                   54
E value
                   7.0e-22
Match length
                   116
% identity
                   88
NCBI Description Rice mRNA for ascorbate peroxidase, complete cds
                   304060
Seq. No.
                   ntr700075769.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2493321
BLAST score
                   183
                   4.0e-22
E value
Match length
                   62
                   77
% identity
                  L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO)
NCBI Description
                   >gi_2129952_pir__S66353 L-ascorbate oxidase (EC 1.10.3.3)
                   precursor - common tobacco >gi_599594_dbj_BAA07734
                   (D43624) ascorbate oxidase precursor [Nicotiana tabacum]
Seq. No.
                   304061
Seq. ID
                   ntr700075809.h1
Method
                   BLASTN
NCBI GI
                   g1870200
BLAST score
                   215
```

E value 1.0e-117 Match length 263 % identity 96

NCBI Description Z.mays cyp71c2 gene

Seq. No. 304062

Seq. ID ntr700075825.h1

Method BLASTX NCBI GI g1362019



BLAST score 188
E value 2.0e-14
Match length 70
% identity 56

NCBI Description zinc finger protein 6 - Arabidopsis thaliana >gi_790683 (L39649) zinc finger protein [Arabidopsis thaliana]

Seq. No. 304063

Seq. ID ntr700075840.h1

Method BLASTX
NCBI GI g2781433
BLAST score 384
E value 2.0e-37
Match length 99
% identity 76

NCBI Description (AF030052) RSW1-like cellulose synthase catalytic subunit

[Oryza sativa subsp. japonica]

Seq. No. 304064

Seq. ID ntr700075880.h1

Method BLASTX
NCBI GI g3415117
BLAST score 331
E value 4.0e-31
Match length 90
% identity 68

NCBI Description (AF081203) villin 3 [Arabidopsis thaliana]

Seq. No. 304065

Seq. ID ntr700075887.h1

Method BLASTX
NCBI GI g129916
BLAST score 368
E value 2.0e-35
Match length 77
% identity 95

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY

phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

Seq. No. 304066

Seq. ID ntr700075892.h1

Method BLASTX
NCBI GI g4220517
BLAST score 196
E value 4.0e-33
Match length 102
% identity 66

NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304067

Seq. ID ntr700075928.h1

Method BLASTX
NCBI GI g3550436
BLAST score 233
E value 1.0e-19



```
Match length
% identity
                  81
NCBI Description
                  (AJ001317) putative transcription repressor HOTR [Hordeum
                  vulgare]
                  304068
Seq. No.
                  ntr700075955.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3021510
BLAST score
                  250
                  1.0e-21
E value
Match length
                  71
                  70
% identity
NCBI Description
                  (AJ001770) glucose-6-phosphate dehydrogenase [Nicotiana
                  tabacum]
                  304069
Seq. No.
                  ntr700075966.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2959767
BLAST score
                  173
E value
                  2.0e-18
Match length
                  101
% identity
                  54
NCBI Description
                  (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi 3738292
                   (AC005309) glutathione-conjugate transporter AtMRP4
                  [Arabidopsis thaliana]
                  304070
Seq. No.
Seq. ID
                  ntr700076014.h1
Method
                  BLASTX
                  g4115359
NCBI GI
BLAST score
                  213
E value
                  3.0e-17
Match length
                  98
% identity
NCBI Description
                  (AC005957) putative disease resistance protein [Arabidopsis
                  thaliana]
Seq. No.
                  304071
Seq. ID
                  ntr700076026.h1
Method
                  BLASTX
NCBI GI
                  q3493460
BLAST score
                  214
E value
                  2.0e-17
Match length
                  49
% identity
                  86
                  (U62485) glycolate oxidase [Nicotiana tabacum]
NCBI Description
```

Seq. No. 304072

ntr700076152.h1 Seq. ID

Method BLASTX NCBI GI q4455356 BLAST score 177 E value 1.0e-13 Match length 63 % identity 51

43005





```
(AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   304073
                  ntr700076205.h1
Seq. ID
                  BLASTX
Method
                   q3668086
NCBI GI
                   149
BLAST score
                   4.0e-10
E value
Match length
                   39
% identity
                   67
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   304074
Seq. No.
                   ntr700076233.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3915866
BLAST score
                   392
                   2.0e-38
E value
Match length
                   80
% identity
                   86
                  GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)
NCBI Description
                   >gi 2995455 emb CAA62901 (X91787) tRNA-glutamine
                   synthetase [Lupinus luteus]
Seq. No.
                   304075
                   ntr700076327.h1
Seq. ID
                   BLASTN
Method
                   g4140643
NCBI GI
BLAST score
                   52
                   2.0e-20
E value
Match length
                   108
                   87
% identity
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   304076
Seq. No.
                   ntr700076333.h1
Seq. ID
                   BLASTX
Method
                   q3043415
NCBI GI
BLAST score
                   365
                   3.0e - 35
E value
                   70
Match length
% identity
                   99
                  (Y17053) At-hsc70-3 [Arabidopsis thaliana]
NCBI Description
                   304077
Seq. No.
                   ntr700076368.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q397395
BLAST score
                   175
E value
                   8.0e-94
```

Match length 179 99 % identity

NCBI Description Z.mays MNB1b mRNA for DNA-binding protein

Seq. No. 304078

ntr700076382.h1 Seq. ID

43006



```
Method
                  BLASTX
NCBI GI
                  g66615
BLAST score
                  321
E value
                  5.0e-30
Match length
                  61
% identity
                  98
                  glutathione transferase (EC 2.5.1.18) I - maize
NCBI Description
                  304079
Seq. No.
Seq. ID
                  ntr700076385.h1
Method
                  BLASTX
NCBI GI
                  g1084415
BLAST score
                  155
E value
                  1.0e-10
Match length
                  59
% identity
                  59
                  RNA-binding protein - Wood tobacco >qi 624925 dbj BAA05170
NCBI Description
                   (D26182) RNA-binding glycine rich protein (RGP-2)
                   [Nicotiana sylvestris]
Seq. No.
                  304080
Seq. ID
                  ntr700076391.h1
Method
                  BLASTN
NCBI GI
                  g500854
BLAST score
                  94
E value
                  1.0e-45
Match length
                  129
% identity
                  94
NCBI Description Maize dissociation element DNA
                  304081
Seq. No.
                  ntr700076431.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3746065
BLAST score
                  240
E value
                  1.0e-20
Match length
                  87
% identity
                  55
NCBI Description
                  (AC005311) putative lipase [Arabidopsis thaliana]
Seq. No.
                  304082
                  ntr700076454.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2117624
BLAST score
                  303
                  7.0e-28
E value
Match length
                  97
% identity
                  62
NCBI Description
                  peroxidase (EC 1.11.1.7) 2 - alfalfa
                  >gi_971564_emb_CAA62228_ (X90695) peroxidase2 [Medicago
```

sativa]

Seq. No. 304083

Seq. ID ntr700076457.h1

Method BLASTN NCBI GI g1063665 BLAST score 102



E value 1.0e-50 Match length 121 % identity 97

NCBI Description Zea mays unknown protein mRNA, complete cds

Seq. No. 304084

Seq. ID ntr700076469.h1

Method BLASTX
NCBI GI g530088
BLAST score 315
E value 3.0e-29
Match length 87
% identity 70

NCBI Description (U12735) aminoalcoholphosphotransferase [Glycine max]

Seq. No. 304085

Seq. ID ntr700076477.h1

Method BLASTX
NCBI GI g554565
BLAST score 361
E value 1.0e-34
Match length 69
% identity 97

NCBI Description (M24889) glutathione S-transferase [Artificial gene]

Seq. No. 304086

Seq. ID ntr700076481.h1

Method BLASTX
NCBI GI g1703201
BLAST score 345
E value 9.0e-33
Match length 89
% identity 72

NCBI Description PROTEIN KINASE AFC3 >gi_601791 (U16178) protein kinase

[Arabidopsis thaliana]

Seq. No. 304087

Seq. ID ntr700076510.h1

Method BLASTX
NCBI GI g2921304
BLAST score 449
E value 6.0e-45
Match length 101
% identity 92

NCBI Description (AF033496) herbicide safener binding protein [Zea mays]

Seq. No. 304088

Seq. ID ntr700076546.h1

Method BLASTX
NCBI GI 94337178
BLAST score 168
E value 5.0e-12
Match length 38
% identity 79

NCBI Description (AC006416) T31J12.5 [Arabidopsis thaliana]

Seq. No. 304089

Match length

% identity

59

95



```
Seq. ID
                   ntr700076617.h1
Method
                   BLASTN
NCBI GI
                   q169818
BLAST score
                   72
E value
                   7.0e-33
Match length
                   108
% identity
                   92
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                   304090
Seq. ID
                   ntr700076634.h1
Method
                   BLASTX
NCBI GI
                   g452593
BLAST score
                   385
E value
                   2.0e-37
Match length
                   101
% identity
                   65
NCBI Description
                  (D21814) ORF [Lilium longiflorum]
Seq. No.
                   304091
Seq. ID
                   ntr700076716.h1
Method
                   BLASTX
NCBI GI
                   g4490750
BLAST score
                   238
E value
                   3.0e-20
Match length
                   60
% identity
                   72
NCBI Description
                  (AL035708) GTP-binding protein GB3 [Arabidopsis thaliana]
Seq. No.
                   304092
Seq. ID
                   ntr700076736.h1
Method
                   BLASTX
NCBI GI
                   g2244850
BLAST score
                   186
E value
                   4.0e-14
Match length
                   91
% identity
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   304093
Seq. ID
                  ntr700076737.h1
Method
                  BLASTX
NCBI GI
                  g2293566
BLAST score
                  389
E value
                  6.0e-38
Match length
                  77
% identity
                  100
NCBI Description
                 (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
Seq. No.
                  304094
Seq. ID
                  ntr700076738.h1
Method
                  BLASTX
NCBI GI
                  g3421087
BLAST score
                  283
E value
                  2.0e-25
```

43009

% identity

95





```
NCBI Description
                  (AF043524) 20S proteasome subunit PAE1 [Arabidopsis
                  thaliana]
                  304095
Seq. No.
                  ntr700076783.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173456
BLAST score
                  218
E value
                  4.0e-18
Match length
                  58
% identity
                  64
NCBI Description
                  SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN
                  D3) (SM-D3) >gi 600750 (U15009) Sm D3 [Homo sapiens]
Seq. No.
                  304096
                  ntr700076845.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567260
BLAST score
                  313
E value
                  4.0e-29
Match length
                  74
                  78
% identity
NCBI Description
                  (AC006841) putative NADPH dependent mannose 6-phosphate
                  reductase [Arabidopsis thaliana]
                  >gi 4582440 gb AAD24825.1 AC007142 3 (AC007142) putative
                  NADPH-dependent mannose-6-phosphate reductase [Arabidopsis
                  thaliana]
                  304097
Seq. No.
                  ntr700076923.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4314361
BLAST score
                  143
E value
                  3.0e-09
Match length
                  32
% identity
                  84
NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]
Seq. No.
                  304098
Seq. ID
                  ntr700076962.h1
Method
                  BLASTN
NCBI GI
                  g1208445
BLAST score
                  59
                  4.0e-25
E value
Match length
                  99
% identity
                  90
NCBI Description Rice (YK426) mRNA, complete cds
Seq. No.
                  304099
Seq. ID
                  ntr700077019.h1
Method
                  BLASTX
NCBI GI
                  q113621
BLAST score
                  286
E value
                  7.0e-26
Match length
                  97
```

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME



>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A
cytoplasmic aldolase [Zea mays]

Seq. No. 304100

Seq. ID ntr700077023.h1

Method BLASTX
NCBI GI g2104446
BLAST score 333
E value 2.0e-31
Match length 101
% identity 61

NCBI Description (Z95396) WD-repeat protein [Schizosaccharomyces pombe]

Seq. No. 304101

Seq. ID ntr700077036.h1

Method BLASTX
NCBI GI g1076414
BLAST score 304
E value 5.0e-28
Match length 91
% identity 67

NCBI Description subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi 757534 emb CAA59963 (X85974)

subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 304102

Seq. ID ntr700077063.h1

Method BLASTX
NCBI GI 94581164
BLAST score 217
E value 8.0e-18
Match length 78
% identity 49

NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No. 304103

Seq. ID ntr700077084.h1

Method BLASTN
NCBI GI g1063665
BLAST score 164
E value 3.0e-87
Match length 229
% identity 99

NCBI Description Zea mays unknown protein mRNA, complete cds

Seq. No. 304104

Seq. ID ntr700077204.h1

Method BLASTX
NCBI GI g2529677
BLAST score 260
E value 2.0e-32
Match length 103
% identity 70

NCBI Description (AC002535) kinesin-like protein, heavy chain [Arabidopsis



thaliana]

Seq. No. 304105 Seq. ID ntr700077211.h1 Method BLASTX q4512664 NCBI GI 276 BLAST score 1.0e-24 E value Match length 63

% identity 81

(AC006931) putative ribose phosphate pyrophosphokinase NCBI Description

[Arabidopsis thaliana]

>gi_4544471_gb_AAD22378.1_AC006580_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]

Seq. No. 304106

ntr700077243.h1 Seq. ID

Method BLASTN q4530610 NCBI GI BLAST score 63 E value 5.0e-27 Match length 79 % identity 95

Oryza sativa subsp. indica serine/threonine protein NCBI Description

phosphatase PP2A-2 catalytic subunit (Pp2A) gene, complete

Seq. No. 304107

ntr700077290.h1 Seq. ID

BLASTX Method q3868758 NCBI GI BLAST score 288 4.0e-26 E value 59 Match length 92 % identity

(D89802) elongation factor 1B gamma [Oryza sativa] NCBI Description

304108 Seq. No.

ntr700077295.h1 Seq. ID

BLASTN Method g4140643 NCBI GI BLAST score 41 7.0e-14 E value 49 Match length 96

Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description

complete sequence

304109 Seq. No.

% identity

Seq. ID ntr700077335.h1

Method BLASTX q4508083 NCBI GI 169 BLAST score 4.0e-12 E value Match length 38 % identity 79

NCBI Description (AC005882) Hypothetical protein [Arabidopsis thaliana]



```
304110
Seq. No.
                  ntr700077359.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4165488
BLAST score
                  149
                  1.0e-18
E value
Match length
                  62
% identity
                  67
NCBI Description (AJ132399) alpha-tubulin 3 [Hordeum vulgare]
                  304111
Seq. No.
                  ntr700077370.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3149952
BLAST score
                  321
                  5.0e-36
E value
                  99
Match length
                  71
% identity
NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]
                  304112
Seq. No.
                  ntr700077420.h1
Seq. ID
Method
                  BLASTX
                  g2493123
NCBI GI
BLAST score
                  140
                  5.0e-09
E value
Match length
                  37
% identity
                  78
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                  SUBUNIT) >qi 1051258 (U36939) vacuolar ATPase catalytic
                  subunit [Hordeum vulgare]
                  304113
Seq. No.
                  ntr700077447.h1
Seq. ID
                  BLASTX
Method
                  g4510345
NCBI GI
BLAST score
                  151
E value
                  5.0e-10
Match length
                  61
% identity
                  46
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
                  304114
Seq. No.
                  ntr700077465.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262224
BLAST score
                  184
                  7.0e-14
E value
                  96
Match length
% identity
                  41
                  (AC006200) putative amino acid or GABA permease
```

304115 Seq. No.

NCBI Description

Seq. ID nwy700443340.hl

Method BLASTN

43013

[Arabidopsis thaliana]



```
g3005705
NCBI GI
BLAST score
                   104
E value
                   6.0e-52
Match length
                   108
% identity
                   99
NCBI Description
                   Homo sapiens clone 23778 autosomal dominant polycystic
                   kidney disease type II protein mRNA, partial cds
                   304116
Seq. No.
Seq. ID
                   nwy700443419.h1
Method
                   BLASTN
NCBI GI
                   g1236938
BLAST score
                   84
E value
                   5.0e-40
Match length
                   92
% identity
                   98
                  Human transcriptional activator mRNA, complete cds
NCBI Description
Seq. No.
                   304117
Seq. ID
                   nwy700443431.h1
Method
                   BLASTN
NCBI GI
                   q189305
BLAST score
                   142
E value
                   3.0e-74
Match length
                   275
% identity
                   97
NCBI Description
                  Human nucleolin gene, complete cds
Seq. No.
                   304118
                   nwy700443450.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4507210
BLAST score
                   92
E value
                   8.0e-45
Match length
                   104
% identity
                   97
NCBI Description
                   Alu RNA-binding protein) (SRP14) mRNA
```

Homo sapiens signal recognition particle 14kD (homologous

>gi_313660_emb_X73459_HSSRP14A H.sapiens mRNA for signal

recognition particle subunit

Seq. No. 304119

Seq. ID nwy700443531.h1

Method BLASTX NCBI GI g1084476 BLAST score 143 2.0e-09 E value Match length 24 100 % identity

NCBI Description catalase (EC 1.11.1.6) - maize >gi_311239_emb_CAA42720_

(X60135) catalase-1 [Zea mays]

Seq. No. 304120

Seq. ID nwy700443622.h1

Method BLASTN NCBI GI g3327165 BLAST score 127

```
1.0e-65
E value
Match length
                  131
                  99
% identity
                  Homo sapiens mRNA for KIAA0676 protein, partial cds
NCBI Description
                  304121
Seq. No.
                  nwy700443686.hl
Seq. ID
Method
                  BLASTX
                  g386786
NCBI GI
BLAST score
                  222
                  5.0e-23
E value
Match length
                  80
% identity
                  80
                  (J04988) 90 kD heat shock protein [Homo sapiens]
NCBI Description
                  304122
                  nwy700443778.hl
                  BLASTX
```

Seq. No. Seq. ID

Method NCBI GI q2645729 BLAST score 320 E value 6.0e-30 Match length 71 % identity 89

(AF033095) testis enhanced gene transcript protein [Homo NCBI Description

sapiens]

304123 Seq. No.

Seq. ID nwy700443789.h1

Method BLASTN g3367508° NCBI GI BLAST score 237 1.0e-131 E value Match length 281 96 % identity

Homo sapiens chromosome 5, BAC clone 45m2 (LBNL H145), NCBI Description

complete sequence [Homo sapiens]

304124 Seq. No.

Seq. ID nwy700443856.hl

Method BLASTX NCBI GI g4520344 BLAST score 139 7.0e-09 E value Match length 63 52 % identity

NCBI Description (AB009288) N-copine [Homo sapiens]

304125 Seq. No.

nwy700443874.h1 Seq. ID

Method BLASTN NCBI GI g1136421 BLAST score 230 E value 1.0e-126 Match length 250 % identity 98

NCBI Description Human mRNA for KIAA0181 gene, partial cds

NCBI Description



```
Seq. No.
                   304126
                  nwy700443958.h1
Seq. ID
                  BLASTN
Method
                  q3928123
NCBI GI
BLAST score
                  73
E value
                   3.0e-33
Match length
                   141
% identity
                  Homo sapiens chromosome 17, clone hRPK.180_P_8, complete
NCBI Description
                   sequence [Homo sapiens]
                   304127
Seq. No.
                   nwy700444094.hl
Seq. ID
                   BLASTN
Method
                   g4378110
NCBI GI
BLAST score
                   175
E value
                   7.0e-94
                   242
Match length
                   94
% identity
                   Human DNA sequence from clone 453C12 on chromosome
NCBI Description
                   20g12-13.12 Contains SDC4 (syndecan 4 (amphiglycan,
                   ryudocan)), predicts a gene like the mouse transcription
                   factor RBP-L, MATN4 (matrilin-4), STS, GSS, CpG island,
                   304128
Seq. No.
                   nwy700444148.h1
Seq. ID
                   BLASTX
Method
                   q4432860
NCBI GI
                   249
BLAST score
E value
                   1.0e-21
                   97
Match length
% identity
                   (AC006300) putative glucose-induced repressor protein
NCBI Description
                   [Arabidopsis thaliana]
                   304129
Seq. No.
Seq. ID
                   nwy700444189.hl
Method
                   BLASTX
                   g2749939
NCBI GI
BLAST score
                   145
E value
                   2.0e-09
Match length
                   62
% identity
                   48
                   (U70999) CCS1 [Chlamydomonas reinhardtii] >gi_2749941
NCBI Description
                   (U71000) CCS1 [Chlamydomonas reinhardtii]
                   304130
Seq. No.
                   nwy700444289.h1
Seq. ID
                   BLASTX
Method
                   g1237102
NCBI GI
                   201
BLAST score
E value
                   3.0e-16
Match length
                   47
                   83
 % identity
```

43016

[Arabidopsis thaliana]

(L40358) calmodulin-binding protein [Arabidopsis thaliana]

>qi 1589171 prf 2210340A calmodulin-binding protein



Seq. No. 304131

Seq. ID nwy700444342.h1

Method BLASTN
NCBI GI g4506930
BLAST score 219
E value 1.0e-120
Match length 282
% identity 95

NCBI Description Homo sapiens SH3-domain GRB2-like 2 (SH3GL2) mRNA, and

translated products >gi_2921407_gb_AF036268_AF036268 Homo

sapiens EEN-B1 mRNA, complete cds

Seq. No. 304132

Seq. ID nwy700444344.h1

Method BLASTN
NCBI GI g2632099
BLAST score 192
E value 1.0e-104
Match length 276
% identity 92

NCBI Description Human DNA sequence from cosmid V389H8 on chromosome X.

Contains mRNA near btk gene involved in

a-gamma-globulinemia, ESTs, STS

Seq. No. 304133

Seq. ID nwy700444353.h1

Method BLASTN
NCBI GI g963091
BLAST score 148
E value 7.0e-78
Match length 216
% identity 93

NCBI Description Human P311 HUM (3.1) mRNA, complete cds

Seq. No. 304134

Seq. ID nwy700444401.h1

Method BLASTX
NCBI GI g1673620
BLAST score 230
E value 3.0e-19
Match length 48
% identity 94

NCBI Description (U76762) Fer [Mus musculus]

Seq. No. 304135

Seq. ID nwy700444490.h1

Method BLASTN
NCBI GI g4103489
BLAST score 83
E value 4.0e-39
Match length 123
% identity 92

NCBI Description Mus musculus glucocorticoid-induced leucine zipper GILZ

protein mRNA, complete cds

Seq. No. 304136

43017



nwy700444534.h1 Seq. ID BLASTN Method g4505968 NCBI GI BLAST score 205 E value 1.0e-111 265 Match length % identity 94 Homo sapiens POU domain, class 6, transcription factor 1 NCBI Description (POU6F1) mRNA >gi_437806_emb_Z21966_HSMPOUHOX H.sapiens mPOU homeobox protein mRNA 304137 Seq. No. nwy700444552.hl Seq. ID BLASTX Method NCBI GI g4558664 BLAST score 235 6.0e-20 E value 95 Match length % identity (AC007063) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 304138 nwy700444554.hl Seq. ID Method BLASTX g4262233 NCBI GI BLAST score 201 9.0e-18 E value Match length 79 % identity (AC006200) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 304139 nwy700444557.hl Seq. ID Method BLASTX g3650033 NCBI GI BLAST score 146 2.0e-09 E value Match length 66 % identity 47 (AC005396) unknown protein [Arabidopsis thaliana] NCBI Description 304140 Seq. No. nwy700444672.h1 Seq. ID Method BLASTX NCBI GI g3970652 BLAST score 355 E value 4.0e-34 Match length 84 75 % identity (X77499) amino acid permease [Arabidopsis thaliana] NCBI Description Seq. No. 304141

nwy700444728.hl Seq. ID

Method BLASTX NCBI GI g3820648 BLAST score 173 E value 9.0e-13



Match length 85 % identity 40

NCBI Description (Y12636) allene oxide synthase [Arabidopsis thaliana]

Seq. No.

304142

Seq. ID

nwy700444756.h1

Method NCBI GI BLASTX q3810596

BLAST score E value 241 1.0e-20

Match length % identity

72 57

NCBI Description

(AC005398) reverse-transcriptase-like protein [Arabidopsis

thaliana]

Seq. No.

304143

Seq. ID

nwy700444791.h1

Method NCBI GI BLAST score BLASTN g4557766 101

E value
Match length

5.0e-50 146

% identity NCBI Description

91 on Homo sapiens methylmalonyl Coenzyme A mutase (MUT), nuclear

gene encoding mitochondrial protein, mRNA

>gi_187451_gb_M65131_HUMMCM Human methylmalonyl-CoA mutase
(MCM) mRNA, complete cds. >gi 1408435 gb G28620_G28620

human STS SHGC-35796

Seq. No.

304144

Seq. ID

nwy700444824.hl

Method NCBI GI BLASTN g3882178

BLAST score

83

E value

4.0e-39

Match length % identity

103 95

NCBI Description

n Homo sapiens mRNA for KIAA0729 protein, partial cds

Seq. No.

304145

Seq. ID

nwy700444871.h1

Method NCBI GI BLASTN g2570261

BLAST score

202

E value Match length 1.0e-110 273

% identity

95

NCBI Description

Human Chromosome 16 BAC clone CIT987SK-A-101F10, complete

sequence [Homo sapiens]

Seq. No.

304146

Seq. ID

nwy700444892.h1

Method NCBI GI BLASTN

BLAST score

g3882192

E value

166

Make a language

1.0e-88

Match length 174

% identity Homo sapiens mRNA for KIAA0736 protein, complete cds NCBI Description 304147 Seq. No. nwy700444969.hl Seq. ID Method BLASTX NCBI GI g2832658 266 BLAST score 1.0e-23 E value Match length 61 80 % identity (AL021710) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 304148 nwy700444984.h1 Seq. ID Method BLASTX g1076678 NCBI GI BLAST score 310 E value 9.0e-29 75 Match length 85 % identity ubiquitin / ribosomal protein S27a - potato (fragment) NCBI Description 304149 Seq. No. Seq. ID nwy700445064.h1 BLASTX g3024018 381 4.0e-37 73 99 % identity INITIATION FACTOR 5A (EIF-5A) (EIF-4D) NCBI Description >gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation initiation factor 5A [Zea mays]

Method NCBI GI BLAST score E value Match length

Seq. No. 304150

nwy700445211.h1 Seq. ID

Method BLASTN NCBI GI q1136227 BLAST score 177 5.0e-95 E value 236 Match length % identity

Human xeroderma pigmentosum group E UV-damaged DNA binding NCBI Description

factor mRNA, complete cds

Seq. No. 304151

nwy700445240.h1 Seq. ID

Method BLASTX g3914382 NCBI GI 173 BLAST score 2.0e-16 E value Match length 53 % identity 77

2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE NCBI Description

(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)





(X75020) phosphoglycerate mutase >gi_1498232_emb_CAA52928 [Prunus dulcis] >gi_1585833_prf__2202194A 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Prunus dulcis]

304152 Seq. No.

nwy700445276.h1 Seq. ID

BLASTN Method g1863998 NCBI GI BLAST score 102 E value 1.0e-50 Match length 110 98 % identity

NCBI Description Maize DNA for Fd VI, complete cds

Seq. No.

304153

nwy700445278.h1 Seq. ID Method BLASTN

NCBI GI g598674 BLAST score 94 E value 7.0e-46Match length 122 95 % identity

Human HepG2 3' region MboI cDNA, clone hmd2g05m3 NCBI Description

304154 Seq. No.

nwy700445343.h1 Seq. ID

Method BLASTX NCBI GI g1362922 BLAST score 175 5.0e-28 E value

Match length 87 % identity 83

Rab protein - human >gi 945223 (L42025) Rev/Rex activation NCBI Description

domain-binding protein [Homo sapiens]

304155 Seq. No.

nwy700445349.h1 Seq. ID

BLASTN Method g2828765 NCBI GI 253 BLAST score E value 1.0e-140 Match length 276 98 % identity

Homo sapiens chromosome 4 clone B227H22 from 4q25, complete NCBI Description

sequence [Homo sapiens]

304156 Seq. No.

nwy700445415.h1 Seq. ID

BLASTN Method g4589543 NCBI GI BLAST score 83 2.0e-39 E value Match length 95 97 % identity

NCBI Description Homo sapiens mRNA for KIAA0950 protein, partial cds

NCBI GI BLAST score

126



```
304157
Seq. No.
                  nwy700445436.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g532623
BLAST score
                  210
                  3.0e-17
E value
Match length
                  40
                  97
% identity
NCBI Description (L35913) lipase [Zea mays]
                  304158
Seq. No.
                  nwy700445470.h1
Seq. ID
                  BLASTX
Method
                  g3080424
NCBI GI
BLAST score
                   437
E value
                  1.0e-43
Match length
                  89
                   96
% identity
NCBI Description (AL022604) NAD+ dependent isoc. e dehydrogenase subunit
                   1 [Arabidopsis thaliana]
                   304159
Seq. No.
                   nwy700445490.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3387923
BLAST score
                   184
                   3.0e-99
E value
Match length
                   269
% identity
                   92
NCBI Description Homo sapiens clone 24422 mRNA sequence
                   304160
Seq. No.
                   nwy700445567.hl
Seq. ID
                   BLASTX
Method
                   g1495804
NCBI GI
BLAST score
                   326
                   1.0e-30
E value
                   82
Match length
                   76
% identity
                  (X96406) 13-lipoxygenase [Solanum tuberosum]
NCBI Description
                   304161
Seq. No.
                   nwy700445574.h1
Seq. ID
                   BLASTX
Method
                   q3413511
NCBI GI
BLAST score
                   212
                   2.0e-17
E value
Match length
                   50
                   80
% identity
                   (AJ000265) glucose-6-phosphate isomerase [Spinacia
NCBI Description
                   oleracea]
                   304162
Seq. No.
                   nwy700445611.hl
Seq. ID
                   BLASTN
Method
                   g6634030
```

43022



E value 5.0e-65 Match length 130 % identity 99

NCBI Description Homo sapiens KIAA0406 mRNA, complete cds

Seq. No. 304163

Seq. ID nwy700445640.h1

Method BLASTN
NCBI GI g5420148
BLAST score 118
E value 3.0e-60
Match length 126
% identity 98

NCBI Description Human DNA sequence from clone 1039K5 on chromosome

22q12.3-13.2 Contains gene similar to PICK1 perinuclear

binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island,

complete s

Seq. No. 304164

Seq. ID nwy700445653.h1

Method BLASTX
NCBI GI g3283220
BLAST score 140
E value 9.0e-09
Match length 33
% identity 70

NCBI Description (AF061241) splicing factor hPRP17 [Homo sapiens]

Seq. No. 304165

Seq. ID nwy700445687.h1

Method BLASTX
NCBI GI g3033400
BLAST score 203
E value 3.0e-20
Match length 77
% identity 66

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 304166

Seq. ID nwy700445770.h1

Method BLASTX
NCBI GI g4093155
BLAST score 183
E value 8.0e-14
Match length 99
% identity 47

NCBI Description (AF088281) phytochrome-associated protein 1 [Arabidopsis

thaliana]

Seq. No. 304167

Seq. ID nwy700445774.h1

Method BLASTX
NCBI GI g3172538
BLAST score 250
E value 1.0e-27



```
Match length
% identity
                  67
                  (AF067789) tSNARE AtTLG2p [Arabidopsis thaliana]
NCBI Description
                  304168
Seq. No.
                  nwy700445778.h1
Seq. ID
Method
                  BLASTX
                  g113217
NCBI GI
                  237
BLAST score
                  3.0e-20
E value
Match length
                  59
                  79
% identity
NCBI Description ACTIN 1 >gi_100149_pir__S07002 actin 1 - carrot
                  304169
Seq. No.
Seq. ID
                  nwy700445919.h1
                  BLASTX
Method
NCBI GI
                  g1255448
                  166
BLAST score
                  7.0e-12
E value
Match length
                  51
% identity
                   67
NCBI Description
                   (D50468) mitogen-activated protein kinase [Arabidopsis
                  thaliana]
                   304170
Seq. No.
                  nwy700445940.hl
Seq. ID
Method
                  BLASTN
                  g34312
NCBI GI
                   129
BLAST score
                   9.0e-67
E value
                   129
Match length
                   100
% identity
NCBI Description Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27)
Seq. No.
                   304171
Seq. ID
                   nwy700446033.h1
Method
                   BLASTX
NCBI GI
                   q3402713
BLAST score
                   195
E value
                   2.0e-15
Match length
                   42
% identity
                   79
                   (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   304172
Seq. ID
                   nwy700446047.h1
Method
                   BLASTX
                   q3928079
NCBI GI
BLAST score
                   249
                   1.0e-21
E value
```

Match length 67 % identity 69

NCBI Description (AC005770) hypothetical protein [Arabidopsis thaliana]

Seq. No.

304173

Seq. ID

nwy700446084.h1

NCBI Description



```
Method
                    BLASTN
                    q242013
NCBI GI
BLAST score
                    84
                    5.0e-40
E value
Match length
                    116
% identity
                    93
NCBI Description
                   PGK1=phosphoglycerate kinase 1 {3' nuclease-sensitive
                    region} [human, Genomic, 3571 nt]
Seq. No.
                    304174
Seq. ID
                    nwy700446107.hl
Method
                    BLASTX
NCBI GI
                    g730449
BLAST score
                    163
E value
                    8.0e-12
Match length
                    27
% identity
                    96
NCBI Description
                    60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A)
                    >gi_480647_pir__S37132 ribosomal protein L13.A - rape
>gi_398918_emb_CAA80341_ (Z22618) cold induced protein
                    (BnC24A) [Brassica napus]
Seq. No.
                    304175
Seq. ID
                    nwy700446114.hl
Method
                    BLASTX
NCBI GI
                    q4582459
BLAST score
                    148
E value
                    5.0e-10
Match length
                    55
                    49
% identity
                    (AC007071) putative RanBP7/importin protein [Arabidopsis
NCBI Description
                    thaliana]
                    304176
Seq. No.
Seq. ID
                    nwy700446275.h1
Method
                    BLASTX
                    g3550661
NCBI GI
                    193
BLAST score
E value
                    5.0e-15
Match length
                    92
% identity
                    48
NCBI Description
                    (AJ001310) 39 kDa EF-Hand containing protein [Solanum
                    tuberosum]
                    304177
Seq. No.
Seq. ID
                    nwy700446314.h1
Method
                    BLASTX
                    q1723514
NCBI GI
BLAST score
                    166
                    7.0e-12
E value
Match length
                    73
% identity
                    38
```

(Z69944) unknown [Schizosaccharomyces pombe]

HYPOTHETICAL 16.7 KD PROTEIN C1F12.10C IN CHROMOSOME I

>gi_2130243_pir__S67453 hypothetical protein - fission
yeast (Schizosaccharomyces pombe) >gi 1217984 emb CAA93814



```
Seq. No.
                   304178
Seq. ID
                  nwy700446405.h1
Method
                  BLASTX
NCBI GI
                  q1076678
BLAST score
                  359
                  1.0e-34
E value
Match length
                  89
                  83
% identity
NCBI Description
                  ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.
                  304179
Seq. ID
                  nwy700446406.hl
Method
                  BLASTN
                  q3687405
NCBI GI
BLAST score
                   45
                  3.0e-16
E value
Match length
                  73
% identity
                  90
NCBI Description Lycopersicon esculentum mRNA for hypothetical protein
                   304180
Seq. No.
                  nwy700446484.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4432835
BLAST score
                   165
                   9.0e-12
E value
Match length
                   55
                   55
% identity
NCBI Description
                  (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                   304181
                   nwy700446524.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1076758
BLAST score
                   164
E value
                   7.0e-12
Match length
                   55
                   62
% identity
                  heat-shock protein precursor - rye >gi 2130093 pir S65776
NCBI Description
                   heat-shock protein, 82K, precursor - rye
                   >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein
                   [Secale cereale]
Seq. No.
                   304182
Seq. ID
                  nwy700446531.h1
Method
                   BLASTX
NCBI GI
                   q576333
BLAST score
                   193
E value
                   2.0e-15
Match length
                   52
% identity
                   65
```

NCBI Description Triticum aestivum

304183 Seq. No.

Seq. ID nwy700446596.h1

Method BLASTX NCBI GI g1122317



BLAST score 166 E value 4.0e-12 Match length 33 % identity 97

NCBI Description (X94193) heat shock protein 17.9 [Pennisetum glaucum]

Seq. No. 304184

Seq. ID nwy700446786.h1

Method BLASTX
NCBI GI g1351974
BLAST score 305
E value 4.0e-28
Match length 62
% identity 100

NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325

ADP-ribosylation factor - maize >gi_1076789_pir__S53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_

(X80042) ADP-ribosylation factor [Zea mays]

Seq. No. 304185

Seq. ID nwy700446811.h1

Method BLASTX
NCBI GI g3876247
BLAST score 220
E value 3.0e-18
Match length 92
% identity 47

NCBI Description (Z71262) similar to serine/threonine kinase; cDNA EST

EMBL:D27596 comes from this gene; cDNA EST EMBL:D75765 comes from this gene; cDNA EST EMBL:D34336 comes from this gene; cDNA EST EMBL:D34931 comes from this gene; cDNA EST E

Seq. No. 304186

Seq. ID nwy700446926.h1

Method BLASTX
NCBI GI g135397
BLAST score 174
E value 1.0e-20
Match length 59
% identity 92

NCBI Description TUBULIN ALPHA-1 CHAIN, BRAIN-SPECIFIC

>gi_37492_emb_CAA25855_ (X01703) alpha-tubulin [Homo

sapiens]

Seq. No. 304187

Seq. ID nwy700446943.h1

Method BLASTX
NCBI GI g3004565
BLAST score 292
E value 1.0e-26
Match length 94
% identity 65

NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 304188

Seq. ID nwy700446972.h1

Method BLASTX

```
NCBI GI
                  a1076678
BLAST score
                  319
                  8.0e-30
E value
Match length
                  75
% identity
                  87
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.
                  304189
Seq. ID
                  nwy700447212.h1
Method
                  BLASTN
NCBI GI
                  q22245
BLAST score
                  137
E value
                  4.0e-71
Match length
                  242
                  95
% identity
NCBI Description
                  Zea mays DNA for cin4 element (showing homology to reverse
                  transcriptase)
Seq. No.
                  304190
Seq. ID
                  nwy700447237.h1
Method
                  BLASTN
NCBI GI
                  q3287465
BLAST score
                  38
                  3.0e-12
E value
Match length
                  86
                  86
% identity
                  Homo sapiens chromosome 17, clone hRPK.1003 J 3, complete
NCBI Description
                  sequence [Homo sapiens]
Seq. No.
                  304191
Seq. ID
                  nwy700447404.h1
Method
                  BLASTN
NCBI GI
                  g2921499
BLAST score
                  148
E value
                  6.0e-78
Match length
                  184
                  95
% identity
                  Human DNA from chromosome 14-specific cosmid containing
NCBI Description
                  XRCC3 DNA repair gene, genomic sequence, complete sequence
                  [Homo sapiens]
                  304192
Seq. No.
Seq. ID
                  nwy700447580.h1
Method
                  BLASTX
NCBI GI
                  g3250675
BLAST score
                  181
                  1.0e-13
E value
Match length
                  70
                  53
% identity
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
                  304193
Seq. No.
Seq. ID
                  nwy700447583.h1
Method
                  BLASTN
```

43028

g22312

70 3.0e-31

NCBI GI BLAST score

E value

```
Match length
% identity
                   90
NCBI Description
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
                   abscisic acid)
Seq. No.
                   304194
                   nwy700447749.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4335735
BLAST score
                   145
E value
                   2.0e-09
Match length
                   39
% identity
                   59
NCBI Description
                  (AC006248) hypothetical protein [Arabidopsis thaliana]
                   304195
Seq. No.
Seq. ID
                   nwy700447770.h1
Method
                   BLASTX
NCBI GI
                   g4335729
BLAST score
                   217
E value
                   7.0e-18
Match length
                   86
% identity
                   47
NCBI Description
                   (AC006248) putative salt-inducible protein [Arabidopsis
                   thaliana]
Seq. No.
                   304196
Seq. ID
                   nwy700447841.hl
Method
                   BLASTX
NCBI GI
                   g1076678
BLAST score
                   193
E value
                   5.0e-15
Match length
                   72
% identity
                   62
NCBI Description
                  ubiquitin / ribosomal protein S27a - potato (fragment)
                   304197
Seq. No.
Seq. ID
                   nwy700447891.h1
Method
                   BLASTX
NCBI GI
                   g3549679
BLAST score
                   224
E value
                   1.0e-18
Match length
                   61
% identity
                   79
NCBI Description
                   (AL031394) putative protein [Arabidopsis thaliana]
Seq. No.
                   304198
Seq. ID
                   nwy700448002.hl
Method
                   BLASTX
NCBI GI
                   g1465735
```

NCBI GI g146573
BLAST score 235
E value 1.0e-34
Match length 89
% identity 78

NCBI Description (U44133) violaxanthin de-epoxidase precursor [Arabidopsis

thaliana] >gi_3063441 (AC003981) F22013.3 [Arabidopsis

thaliana]



```
304199
Seq. No.
Seq. ID
                   nwy700448013.h1
Method
                   BLASTX
NCBI GI
                   g2570203
BLAST score
                   169
                   3.0e-12
E value
Match length
                   92
                   39
% identity
                   (U59235) unknown [Synechococcus PCC7942]
NCBI Description
Seq. No.
                   304200
Seq. ID
                   nwy700448052.h1
Method
                   BLASTX
                   q587566
NCBI GI
BLAST score
                   157
E value
                   6.0e-20
Match length
                   90
% identity
                   57
NCBI Description
                   (X80237) mitochondrial processing peptidase [Solanum
                   tuberosum]
Seq. No. Seq. ID
                   304201
                   nwy700448108.h1
Method
                   BLASTN
NCBI GI
                   q206738
BLAST score
                   114
E value
                   9.0e-58
Match length
                   134
% identity
                   96
NCBI Description Rat ribosomal protein S11 mRNA, complete cds
Seq. No.
                   304202
Seq. ID
                   nwy700448122.h1
Method
                   BLASTN
NCBI GI
                   q3282162
BLAST score
                   39
E value
                   1.0e-12
                   59
Match length
                   92
% identity
NCBI Description
                  Homo sapiens chromosome 5, P1 clone 737H5 (LBNL H36),
                  complete sequence [Homo sapiens]
Seq. No.
                   304203
Seq. ID
                  nwy700448163.h1
Method
                  BLASTX
NCBI GI
                  g2723473
BLAST score
                  278
                  5.0e-25
E value
Match length
                  61
% identity
                  92
NCBI Description
                   (D89726) defender against apoptotic death 1 protein [Oryza
                  sativa] >gi 2723883 dbj BAA24104 (D89727) defender against
```

Seq. No. 304204

Seq. ID nwy700448206.h1

43030

apoptotic death 1 protein [Oryza sativa]



Method BLASTX
NCBI GI g1709551
BLAST score 539
E value 2.0e-55
Match length 103
% identity 97

NCBI Description CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) / LYSOPHOSPHOLIPASE >gi_967278_bbs_166307 (S77829) phospholipase A2, PLA2 [rats, brain, Peptide, 752

aa] [Rattus sp.]

Seq. No. 304205

Seq. ID nwy700448214.h1

Method BLASTN
NCBI GI 94503014
BLAST score 137
E value 2.0e-71
Match length 185
% identity 94

NCBI Description Homo sapiens copine III (CPNE3) mRNA

>gi_3327085_dbj_AB014536_AB014536 Homo sapiens mRNA for

KIAA0636 protein, complete cds

Seq. No. 304206

Seq. ID nwy700448233.h1

Method BLASTN
NCBI GI g2641953
BLAST score 125
E value 3.0e-64
Match length 145
% identity 97

NCBI Description Rattus norvegicus mRNA for antizyme inhibitor, complete cds

Seq. No. 304207

Seq. ID nwy700448267.h1

Method BLASTX
NCBI GI g4505307
BLAST score 218
E value 1.0e-19
Match length 92
% identity 58

NCBI Description myosin VIIA (Usher syndrome 1B (autosomal recessive,

severe)) >gi_1235670 (U39226) myosin VIIA [Homo sapiens]

Seq. No. 304208

Seq. ID nwy700448294.h1

Method BLASTN
NCBI GI g1673440
BLAST score 169
E value 2.0e-90
Match length 185
% identity 98

NCBI Description M.musculus 94kb genomic sequence encoding Tsx gene

Seq. No. 304209

Seq. ID nwy700448317.h1

Method BLASTN

```
NCBI GI
                    g510910
                   79
BLAST score
                   1.0e-36
E value
                   178
Match length
                   87
% identity
NCBI Description
                   L.temulentum mRNA for histone H3
                   304210
Seq. No.
                   nwy700448369.h1
Seq. ID
Method
                   BLASTN
                   g687711
NCBI GI
BLAST score
                   104
                   9.0e-52
E value
Match length
                   164
% identity
                   93
                   Rattus norvegicus lens epithelial protein mRNA, complete
NCBI Description
Seq. No.
                   304211
Seq. ID
                   nwy700448388.hl
Method
                   BLASTX
NCBI GI
                   q1710546
BLAST score
                   147
E value
                   1.0e-09
Match length
                   53
                   58
% identity
                   60S RIBOSOMAL PROTEIN L36 >qi 1276967 (U47095) putative
NCBI Description
                   ribosomal protein [Daucus carota]
                   304212
Seq. No.
                   nwy700448391.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1170084
                   240
BLAST score
E value
                   6.0e-33
Match length
                   82
% identity
                   91
                   GLUTATHIONE S-TRANSFERASE YC-1 (CHAIN 2) (GST YC1)
NCBI Description
                    (CLASS-ALPHA) >gi_92307_pir_ A26753 glutathione transferase (EC 2.5.1.18) Yc1 - rat >gi_204517 (K01932) glutathione
                   S-transferase Yc subunit [Rattus norvegicus]
                   >gi 576438 emb CAA55405 (X78848) glutathione transferase
                    [Rattus norvegicus]
                   304213
Seq. No.
Seq. ID
                   nwy700448459.h1
```

Method BLASTX NCBI GI g2459448

BLAST score 281 E value 3.0e-25 Match length 82 % identity 67

NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis

thaliana]

Seq. No. 304214

Seq. ID nwy700448461.h1



```
* Method
                     BLASTX
  NCBI GI
                     q2316016
  BLAST score
                     211
  E value
                     4.0e-17
  Match length
                     101
                     44
  % identity
                     (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                     304215
  Seq. ID
                     pmx700081823.h1
  Method
                     BLASTN
  NCBI GI
                     g22274
  BLAST score
                     66
  E value
                     8.0e-29
  Match length
                     66
                     100
  % identity
                     Maize 26S - 17S rDNA spacer region from Black Mexican Sweet
  NCBI Description
                     (BMS) suspension cells
  Seq. No.
                     304216
  Seq. ID
                     pmx700081830.hl
  Method
                     BLASTX
  NCBI GI
                     q3924609
  BLAST score
                     146
                     1.0e-11
  E value
  Match length
                     94
  % identity
                     41
                     (AF069442) putative polyprotein of LTR transposon
  NCBI Description
                     [Arabidopsis thaliana]
                     304217
  Seq. No.
  Seq. ID
                     pmx700081840.h1
  Method
                     BLASTX
  NCBI GI
                     g2119927
  BLAST score
                     401
  E value
                     2.0e-39
  Match length
                     94
                     81
  % identity
  NCBI Description translation elongation factor G, chloroplast - soybean
  Seq. No.
                     304218
  Seq. ID
                     pmx700081860.h1
  Method
                     BLASTX
  NCBI GI
                     g3021348
  BLAST score
                     266
                     9.0e-24
  E value
  Match length
                     66
  % identity
                     77
                     (AJ004961) ribosomal protein L18 [Cicer arietinum]
  NCBI Description
                     304219
  Seq. No.
  Seq. ID
                     pmx700081884.h1
                     BLASTX
  Method
  NCBI GI
                     g2459426
  BLAST score
                     140
                     4.0e-16
  E value
```

95

Match length



% identity

NCBI Description (AC002332) putative splicing factor U2AF large chain

[Arabidopsis thaliana]

Seq. No. 304220

Seq. ID pmx700081885.h1

Method BLASTX NCBI GI g4262174 BLAST score 319 E value 1.0e-29 Match length 101 % identity 57

NCBI Description (AC005508) 9058 [Arabidopsis thaliana]

Seq. No. 304221

Seq. ID pmx700081909.h1

Method BLASTX NCBI GI g3913018 BLAST score 339 E value 4.0e-32 Match length 67 % identity 97

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

(ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic

aldolase [Oryza sativa]

Seq. No. 304222

Seq. ID pmx700081934.h1

Method BLASTX NCBI GI g129708 BLAST score 144 E value 3.0e-09 Match length 43

% identity 65

NCBI Description PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR (PCR)

(NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE)

>gi_82417_pir__S04783 protochlorophyllide reductase (EC
1.3.1.33) precursor - barley >gi_19061_emb_CAA33879
(X15869) precursor peptide (AA -74 to 314) [Hordeum vulgare] >gi_227065_prf__1613434A protochlorophyllide

oxidoreductase [Hordeum vulgare var. distichum]

Seq. No. 304223

Seq. ID pmx700081951.h1

Method BLASTXNCBI GI g4099919 BLAST score 154 2.0e-10 E value Match length 58 55 % identity

NCBI Description (U91981) pollen allergen homolog [Triticum aestivum]

Seq. No. 304224

Seq. ID pmx700081971.h1

Method BLASTX NCBI GI g2398831 BLAST score 309

```
E value
                    .0e-28
Match length
                   63
% identity
                  87
                  (X75542) 4-coumarate:CoA ligase [Vanilla planifolia]
NCBI Description
Seq. No.
                  304225
Seq. ID
                  pmx700081989.hl
Method
                  BLASTX
                  g419789
NCBI GI
BLAST score
                  153
E value
                  2.0e-10
Match length
                   56
% identity
                   52
NCBI Description hypothetical protein - potato
Seq. No.
                  304226
Seq. ID
                  pmx700082038.h1
Method
                  BLASTX
NCBI GI
                  q4454012
BLAST score
                  316
E value
                   1.0e-29
Match length
                  77
% identity
                  70
NCBI Description
                   (AL035396) Pollen-specific protein precursor like
                   [Arabidopsis thaliana]
Seq. No.
                  304227
Seq. ID
                  pmx700082065.h1
Method
                  BLASTX
NCBI GI
                  g1076685
BLAST score
                  159
E value
                  3.0e-11
Match length
                   41
% identity
                   63
NCBI Description
                  SPF1 protein - sweet potato >gi 484261 dbj BAA06278
                   (D30038) SPF1 protein [Ipomoea batatas]
Seq. No.
                  304228
Seq. ID
                  pmx700082072.h1
Method
                  BLASTX
NCBI GI
                  g4063760
BLAST score
                  192
E value
                  7.0e-15
Match length
                  91
% identity
                  46
NCBI Description
                  (AC005561) putative POL3 protein [Arabidopsis thaliana]
Seq. No.
                  304229
Seq. ID
                  pmx700082075.h1
Method
                  BLASTX
NCBI GI
                  g481762
```

Method BLASTX
NCBI GI g481762
BLAST score 149
E value 8.0e-10
Match length 81
% identity 36

NCBI Description beta-adaptin 1 - fruit fly (Drosophila melanogaster)

>gi_434902_emb_CAA53509_ (X75910) beta-adaptin Drosophila 1



[Drosophila melanogaster]

```
304230
Seq. No.
Seq. ID
                   pmx700082113.h1
Method
                   BLASTX
NCBI GI
                   g4512624
BLAST score
                   411
                   1.0e-40
E value
                   98
Match length
                   79
% identity
                   (AC004793) Strong similarity to gi 3033401 F19I3.29
NCBI Description
                   putative potassium transporter from Arabidopsis thaliana
                   BAC gb AC004238
Seq. No.
                   304231
Seq. ID
                   pmx700082118.h1
Method
                   BLASTX
NCBI GI
                   g4056478
BLAST score
                   197
E value
                   2.0e-22
Match length
                   100
% identity
                   61
NCBI Description
                   (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                   304232
Seq. ID
                   pmx700082123.h1
Method
                   BLASTN
NCBI GI
                   q4140643
BLAST score
                   57
                   2.0e-23
E value
Match length
                   93
% identity
                   90
NCBI Description
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                   complete sequence
Seq. No.
                   304233
Seq. ID
                   pmx700082162.h1
Method
                   BLASTX
                   q4099092
NCBI GI
BLAST score
                   269
                   8.0e-24
E value
                   77
Match length
                   65
% identity
NCBI Description
                   (U83179) unknown [Arabidopsis thaliana]
Seq. No.
                   304234
Seq. ID
                   pmx700082222.h1
Method
                   BLASTX
NCBI GI
                   g4006869
BLAST score
                   166
                   2.0e-18
E value
                   77
Match length
                   62
% identity
NCBI Description
                  (Z99707) patatin-like protein [Arabidopsis thaliana]
```

43036

304235

pmx700082281.h1

Seq. No. Seq. ID



```
Method
                   BLASTN
NÇBI GI
                   q3821780
BLAST score
                   36
E value
                   4.0e-11
Match length
                   36
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   304236
Seq. No.
Seq. ID
                   pmx700082285.h1
Method
                   BLASTX
NCBI GI
                   q729135
BLAST score
                   215
E value
                   6.0e-18
Match length
                   54
% identity
                   83
NCBI Description
                   CAFFEIC ACID 3-O-METHYLTRANSFERASE
                    (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC \overline{2.1.1.6}) - maize
                   >gi_168532 (M73235) O-methyltransferase [Zea mays]
Seq. No.
                   304237
Seq. ID
                   pmx700082292.h1
Method
                   BLASTX
NCBI GI
                   q3059131
BLAST score
                   200
E value
                   7.0e-16
Match length
                   73
% identity
                   55
                   (AJ000478) cytochrome P450 [Helianthus tuberosus]
NCBI Description
Seq. No.
                   304238
Seq. ID
                   pmx700082318.hl
Method
                   BLASTX
                   g3283026
NCBI GI
BLAST score
                   162
E value
                   3.0e-11
Match length
                   86
                   44
% identity
NCBI Description
                   (AF051562) putative transposase [Arabidopsis thaliana]
Seq. No.
                   304239
Seq. ID
                   pmx700082381.h1
Method
                   BLASTX
NCBI GI
                   g3063706
BLAST score
                   227
                   5.0e-19
E value
Match length
                   83
                   49
% identity
                   (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 304240

Seq. ID pmx700082412.h1

Method BLASTX NCBI GI g4263717 BLAST score 201

E value 6.0e-16 Match length 94 % identity 49

(AC006223) putative inositol polyphosphate 5-phosphatase NCBI Description

[Arabidopsis thaliana]

Seq. No. 304241

Seq. ID pmx700082502.h1

Method BLASTN NCBI GI q2662346 BLAST score 36 E value 6.0e-11 Match length 64

89 % identity

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

304242 Seq. No.

Seq. ID pmx700082563.h1

Method BLASTX NCBI GI g114268 190 BLAST score E value 6.0e-15 Match length 54 % identity 54

L-ASCORBATE OXIDASE HOMOLOG PRECURSOR (ASCORBASE) NCBI Description

>gi_541907_pir__S23763 gene Bp10 protein - rape

>gi_17789_emb_CAA45554_ (X64257) protein homologous to

ascorbate oxidase [Brassica napus]

304243 Seq. No.

pmx700082565.h1 Seq. ID

Method BLASTN NCBI GI q1185553 BLAST score 43 E value 5.0e-15 Match length 91 % identity 54

Zea mays qlyceraldehyde-3-phosphate dehydrogenase (gpc2) NCBI Description

gene, complete cds

Seq. No. 304244

Seq. ID pmx700082587.h1

Method BLASTX NCBI GI g2262159 BLAST score 144 E value 1.0e-09 Match length 48 % identity 62

(AC002329) predicted protein similar to S.pombe protein NCBI Description

C5H10.03 [Arabidopsis thaliana]

304245 Seq. No.

Seq. ID pmx700082591.h1

Method BLASTX NCBI GI g4239821 BLAST score 346 7.0e-33 E value



Match length 84
% identity 79
NCBI Description (AB010876) germin-like protein 1 [Oryza sativa]
Seq. No. 304246
Seq. ID 9mx700082595.h1

Method BLASTN
NCBI GI 94234845
BLAST score 141
E value 2.0e-73

E value 2.0eMatch length 141
% identity 100
NCBL Description 7ea n

NCBI Description Zea mays copia-like retrotransposon Sto-17, partial

sequence

Seq. No. 304247

Seq. ID pmx700082616.h1

Method BLASTX
NCBI GI g1296955
BLAST score 255
E value 2.0e-22
Match length 75
% identity 40

NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]

Seq. No. 304248

Seq. ID pmx700082619.h1

Method BLASTX
NCBI GI g131770
BLAST score 232
E value 1.0e-19
Match length 61
% identity 70

% identity

NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)

(VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024

ribosomal protein S9.e - slime mold (Dictyostelium

discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein

[Dictyostelium discoideum]

Seq. No. 304249

Seq. ID pmx700082632.h1

Method BLASTX
NCBI GI 94544423
BLAST score 258
E value 1.0e-22
Match length 66
% identity 70

NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304250

Seq. ID pmx700082652.h1

Method BLASTX
NCBI GI g627468
BLAST score 211
E value 4.0e-17
Match length 84
% identity 49





NCBI Description hypothetical protein 1 - human >gi_285983_dbj_BAA02799_ (D13635) KIAA0010 [Homo sapiens]

Seq. No. 304251

Seq. ID pmx700082679.h1

Method BLASTX
NCBI GI g120670
BLAST score 353
E value 8.0e-34
Match length 67
% identity 100

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_100879_pir__S06879 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12) C - maize

>gi_295853_emb_CAA33620 (X15596) GAPDH [Zea mays]

Seq. No. 304252

Seq. ID pmx700082703.h1

Method BLASTX
NCBI GI g3047114
BLAST score 369
E value 2.0e-35
Match length 104
% identity 67

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 304253

Seq. ID pmx700082835.h1

Method BLASTX
NCBI GI g140701
BLAST score 163
E value 2.0e-11
Match length 100
% identity 36

NCBI Description HYPOTHETICAL 26.5 KD PROTEIN IN TOLC-RIBB INTERGENIC REGION

(ORFB) (O265) >gi_96076_pir__S22363 hypothetical protein B - Escherichia coli >gi_146680 (M77129) ORFB [Escherichia coli] >gi_1789419 (AE000386) orf, hypothetical protein

[Escherichia coli]

Seq. No. 304254

Seq. ID pmx700082865.h1

Method BLASTX
NCBI GI g2654212
BLAST score 294
E value 8.0e-27
Match length 59
% identity 97

NCBI Description (AF035458) heat shock 70 protein [Spinacia oleracea]

>gi_2773052 (AF039084) heat shock 70 protein [Spinacia

oleracea]

Seq. No. 304255

Seq. ID pmx700082877.h1

Method BLASTX
NCBI GI g3341694
BLAST score 266



E value Match length 100 % identity

NCBI Description (AC003672) PREG-like protein [Arabidopsis thaliana]

Seq. No.

304256 Seq. ID pmx700082932.h1

Method BLASTX NCBI GI q3135493 BLAST score 210 E value 6.0e-17 Match length 103 % identity 45

NCBI Description (AF060248) unknown [Arabidopsis thaliana]

Seq. No.

pmx700082940.h1 Seq. ID

304257

Method BLASTN NCBI GI q22324 BLAST score 187 E value 1.0e-101 Match length 262 % identity 93

NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No. 304258

pmx700082958.h1 Seq. ID

Method BLASTX NCBI GI q1730674 BLAST score 194 E value 4.0e-15 Match length 57 % identity 61

NCBI Description HYPOTHETICAL 62.7 KD PROTEIN IN SEC12-SSK2 INTERGENIC

REGION >gi_2132801_pir__S63361 probable membrane protein

YNR030w - yeast (Saccharomyces cerevisiae) >gi_1302525_emb_CAA96310_ (Z71645) ORF YNR030w [Saccharomyces cerevisiae]

Seq. No. 304259

Seq. ID pmx700082972.h1

Method BLASTX NCBI GI g3859602 BLAST score 249 E value 2.0e-21 Match length 87 % identity 48

NCBI Description (AF104919) contains similarity to human

DHHC-domain-containing cysteine-rich protein (GB:U90653) and several S. cerevisiae probable membrane proteins (GB:U20865, Z48758, U43491) [Arabidopsis thaliana]

Seq. No. 304260

Seq. ID pmx700082985.h1

Method BLASTX NCBI GI g3021270 BLAST score 147

```
1.0e-
```

E value 1.0e-09
Match length 71
% identity 42

NCBI Description (AL022347) serine/threonine kinase -like protein

[Arabidopsis thaliana]

Seq. No. 304261

Seq. ID pmx700082988.h1

Method BLASTX
NCBI GI g2880051
BLAST score 196
E value 2.0e-15
Match length 84

% identity 50

NCBI Description (AC002340) putative protein kinase [Arabidopsis thaliana]

Seq. No. 304262

Seq. ID pmx700083002.h1

Method BLASTX
NCBI GI g1705924
BLAST score 221
E value 3.0e-18
Match length 94
% identity 45

NCBI Description CLPB PROTEIN >gi_885934 (U20646) ClpB [Synechococcus sp.]

Seq. No. 304263

Seq. ID pmx700083021.h1

Method BLASTX
NCBI GI g509810
BLAST score 429
E value 1.0e-42
Match length 93
% identity 87

NCBI Description (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No. 304264

Seq. ID pmx700083041.h1

Method BLASTX
NCBI GI g3241944
BLAST score 320
E value 6.0e-30
Match length 87
% identity 63

NCBI Description (AC004625) DNA-(apurinic or apyrimidinic site) lyase, ARP

[Arabidopsis thaliana]

Seq. No. 304265

Seq. ID pmx700083108.h1

Method BLASTX
NCBI GI g3461836
BLAST score 395
E value 1.0e-38
Match length 105
% identity 70

NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana] >gi_3927841 (AC005727) putative protein kinase [Arabidopsis



thaliana]

 Seq. No.
 304266

 Seq. ID
 pmx700083123.h1

 Method
 BLASTX

 NODI GI
 pmx700016

NCBI GI g129916 BLAST score 379 E value 1.0e-36 Match length 78 % identity 96

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY

phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
>gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

Seq. No. 304267

Seq. ID pmx700083130.h1

Method BLASTX
NCBI GI g3242785
BLAST score 265
E value 2.0e-23
Match length 93
% identity 55

NCBI Description (AF055355) respiratory burst oxidase protein C [Arabidopsis

thaliana]

Seq. No. 304268

Seq. ID pmx700083236.h1

Method BLASTX
NCBI GI g3786007
BLAST score 187
E value 3.0e-14
Match length 87
% identity 44

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304269

Seq. ID pmx700083238.h1

Method BLASTX
NCBI GI g3292826
BLAST score 147
E value 2.0e-09
Match length 30
% identity 87

NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304270

Seq. ID pmx700083275.h1

Method BLASTX
NCBI GI g3914056
BLAST score 303
E value 6.0e-28
Match length 93
% identity 65

NCBI Description DNA MISMATCH REPAIR PROTEIN MSH2 >gi 2522362 (AF002706)

MutS homolog 2 [Arabidopsis thaliana] >gi_2522364 (AF003005) MutS homolog 2 [Arabidopsis thaliana]



>gi_2547236 (AF026549) DNA mismatch repair protein MSH2
[Arabidopsis thaliana]

 Seq. No.
 304271

 Seq. ID
 pmx700083294.h1

 Method
 BLASTX

 NCBI GI
 g1345132

 BLAST score
 314

E value 3.0e-29 Match length 89 69

NCBI Description (U47029) ERECTA [Arabidopsis thaliana]

>gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase

[Arabidopsis thaliana] >gi_3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 304272

Seq. ID pmx700083316.h1

Method BLASTX
NCBI GI g3176965
BLAST score 194
E value 1.0e-32
Match length 89
% identity 77

NCBI Description (AF067967) pyrroline-5-carboxylate synthetase

[Mesembryanthemum crystallinum]

Seq. No. 304273

Seq. ID pmx700083338.h1

Method BLASTX
NCBI GI g2147484
BLAST score 468
E value 3.0e-47
Match length 100
% identity 89

NCBI Description homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)

homeobox protein [Phalaenopsis sp. 'hybrid SM9108']

Seq. No. 304274

Seq. ID pmx700083382.h1

Method BLASTX
NCBI GI g1707020
BLAST score 235
E value 4.0e-20
Match length 79
% identity 52

NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304275

Seq. ID pmx700083430.h1

Method BLASTX
NCBI GI g2642648
BLAST score 266
E value 4.0e-25
Match length 78
% identity 85

NCBI Description (AF033852) cytosolic heat shock 70 protein; HSC70-3





[Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No. 304276

Seq. ID pmx700083446.h1

Method BLASTX
NCBI GI g4220528
BLAST score 325
E value 2.0e-30
Match length 81
% identity 75

NCBI Description (AL035356) glucose-6-phosphate isomerase [Arabidopsis

thaliana]

Seq. No. 304277

Seq. ID pmx700083456.h1

Method BLASTX
NCBI GI g1184774
BLAST score 231
E value 2.0e-19
Match length 52
% identity 87

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 304278

Seq. ID pmx700083528.h1

Method BLASTX
NCBI GI g122007
BLAST score 142
E value 3.0e-12
Match length 45
% identity 73

NCBI Description HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley

>gi_20448_emb_CAA37828 (X53831) H2A histone protein (AA 1

- 149) [Petroselinum crispum]

Seq. No. 304279

Seq. ID pmx700083542.h1

Method BLASTX
NCBI GI g1655536
BLAST score 175
E value 4.0e-13
Match length 40
% identity 75

NCBI Description (Y09095) chloride channel [Arabidopsis thaliana]

>gi_1742957_emb_CAA96059_ (Z71447) CLC-c chloride channel

protein [Arabidopsis thaliana]

Seq. No. 304280

Seq. ID pmx700083555.h1

Method BLASTX
NCBI GI g4220474
BLAST score 192
E value 8.0e-15
Match length 45



% identity 82

NCBI Description (AC006069) putative myosin heavy chain [Arabidopsis

thaliana]

Seq. No.

304281

Seq. ID

pmx700083635.hl

Method NCBI GI BLASTX g3540206

BLAST score

326

E value Match length % identity 1.0e-30 83 66

NCBI Description

(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.

304282

Seq. ID

pmx700083683.h1

Method NCBI GI BLASTX g1705463 226

BLAST score E value Match length

3.0e-30

% identity

75 91

NCBI Description

BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir__S71201 biotin sythase - Arabidopsis thaliana >gi_1045316 (U24147) biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806) BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413) biotin synthase [Arabidopsis thaliana] >gi_1769457 (L34413)

biotin synthase [Arabidopsis thaliana] >gi_2288983 (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]

>gi_1589016_prf__2209438A biotin synthase [Arabidopsis thaliana

thaliana]

Seq. No.

304283

Seq. ID

pmx700083694.h1

Method NCBI GI BLAST score BLASTX g3402749 158

E value Match length % identity

4.0e-16 84

51

NCBI Description

(AL031187) putative protein [Arabidopsis thaliana]

Seq. No.

304284

Seq. ID

pmx700083705.h1

Method NCBI GI BLASTX g3249105

BLAST score E value Match length

181 7.0e-14

% identity

40 82

NCBI Description

(AC003114) Contains similarity to protein phosphatase 2C

(ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.

304285

Seq. ID

pmx700083716.h1

Method NCBI GI BLASTX q3874685

BLAST score

1̃71



E value 2.0e-12
Match length 89
% identity 35

NCBI Description (Z78539) Similarity to S.pombe hypothetical protein C4G8.04

(SW:YAD4_SCHPO); cDNA EST EMBL:D27846 comes from this gene; cDNA EST EMBL:D27845 comes from this gene; cDNA EST

cDNA EST EMBL:D27845 comes from this gene; cDNA EST yk202h7.3 comes from this gene; cDNA EST yk202h7.5 come

Seq. No. 304286

Seq. ID pmx700083750.h1

Method BLASTX
NCBI GI g2244807
BLAST score 229
E value 3.0e-19
Match length 81
% identity 52

NCBI Description (297336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304287

Seq. ID pmx700083765.h1

Method BLASTX
NCBI GI g3249113
BLAST score 287
E value 5.0e-26
Match length 92
% identity 71

NCBI Description (AC003114) Strong similarity to kinesin homolog IG002P16.12

gb_2191180 from A. thaliana BAC gb AF007270. [Arabidopsis

thaliana]

Seq. No. 304288

Seq. ID pmx700083782.h1

Method BLASTX
NCBI GI g3831457
BLAST score 311
E value 7.0e-29
Match length 90
% identity 67

NCBI Description (AC005700) putative ion channel protein [Arabidopsis

thaliana]

Seq. No. 304289

Seq. ID pmx700083813.h1

Method BLASTX
NCBI GI g2583123
BLAST score 300
E value 2.0e-27
Match length 94
% identity 62

NCBI Description (AC002387) putative nucleotide sugar epimerase [Arabidopsis

thaliana]

Seq. No. 304290

Seq. ID pmx700083827.h1

Method BLASTX
NCBI GI g2244772
BLAST score 186

```
E value 3.0e-14
Match length 72
% identity 53
NCBI Description (Z97335) transport protein [Arabidopsis thaliana]
Seq. No. 304291
Seq. ID pmx700083862.h1
```

Method BLASTX
NCBI GI g3056595
BLAST score 201
E value 6.0e-16
Match length 91
% identity 51

NCBI Description (AC004255) T1F9.16 [Arabidopsis thaliana]

Seq. No. 304292

Seq. ID pmx700083867.h1

Method BLASTX
NCBI GI g282994
BLAST score 395
E value 1.0e-38
Match length 83
% identity 86

NCBI Description Sip1 protein - barley >gi 167100 (M77475) seed imbibition

protein [Hordeum vulgare]

Seq. No. 304293

Seq. ID pmx700083913.h1

Method BLASTX
NCBI GI g2702273
BLAST score 180
E value 2.0e-13
Match length 100
% identity 43

NCBI Description (AC003033) carrot B2 protein-like [Arabidopsis thaliana]

Seq. No. 304294

Seq. ID pmx700083939.h1

Method BLASTN
NCBI GI g21800
BLAST score 80
E value 3.0e-37
Match length 195
% identity 76

NCBI Description T.aestivum L mRNA for histone H2B

Seq. No. 304295

Seq. ID pmx700083949.h1

Method BLASTX
NCBI GI g1617270
BLAST score 397
E value 8.0e-39
Match length 109
% identity 67

NCBI Description (X94624) acyl-CoA synthetase [Brassica napus]

Seq. No. 304296

Seq. No.

Seq. ID

304301

pmx700084087.h1



```
Seq. ID
                   pmx700083955.h1
Method
                   BLASTX
NCBI GI
                   a4530126
BLAST score
                   172
E value
                   2.0e-12
Match length
                   74
% identity
                   49
NCBI Description
                   (AF078082) receptor-like protein kinase homolog RK20-1
                   [Phaseolus vulgaris]
Seq. No.
                   304297
Seq. ID
                   pmx700083974.h1
Method
                   BLASTX
NCBI GI
                   g4019300
BLAST score
                   155
E value
                   2.0e-10
Match length
                   97
% identity
                   16
NCBI Description
                   (AF083424) orf 73 [Ateline herpesvirus 3]
Seq. No.
                   304298
Seq. ID
                   pmx700083986.h1
Method
                   BLASTX
NCBI GI
                   g2244898
BLAST score
                   285
E value
                   1.0e-25
Match length
                   103
% identity
                   50
NCBI Description
                   (Z97338) strong similarity to protein phosphatase 2A
                   regulatory chain, 74K [Arabidopsis thaliana]
Seq. No.
                   304299
Seq. ID
                   pmx700084030.h1
Method
                   BLASTX
NCBI GI
                   g2792214
BLAST score
                   152
E value
                   3.0e-10
Match length
                   81
% identity
                   41
NCBI Description
                   (AF032685) NBS-LRR type resistance protein [Hordeum
                   vulgare]
Seq. No.
                   304300
Seq. ID
                   pmx700084059.h1
Method
                   BLASTX
NCBI GI
                   g140207
BLAST score
                   208
E value
                   9.0e-17
Match length
                   58
% identity
                   64
NCBI Description
                   PROBABLE 40S RIBOSOMAL PROTEIN S9 >gi 102109 pir S12674
                   ribosomal protein S9.e - Trypanosoma brucei >gi_10399_emb_CAA36818_ (X52586) ald orfU protein (AA 1 -
                   190) [Trypanosoma brucei]
```



```
Method
NCBI GI
                  q4371296
BLAST score
                  166
E value
                  7.0e-12
Match length
                  74
% identity
                  49
NCBI Description
                  (AC006260) putative receptor protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  304302
Seq. ID
                  pmx700084088.h1
Method
                  BLASTX
NCBI GI
                  g2149640
BLAST score
                  162
E value
                  2.0e-11
Match length
                  41
                  76
% identity
NCBI Description
                  (U91995) Argonaute protein [Arabidopsis thaliana]
                  304303
Seq. No.
                  pmx700084102.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  7.0e-11
Match length
                  48
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  304304
                  pmx700084125.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4581207
BLAST score
                  164
E value
                  2.0e-11
Match length
                  75
% identity
                  40
NCBI Description
                  (Y17914) cyclic nucleotide and calmodulin-regulated ion
                  channel [Arabidopsis thaliana]
Seq. No.
                  304305
Seq. ID
                  pmx700084302.h1
Method
                  BLASTX
NCBI GI
                  q4539458
BLAST score
                  149
E value
                  9.0e-10
Match length
                  101
% identity
                  39
NCBI Description
                  (AL049500) hypothetical protein [Arabidopsis thaliana]
```

304306 Seq. No. Seq. ID pmx700084309.h1

Method BLASTX NCBI GI g4580398 BLAST score 180

2.0e-13

Match length 63

E value



```
% identity
NCBI Description
                   (AC007171) putative protein kinase APK1A [Arabidopsis
                   thaliana]
                   304307
Seq. No.
Seq. ID
                   pmx700084322.h1
Method
                   BLASTX
NCBI GI
                   g2911048
BLAST score
                   177
                   4.0e-13
E value
Match length
                   90
% identity
                   50
NCBI Description
                  (AL021961) hypothetical protein [Arabidopsis thaliana]
                   304308
Seq. No.
Seq. ID
                   pmx700084491.h1
Method
                   BLASTN
NCBI GI
                   g940880
BLAST score
                   39
E value
                   1.0e-12
Match length
                   99
% identity
                   85
NCBI Description Z.mays zag2 gene
Seq. No.
                   304309
Seq. ID
                   pmx700084512.h1
Method
                   BLASTX
NCBI GI
                   q4454012
BLAST score
                   249
                   2.0e-21
E value
Match length
                   75
                   59
% identity
                   (AL035396) Pollen-specific protein precursor like
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   304310
Seq. ID
                   pmx700084547.h1
Method
                   BLASTX
NCBI GI
                   g3549667
BLAST score
                   328
E value
                   9.0e-31
Match length
                   87
% identity
                  72
NCBI Description
                   (AL031394) Arabidopsis dynamin-like protein ADL2
                   [Arabidopsis thaliana]
Seq. No.
                   304311
Seq. ID
                  pmx700084574.h1
Method
                  BLASTN
```

NCBI GI g22312 BLAST score 69 E value 5.0e-31 Match length 117 % identity 90

NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)



```
Seq. No.
                   304312
Seq. ID
                   pmx700084577.h1
Method
                   BLASTX
NCBI GI
                   q4539320
BLAST score
                   324
E value
                   3.0e-30
Match length
                   103
% identity
                   56
NCBI Description
                   (AL035679) putative endo-1, 4-beta-glucanase [Arabidopsis
Seq. No.
                   304313
Seq. ID
                   pmx700084604.h1
Method
                   BLASTX
NCBI GI
                   g3021280
BLAST score
                   249
E value
                   2.0e-21
Match length
                   108
% identity
                   47
                   (AL022347) serine /threonine kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   304314
Seq. ID
                   pmx700084671.h1
Method
                   BLASTX
                   q3411227
NCBI GI
BLAST score
                   212
E value
                   3.0e-17
Match length
                   89
% identity
                   48
NCBI Description
                   (AF078874) NBS-LRR type disease resistance protein O2
                   [Avena sativa]
Seq. No.
                   304315
Seq. ID
                   pmx700084705.h1
                   BLASTN
Method
NCBI GI
                   g1206012 -
BLAST score
                   45
E value
                   1.0e-16
Match length
                   45
% identity
                   100
NCBI Description
                  Zea mays beta-D-glucosidase precursor (glu2) mRNA, complete
                   cds
                   304316
Seq. No.
Seq. ID
                   pmx700084742.hl
Method
                   BLASTX
NCBI GI
                   q1172836
BLAST score
                   415
                   6.0e-41
E value
                  78
Match length
                  97
% identity
```

GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787) NCBI Description

small ras-related protein [Nicotiana tabacum]

Seq. No.

304317

Seq. ID

pmx700084743.h1

Match length

% identity

91

```
Method
NCBI GI
                   q2088726
BLAST score
                   146
E value
                   2.0e-09
                   63
Match length
% identity
                   44
NCBI Description
                  (AF003140) C44E4.1b gene product [Caenorhabditis elegans]
Seq. No.
                   304318
                   pmx700084784.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2062705
BLAST score
                   35
E value
                   3.0e-10
                   35
Match length
                   100
% identity
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
                   304319
Seq. No.
Seq. ID
                   pmx700084826.h1
Method
                   BLASTX
NCBI GI
                   q4585924
BLAST score
                   189
E value
                   2.0e-14
Match length
                   103
% identity
                   47
NCBI Description
                  (AC007211) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   304320
Seq. ID
                   pmx700084896.h1
Method
                   BLASTX
NCBI GI
                   q3395431
BLAST score
                   257
E value
                   2.0e-22
Match length
                   72
% identity
                   67
NCBI Description
                  (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   304321
Seq. ID
                   pmx700084920.h1
Method
                   BLASTX
NCBI GI
                   g2673911
BLAST score
                   223
E value
                   2.0e-18
Match length
                   66
% identity
                   67
NCBI Description
                   (AC002561) putative squamosa-promoter binding protein
                   [Arabidopsis thaliana]
                   304322
Seq. No.
Seq. ID
                  pmx700084929.hl
Method
                  BLASTX
NCBI GI
                  g3860251
BLAST score
                  346
                  6.0e-33
E value
```





```
NCBI Description
                  (AC005824) putative permease [Arabidopsis thaliana]
                  304323
Seq. No.
Seq. ID
                  pmx700084952.h1
Method
                  BLASTX
NCBI GI
                  q417745
BLAST score
                  142
E value
                  5.0e-25
Match length
                  77
                  86
% identity
NCBI Description
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                  HYDROLASE) (ADOHCYASE) >gi_170773 (L11872)
                  S-adenosyl-L-homocysteine Hydrolase [Triticum aestivum]
Seq. No.
                  304324
                  pmx700084958.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3757523
BLAST score
                  333
E value
                  2.0e-31
Match length
                  103
% identity
                  63
NCBI Description (AC005167) putative transportin [Arabidopsis thaliana]
Seq. No.
                  304325
Seq. ID
                  pmx700084987.h1
Method
                  BLASTX
NCBI GI
                  g4008006
BLAST score
                  141
                  3.0e-09
E value
Match length
                  42
                  69
% identity
                  (AF084034) receptor-like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  304326
Seq. ID
                  pmx700085009.h1
Method
                  BLASTX
NCBI GI
                  g1151244
BLAST score
                  194
E value
                  4.0e-15
Match length
                  60
% identity
                  62
NCBI Description (U43377) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                  304327
Seq. ID
                  pmx700085039.h1
```

Method BLASTN NCBI GI g575730 BLAST score 178 1.0e-95 E value Match length 243 % identity 95

NCBI Description Z.mays mRNA for transmembrane protein

Seq. No. 304328

Seq. ID pmx700085075.h1



```
Method
                  BLASTN
NCBI GI
                  q4388782
BLAST score
                  112
E value
                  3.0e-56
                  274
Match length
                  97
% identity
NCBI Description
                  Zea mays 40S ribosomal protein S27 homolog mRNA, complete
                  304329
Seq. No.
Seq. ID
                  pmx700085120.h1
Method
                  BLASTX
                  g3800952
NCBI GI
BLAST score
                  174
E value
                  8.0e-13
Match length
                  88
                  44
% identity
NCBI Description
                  (AF100657) No definition line found [Caenorhabditis
                  elegans]
                  304330
Seq. No.
Seq. ID
                  pmx700085180.h1
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  6.0e-11
Match length
                  48
% identity
                  67
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                  304331
Seq. ID
                  pmx700085183.h1
Method
                  BLASTX
NCBI GI
                  g3335354
BLAST score
                  237
                  3.0e-20
E value
Match length
                  83
% identity
                  58
NCBI Description
                  (AC004512) This gene is continued from gene F5I14.1 from
                  BAC sequence gb AC001229 from A. thaliana. EST gb AA585814
                  comes from this gene. [Arabidopsis thaliana]
                  304332
Seq. No.
Seq. ID
                  pmx700085238.h1
Method
                  BLASTX
NCBI GI
                  q4006910
BLAST score
                  152
E value
                  2.0e-10
Match length
                  33
% identity
                  82
NCBI Description
                  (Z99708) putative protein [Arabidopsis thaliana]
```

Seq. No. 304333

Seq. ID pmx700085269.h1

Method BLASTX NCBI GI g3367517 BLAST score 233

```
E value
Match length
                   62
% identity
NCBI Description
                   (AC004392) Similar to F4I1.26 putative beta-glucosidase
                  gi_3128187 from A. thaliana BAC gb_AC004521. ESTs
                  gb N97083, gb F19868 and gb F15482 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  304334
Seq. ID
                  pmx700085374.h1
Method
                  BLASTN
NCBI GI
                  q168722
BLAST score
                  35
E value
                  3.0e-10
Match length
                  35
                  100
% identity
NCBI Description Z.mays protein phosphatase-1 (ZmPP1) mRNA, complete cds
                  304335
Seq. No.
                  pmx700085427.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2369714
BLAST score
                  393
E value
                  2.0e-38
Match length
                  86
% identity
                  86
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                  304336
Seq. ID
                  pmx700085504.h1
Method
                  BLASTX
NCBI GI
                  g2914703
BLAST score
                  313
E value
                  5.0e-29
Match length
                  101
% identity
                  56
NCBI Description
                  (AC003974) unknown protein [Arabidopsis thaliana]
Seq. No.
                  304337
Seq. ID
                  pmx700085523.h1
Method
                  BLASTN
                  g473602
NCBI GI
BLAST score
                  107
E value
                  3.0e-53
Match length
                  203
% identity
                  88
NCBI Description Zea mays W-22 histone H2A mRNA, complete cds
Seq. No.
                  304338
Seq. ID
                  pmx700085525.h1
Method
                  BLASTX
```

NCBI GI g2943742 BLAST score 159 E value 6.0e-11 91 Match length % identity 41

NCBI Description (AB002266) XA1 [Oryza sativa]



Seq. No. 304339

Seq. ID pmx700085542.h1

Method BLASTX
NCBI GI g2244990
BLAST score 327
E value 1.0e-30
Match length 94
% identity 72

NCBI Description (Z97340) similarity to LIM homeobox protein -

Caenorhabditis [Arabidopsis thaliana]

Seq. No. 304340

Seq. ID pmx700085564.h1

Method BLASTX
NCBI GI g3834302
BLAST score 358
E value 3.0e-34
Match length 80
% identity 81

NCBI Description (AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase

from Oryza sativa. ESTs gb F14272 and gb F14273 come from

this gene. [Arabidopsis thaliana]

Seq. No. 304341

Seq. ID pmx700085584.h1

Method BLASTX
NCBI GI g2244835
BLAST score 309
E value 1.0e-28
Match length 92
% identity 62

NCBI Description (297337) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 304342

Seq. ID pmx700085644.h1

Method BLASTX
NCBI GI g542179
BLAST score 530
E value 2.0e-54
Match length 98
% identity 100

NCBI Description alpha tubulin - maize >gi_629837_pir__S39998 tubulin alpha

chain - maize (fragment) >gi_393401_emb_CAA52158_ (X73980)

alpha tubulin [Zea mays]

Seq. No. 304343

Seq. ID pmx700085692.h1

Method BLASTX
NCBI GI g1184776
BLAST score 399
E value 4.0e-39
Match length 77
% identity 100

NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC4 [Zea mays]

NCBI GI

E value

BLAST score

g3183426

4.0e-09

143



```
Seq. No.
                   304344
                   pmx700085712.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2345154
BLAST score
                   351
E value
                   2.0e-33
Match length
                   67
% identity
                   100
NCBI Description
                  (AF015522) ribsomal protein S4 [Zea mays]
                   304345
Seq. No.
Seq. ID
                   pmx700085715.h1
Method
                   BLASTX
NCBI GI
                   g4191797
BLAST score
                   154
E value
                   2.0e-10
Match length
                   98
                   34
% identity
NCBI Description
                   (AC005917) putative receptor protein kinase, 3' partial
                   [Arabidopsis thaliana]
Seq. No.
                   304346
Seq. ID
                   pmx700085722.h1
Method
                   BLASTX
                   g3757520
NCBI GI
BLAST score
                   151
E value
                   5.0e-10
Match length
                   56
% identity
                   59
NCBI Description
                   (AC005167) unknown protein [Arabidopsis thaliana]
Seq. No.
                   304347
Seq. ID
                   pmx700085770.h1
Method
                   BLASTX
NCBI GI
                   g3953475
BLAST score
                   181
E value
                   8.0e-14
Match length
                   65
% identity
                   49
NCBI Description
                   (AC002328) F2202.20 [Arabidopsis thaliana]
Seq. No.
                   304348
Seq. ID
                   pmx700085802.h1
Method
                   BLASTX
NCBI GI
                   g3928092
BLAST score
                   169
E value
                   4.0e-12
Match length
                   41
% identity
NCBI Description
                  (AC005770) unknown protein [Arabidopsis thaliana]
Seq. No.
                  304349
Seq. ID
                  pmx700085848.h1
Method
                  BLASTX
```



Match length 54 % identity 48

NCBI Description HYPOTHETICAL PROTEIN MJ1559 >gi_2128936_pir__F64494

hypothetical protein MJ1559 - Methanococcus jannaschii >gi_1500452 (U67596) conserved hypothetical protein

[Methanococcus jannaschii]

Seq. No. 304350

Seq. ID pmx700085868.h1

Method BLASTX
NCBI GI g3033400
BLAST score 309
E value 1.0e-28
Match length 102
% identity 58

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 304351

Seq. ID pmx700085874.h1

Method BLASTX
NCBI GI g3676071
BLAST score 403
E value 1.0e-39
Match length 103
% identity 71

NCBI Description (Y17969) ERG protein [Arabidopsis thaliana]

Seq. No. 304352

Seq. ID pmx700085908.h1

Method BLASTX
NCBI GI g2494175
BLAST score 151
E value 5.0e-20
Match length 86
% identity 65

NCBI Description GLUTAMATE DECARBOXYLASE 2 (GAD 2) >gi_1184960 (U46665)

glutamate decarboxylase 2 [Arabidopsis thaliana]

>gi 1236619 (U49937) glutamate decarboxylase [Arabidopsis

thaliana]

Seq. No. 304353

Seq. ID pmx700085931.h1

Method BLASTX
NCBI GI g3024018
BLAST score 266
E value 2.0e-23
Match length 56
% identity 93

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 304354

Seq. ID pmx700085935.h1

Method BLASTX

Match length

% identity

251



```
NCBI GI
                      q4406759
   BLAST score
                      248
   E value
                      2.0e-21
   Match length
                      76
   % identity
                      67
                     (AC006836) hypothetical protein [Arabidopsis thaliana]
   NCBI Description
                      304355
   Seq. No.
                     pmx700085950.h1
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      q4200122
   BLAST score
                      346
   E value
                     7.0e-33
   Match length
                     83
   % identity
                      80
   NCBI Description
                     (AJ009555) hypothetical protein [Arabidopsis thaliana]
   Seq. No.
                      304356
                     pmx700085975.h1
Seq. ID
   Method
                      BLASTN
   NCBI GI
                      g1213276
   BLAST score
                      93
   E value
                     7.0e-45
   Match length
                     101
   % identity
                      98
   NCBI Description
                     Z.mays ZEMa gene
   Seq. No.
                      304357
                     pmx700085984.h1
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                     g1076777
   BLAST score
                     159
   E value
                      6.0e-11
   Match length
                     55
   % identity
                      62
                     protein H2A - wheat >gi_536890_dbj_BAA07277_ (D38088)
   NCBI Description
                     protein H2A [Triticum aestivum]
   Seq. No.
                      304358
   Seq. ID
                     pmx700086001.h1
   Method
                     BLASTX
   NCBI GI
                     g3080420
   BLAST score
                     159
   E value
                      6.0e-11
   Match length
                     55
   % identity
                      64
   NCBI Description
                      (AL022604) putative sugar transporter protein [Arabidopsis
                     thaliana]
   Seq. No.
                     304359
   Seq. ID
                     pmx700086013.hl
   Method
                     BLASTN
   NCBI GI
                     g397395
   BLAST score
                     251
   E value
                     1.0e-139
```





NCBI Description Z.mays MNB1b mRNA for DNA-binding protein

Seq. No. 304360

Seq. ID pmx700086025.h1

Method BLASTX
NCBI GI g122022
BLAST score 155
E value 2.0e-10
Match length 60
% identity 58

NCBI Description HISTONE H2B >gi_283025_pir_ S22323 histone H2B - wheat

>gi_21801_emb_CAA42530_ (X59873) histone H2B [Triticum

aestivum]

Seq. No. 304361

Seq. ID pmx700086035.h1

Method BLASTX
NCBI GI g3915866
BLAST score 305
E value 4.0e-28
Match length 98
% identity 82

NCBI Description GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)

>gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine

synthetase [Lupinus luteus]

Seq. No. 304362

Seq. ID pmx700086038.h1

Method BLASTX
NCBI GI g4539452
BLAST score 382
E value 4.0e-37
Match length 96
% identity 69

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No. 304363

Seq. ID pmx700086044.h1

Method BLASTX
NCBI GI g1362060
BLAST score 276
E value 1.0e-24
Match length 90
% identity 59

NCBI Description dehydroquinase-shikimate dehydrogenase - garden pea

Seq. No. 304364

Seq. ID pmx700086107.h1

Method BLASTX
NCBI GI g4115383
BLAST score 223
E value 1.0e-18
Match length 84
% identity 52

NCBI Description (AC005967) receptor-like protein kinase [Arabidopsis

thaliana]



```
304365
Seq. No.
Seq. ID
                  pmx700086109.h1
Method
                  BLASTX
NCBI GI
                  q3894157
BLAST score
                  317
E value
                  1.0e-29
Match length
                  85
% identity
                  74
NCBI Description
                   (AC005312) putative protein kinase, 3' partial [Arabidopsis
                  thaliana]
Seq. No.
                  304366
Seq. ID
                  pmx700086121.h1
Method
                  BLASTX
NCBI GI
                  q134598
BLAST score
                  228
                   4.0e-19
E value
Match length
                  53
% identity
                  87
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)
Seq. No.
                  304367
Seq. ID
                  pmx700086124.h1
Method
                  BLASTX
NCBI GI
                  g1565223
BLAST score
                  293
E value
                  6.0e-33
Match length
                  83
% identity
                  93
NCBI Description
                  (Y08301) MCM2-related protein [Arabidopsis thaliana]
Seq. No.
                  304368
Seq. ID
                  pmx700086147.h1
Method
                  BLASTX
NCBI GI
                  g2947062
BLAST score
                  169
E value
                  3.0e-12
Match length
                  53
% identity
                  58
NCBI Description
                  (AC002521) unknown protein [Arabidopsis thaliana]
                  304369
Seq. No.
Seq. ID
                  pmx700086157.h1
Method
                  BLASTX
NCBI GI
                  q3334756
BLAST score
                  260
E value
                  8.0e-23
Match length
                  67
% identity
                  76
NCBI Description
                  (Y16672) putative arginine/serine-rich splicing factor
                  [Medicago sativa]
```

Seq. No. 304370

Seq. ID pmx700086165.h1

Method BLASTN NCBI GI g2687430



BLAST score 63 E value 2.0e-27 Match length 83 % identity 95

NCBI Description Acorus gramineus large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No. 304371

Seq. ID pmx700086166.h1

Method BLASTX
NCBI GI g4028970
BLAST score 193
E value 6.0e-15
Match length 85
% identity 47

NCBI Description (AF060248) pollenless3 [Arabidopsis thaliana]

Seq. No. 304372

Seq. ID pmx700086175.h1

Method BLASTX
NCBI GI g2984709
BLAST score 207
E value 1.0e-17
Match length 68
% identity 71

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 304373

Seq. ID pmx700086257.h1

Method BLASTX
NCBI GI g2341033
BLAST score 446
E value 1.0e-44
Match length 111
% identity 71

NCBI Description (AC000104) Similar to Babesia aldo-keto reductase

(gb_M93122). [Arabidopsis thaliana]

Seq. No. 304374

Seq. ID pmx700086264.h1

Method BLASTX
NCBI GI g3241944
BLAST score 174
E value 1.0e-12
Match length 51
% identity 55

NCBI Description (AC004625) DNA-(apurinic or apyrimidinic site) lyase, ARP

[Arabidopsis thaliana]

Seq. No. 304375

Seq. ID pmx700086293.h1

Method BLASTX
NCBI GI g3702323
BLAST score 371
E value 8.0e-36
Match length 103
% identity 68





```
NCBI Description
                  (AC005397) unknown protein [Arabidopsis thaliana]
                   304376
Seq. No.
Seq. ID
                   pmx700086326.h1
Method
                   BLASTX
NCBI GI
                   q4191774
BLAST score
                   274
E value
                   8.0e-28
Match length
                   95
% identity
                   67
                   (AC005917) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                   304377
Seq. No.
Seq. ID
                   pmx700086348.hl
Method
                   BLASTX
NCBI GI
                   g2129773
BLAST score
                   257
E value
                   2.0e-22
Match length
                   60
% identity
                   70
NCBI Description
                  xyloglucan endotransglycosylase-related protein XTR3 -
                  Arabidopsis thaliana (fragment) >gi_1244752 (U43485)
                  xyloglucan endotransglycosylase-related protein
                   [Arabidopsis thaliana]
Seq. No.
                   304378
Seq. ID
                  pmx700086394.h1
Method
                  BLASTX
NCBI GI
                  g3377823
BLAST score
                  247
E value
                  3.0e-21
Match length
                  99
                  57
% identity
                   (AF076275) Arabidopsis thaliana mitogen-activated protein
NCBI Description
                  kinase (GB:D50468) [Arabidopsis thaliana]
Seq. No.
                  304379
Seq. ID
                  pmx700086412.h1
Method
                  BLASTX
NCBI GI
                  g584892
BLAST score
                  424
E value
                  5.0e-42
Match length
                  100
% identity
                  80
NCBI Description
                  SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
```

>gi_629805_pir__S43516 serine carboxypeptidase I - rice
>gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I

[Oryza sativa]

Seq. No. 304380

Seq. ID pmx700086418.h1

Method BLASTX NCBI GI g2501189 BLAST score 288 E value 3.0e-26 Match length 65



% identity 89

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

>gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
- maize >gi_596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 304381

Seq. ID pmx700086442.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 48

Match length 48 % identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 304382

Seq. ID pmx700086449.h1

Method BLASTX
NCBI GI g3810596
BLAST score 162
E value 2.0e-11
Match length 51
% identity 51

NCBI Description (AC005398) reverse-transcriptase-like protein [Arabidopsis

thaliana]

Seq. No. 304383

Seq. ID pmx700086571.h1

Method BLASTX
NCBI GI g2501021
BLAST score 319
E value 1.0e-29
Match length 93

% identity 65

NCBI Description LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)

>gi_1652562_dbj_BAA17483_ (D90906) lysyl-tRNA synthetase

¥**

[Synechocystis sp.]

Seq. No. 304384

Seq. ID pmx700086604.h1

Method BLASTN
NCBI GI g1143863
BLAST score 35
E value 8.0e-11
Match length 95

% identity 84

NCBI Description Oryza sativa beta-glucosidase mRNA, nuclear gene encoding

chloroplast protein, complete cds

Seq. No. 304385

Seq. ID pmx700086629.h1

Method BLASTX
NCBI GI g3047117
BLAST score 158
E value 4.0e-11
Match length 32



% identity 94

NCBI Description (AF058919) similar to ATP-dependent RNA helicases

[Arabidopsis thaliana]

Seq. No. 304386

Seq. ID pmx700086653.h1

Method BLASTX
NCBI GI g112994
BLAST score 166
E value 4.0e-12
Match length 46
% identity 74

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]

>gi 226091 prf 1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 304387

Seq. ID pmx700086661.h1

Method BLASTX
NCBI GI g4006835
BLAST score 151
E value 4.0e-10
Match length 87
% identity 19

NCBI Description (AC005970) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304388

Seq. ID pmx700086690.h1

Method BLASTX
NCBI GI g4587584
BLAST score 172
E value 1.0e-12
Match length 94
% identity 41

NCBI Description (AC007232) unknown protein [Arabidopsis thaliana]

Seq. No. 304389

Seq. ID pmx700086702.h1

Method BLASTX
NCBI GI g2583120
BLAST score 270
E value 6.0e-24
Match length 102
% identity 54

NCBI Description (AC002387) putative receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 304390

Seq. ID pmx700086730.h1

Method BLASTX
NCBI GI g3451075
BLAST score 388
E value 9.0e-38
Match length 103



```
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                  304391
Seq. No.
                  pmx700086732.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642165
                  148
BLAST score
                  1.0e-09
E value
Match length
                  41
% identity
                  54
NCBI Description
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  304392
                  pmx700086736.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3420038
BLAST score
                  81
E value
                  1.0e-37
Match length
                  269
% identity
                  83
NCBI Description
                  Zea mays gypsy/Ty3-type retrotransposon Tekay, complete
                  sequence
Seq. No.
                  304393
                  pmx700086741.h1
Seq. ID
Method
                  BLASTX
                  g3128234
NCBI GI
BLAST score
                  291
                  2.0e-26
E value
                  59
Match length
% identity
                  88
                  (AC004077) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  304394
Seq. No.
                  pmx700086772.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2130082
BLAST score
                  278
                  7.0e-25
E value
Match length
                  97
% identity
                  56
NCBI Description
                  protein kinase Xa21 (EC 2.7.1.-) - rice >gi 1122443
                   (U37133) receptor kinase-like protein [Oryza sativa]
                  >gi 2586085 (U72723) receptor kinase-like protein [Oryza
                  longistaminata] >gi_1586408_prf__2203451A receptor
                  kinase-like protein [Oryza sativa]
Seq. No.
                  304395
Seq. ID
                  pmx700086865.h1
Method
                  BLASTX
NCBI GI
                  g4314358
BLAST score
                  314
                  4.0e-29
E value
Match length
                  96
```

% identity 60 NCBI Description (AC006340) putative kinesin heavy chain protein



[Arabidopsis thaliana]

```
304396
Seq. No.
Seq. ID
                  pmx700086868.h1
                  BLASTX
Method
NCBI GI
                  q1321941
BLAST score
                  229
                  3.0e-19
E value
Match length
                  81
% identity
                  52
                  (Z48564) dihydrolipoamide dehydrogenase [Synechocystis
NCBI Description
                  PCC6803]
                  304397
Seq. No.
                  pmx700086921.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263821
BLAST score
                  310
                  1.0e-28
E value
                  87
Match length
% identity
                  72
NCBI Description
                  (AC006067) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  304398
                  pmx700086948.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2673908
BLAST score
                  344
                  1.0e-32
E value
                  103
Match length
% identity
                  55
                  (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  304399
Seq. No.
Seq. ID
                  pmx700086975.h1
Method
                  BLASTX
                 - q3695379
NCBI GI
BLAST score
                  354
                  6.0e-34
E value
Match length
                  87
                  79
% identity
                  (AF096370) contains similarity to a C. elegans hypothetical
NCBI Description
                  protein F44G4.1 (GB:Z49910) and several yeast hypothetical
                  proteins such as 35.1 KD protein in NAM8-GAR1 intergenic
                  region (SP:P38805) [Arabidopsis thaliana]
                  304400
Seq. No.
Seq. ID
                  pmx700086990.h1
Method
                  BLASTX
                  g112994
NCBI GI
BLAST score
                  234
                  7.0e-20
E value
Match length
                  63
                  79
% identity
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
```



ABA-inducible gene protein [Zea mays] >gi_226091_prf__1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 304401

Seq. ID pmx700086993.h1

Method BLASTX
NCBI GI g417103
BLAST score 234
E value 1.0e-23
Match length 63
% identity 92

NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]

>gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]

>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]

>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755 emb_CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 304402

Seq. ID pmx700087016.h1

Method BLASTX
NCBI GI g2982942
BLAST score 311
E value 8.0e-29
Match length 100
% identity 58

NCBI Description (AE000679) GMP synthase [Aquifex aeolicus]

Seq. No. 304403

Seq. ID pmx700087019.h1

Method BLASTX
NCBI GI 94490335
BLAST score 269
E value 7.0e-24
Match length 100
% identity 58

NCBI Description (AL035656) receptor kinase-like protein [Arabidopsis

thaliana]

Seq. No. 304404

Seq. ID pmx700087076.h1

Method BLASTX NCBI GI g4204265

Match length

NCBI Description

% identity

68

47



```
BLAST score
                  2.0e-37
E value
                  86
Match length
% identity
                  77
                  (AC005223) 45643 [Arabidopsis thaliana]
NCBI Description
                  304405
Seq. No.
Seq. ID
                  pmx700087130.h1
Method
                  BLASTN
NCBI GI
                  q451192
BLAST score
                  77
E value
                  2.0e-35
Match length
                  144
% identity
                  89
NCBI Description Triticum aestivum (wali7) mRNA, 3' end, partial cds
Seq. No.
                  304406
                  pmx700087145.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827141
BLAST score
                  155
E value
                  1.0e-10
Match length
                  89
% identity
                  42
NCBI Description
                  (AF027173) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                  304407
                  pmx700087165.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4102600
BLAST score
                  213
E value
                  1.0e-35
Match length
                  99
% identity
                  77
                  (AF013467) ARF6 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  304408
Seq. ID
                  pmx700087166.h1
Method
                  BLASTN
NCBI GI
                  g602252
BLAST score
                  43
E value
                  2.0e-15
Match length
                  55
                  95
% identity
NCBI Description Zea mays enolase (eno2) mRNA, complete cds
Seq. No.
                  304409
Seq. ID
                  pmx700087222.h1
Method
                  BLASTX
NCBI GI
                  g3769673
BLAST score
                  180
E value
                  2.0e-13
```

43070

(AF095285) Tic20 [Pisum sativum]

```
304410
Seq. No.
                  pmx700087233.h1
Seq. ID
                  BLASTX
Method
                  g2894612
NCBI GI
                   336
BLAST score
E value
                  1.0e-31
                  88
Match length
% identity
                   69
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   304411
Seq. ID
                  pmx700087251.h1
Method
                  BLASTX
NCBI GI
                  q2352084
BLAST score
                   423
                   5.0e-42
E value
Match length
                   94
% identity
                   81
                   (U96613) serine/threonine kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   304412
Seq. ID
                   pmx700087346.h1
Method
                   BLASTX
NCBI GI
                   q4249382
BLAST score
                   141
E value
                   3.0e-09
Match length
                   44
                   75
% identity
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
Seq. No.
                   304413
                   pmx700087386.h1
Seq. ID
Method
                   BLASTX
                   g1362103
NCBI GI
BLAST score
                   210
                   6.0e-17
E value
                   64
Match length
                   62
% identity
                   ubiquitin conjugating enzyme - tomato
NCBI Description
                   >gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating
                   enzyme [Lycopersicon esculentum]
                   304414
Seq. No.
                   pmx700087390.h1
Seq. ID
Method
                   BLASTX
                   g3327204
NCBI GI
BLAST score
                   174
```

1.0e-12 E value 81 Match length 41 % identity

(AB014595) KIAA0695 protein [Homo sapiens] NCBI Description

304415 Seq. No.

Seq. ID pmx700087402.h1

Method BLASTX



```
NCBI GI
                  q3004564
BLAST score
                  139
                   6.0e-09
E value
Match length
                   36
                   75
% identity
                   (AC003673) putative receptor Ser/Thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  304416
Seq. No.
Seq. ID
                  pmx700087447.h1
Method
                  BLASTX
NCBI GI
                  q3136048
BLAST score
                   334
                   2.0e-31
E value
                  100
Match length
% identity
                   66
                  (AL023592) putative helicase [Schizosaccharomyces pombe]
NCBI Description
                   304417
Seq. No.
Seq. ID
                  pmx700087453.h1
Method
                  BLASTX
NCBI GI
                   q1906828
BLAST score
                   365
E value
                   4.0e-35
                  74
Match length
                   96
% identity
                  (Y11828) heat shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   304418
Seq. ID
                  pmx700087474.h1
Method
                   BLASTN
NCBI GI
                   q902585
BLAST score
                   34
E value
                   1.0e-09
Match length
                   74
% identity
                   86
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds
Seq. No.
                   304419
                   pmx700087558.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3548805
BLAST score
                   188
E value
                   2.0e-14
Match length
                   68
% identity
                   56
NCBI Description
                  (AC005313) unknown protein [Arabidopsis thaliana]
                   304420
Seq. No.
Seq. ID
                   pmx700087582.h1
Method
                  BLASTX
                   q3747046
NCBI GI
BLAST score
                   164
E value
                  1.0e-11
```

Match length 42 % identity 79

NCBI Description (AF093538) voltage-dependent anion-selective channel



protein [Zea mays]

```
304421
Seq. No.
                  pmx700087587.h1
Seq. ID
Method
                  BLASTX
                  g2459424
NCBI GI
BLAST score
                  163
                  2.0e-11
E value
                  83
Match length
                  37
% identity
                  (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  304422
                  pmx700087646.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2664204
BLAST score
                  165
E value
                  1.0e-11
Match length
                  45
                   67
% identity
                  (AJ003218) GTL1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   304423
Seq. ID
                  pmx700087712.h1
Method
                  BLASTX
                   q1706260
NCBI GI
                   309
BLAST score
                   1.0e-28
E value
Match length
                   83
                   75
% identity
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597
NCBI Description
                   cysteine proteinase 1 precursor - maize
                   >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                  mays]
Seq. No.
                   304424
Seq. ID
                   pmx700087716.h1
Method
                   BLASTX
NCBI GI
                   q2668742
BLAST score
                   218
E value
                   6.0e-18
Match length
                   62
% identity
                   71
NCBI Description
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
                   304425
Seq. ID
                   pmx700087743.h1
Method
                   BLASTX
NCBI GI
                   g2827715
BLAST score
                   193
                   2.0e-20
E value
Match length
                   81
% identity
                   65
```

304426

[Arabidopsis thaliana]

NCBI Description

Seq. No.

(AL021684) receptor protein kinase - like protein



```
pmx700087789.h1
Seq. ID
                  BLASTX
Method
                  g4309759
NCBI GI
                  349
BLAST score
                  3.0e - 33
E value
                  70
Match length
                  94
% identity
                  (AC006217) unknown protein with Src homology 3 (SH3) domain
NCBI Description
                  profile (PDOC50002) [Arabidopsis thaliana]
                  304427
Seq. No.
                  pmx700087824.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3874039
                  190
BLAST score
                  1.0e-14
E value
                  60
Match length
                  53
% identity
                  (Z75526) Weak similarity to Staphyloccus autolysin gene
NCBI Description
                   (TR:G765072); cDNA EST EMBL:M89336 comes from this gene;
                  cDNA EST yk505d12.3 comes from this gene [Caenorhabditis
                  elegans]
                  304428
Seq. No.
                  pmx700087845.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3341647
                  43
BLAST score
                   4.0e-15
E value
Match length
                  47
                  98
% identity
NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase
                   304429
Seq. No.
                  pmx700087870.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                  q168492
BLAST score
                   54
                   1.0e-21
E value
Match length
                   58
                   98
% identity
NCBI Description Corn histone H3 (H3C3) gene, complete cds
                   304430
Seq. No.
Seq. ID
                   pmx700087872.h1
Method
                   BLASTN
NCBI GI
                   q22275
BLAST score
                   152
E value
                   4.0e-80
```

Match length 172 % identity 97

NCBI Description Maize mRNA for ferritin (clone FM1)

Seq. No. 304431

Seq. ID pmx700087874.h1

Method BLASTX NCBI GI g2494129

```
BLAST score
                   3.0e-23
E value
Match length
                   91
                   49
% identity
                   (AC002376) T1G11.3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   304432
                   pmx700087875.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4544450
BLAST score
                   252
```

Match length 95 % identity 51

E value

Seq. No.

NCBI Description (AC006592) hypothetical protein [Arabidopsis thaliana]

 Seq. ID
 pmx700087882.h1

 Method
 BLASTX

 NCBI GI
 g1514643

 BLAST score
 285

7.0e-22

304433

BLAST score 285
E value 8.0e-26
Match length 80
% identity 68

NCBI Description (270524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No. 304434

Seq. ID pmx700087929.h1

Method BLASTX
NCBI GI g2583127
BLAST score 155
E value 1.0e-10
Match length 43
% identity 67

NCBI Description (AC002387) putative sialoglycoprotease [Arabidopsis

thaliana]

Seq. No. 304435

Seq. ID pmx700087979.h1

Method BLASTX
NCBI GI g542142
BLAST score 218
E value 3.0e-18
Match length 42
% identity 93

NCBI Description 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) -

rice >gi 294704 (M96673) 1-aminocyclopropane-1-carboxylate

synthase [Oryza sativa]

Seq. No. 304436

Seq. ID pmx700087990.h1

Method BLASTX
NCBI GI g4263654
BLAST score 152
E value 4.0e-10
Match length 49
% identity 59



(AC006136) putative reverse transcriptase [Arabidopsis NCBI Description thalianal

304437 Seq. No.

pmx700088007.h1 Seq. ID

Method BLASTX NCBI GI g2654226 BLAST score 198 E value 1.0e-15 Match length 46 % identity 89

NCBI Description (AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis

thaliana]

Seq. No. 304438

Seq. ID pmx700088022.h1

Method BLASTN NCBI GI q2564045 BLAST score 35 E value 3.0e-10 Match length 91 85 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K8K14, complete sequence [Arabidopsis thaliana]

Seq. No. 304439

Seq. ID pmx700088033.h1

Method BLASTX NCBI GI q4559333 BLAST score 320 7.0e-30 E value Match length 95

% identity 34

(AC007087) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 304440

pmx700088065.h1 Seq. ID

Method BLASTX NCBI GI g1362086 BLAST score 348 3.0e-33 E value 73 Match length 92 % identity

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi 2129919 pir S65957

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase

[Catharanthus roseus]

304441 Seq. No.

Seq. ID pmx700088088.h1

BLASTX Method NCBI GI g1127575 BLAST score 244 E value 5.0e-21

```
59
```

% identity (U33817) dhurrinase [Sorghum bicolor] NCBI Description

304442 Seq. No. pmx700088108.h1 Seq. ID

Match length

BLASTX Method q4102600 NCBI GI BLAST score 475 5.0e-48 E value 94 Match length

% identity NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]

Seq. No. 304443

pmx700088109.h1 Seq. ID

94

BLASTX Method g1172836 NCBI GI 272 BLAST score 3.0e-24 E value 53 Match length 96

% identity GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787) NCBI Description

small ras-related protein [Nicotiana tabacum]

Seq. No. 304444

pmx700088115.h1 Seq. ID

Method BLASTX g2832657 NCBI GI 187 BLAST score 3.0e-14E value 90 Match length 25 % identity

(AL021710) putative protein [Arabidopsis thaliana] NCBI Description

304445 Seq. No.

pmx700088173.h1 Seq. ID Method BLASTN

g514945 NCBI GI BLAST score 58 E value 2.0e-24 86 Match length 92 % identity

NCBI Description Zea mays sucrose synthase (Sus1) mRNA, complete cds

304446 Seq. No.

pmx700088185.h1 Seq. ID

BLASTX Method NCBI GI q2827663 165 BLAST score E value 1.0e-11 89 Match length 36 % identity

(AL021637) membrane-associated salt-inducible-like protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 304447



```
pmx700088188.hl
Seq. ID
Method
                  BLASTX
                  q4507703
NCBI GI
                  182
BLAST score
                  1.0e-13
E value
Match length
                  74
                  45
% identity
                  tumor suppressing subtransferable candidate 1
NCBI Description
                  >gi_2655037_gb_AAC51911_ (AF019952) tumor suppressing STF
                  cDNA 1 [Homo sapiens]
                  304448
Seq. No.
                  pmx700088213.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q818849
                  553
BLAST score
                  4.0e-57
E value
                  108
Match length
                  85
% identity
                  (U25430) nucleotide pyrophosphatase precursor [Oryza
NCBI Description
                  sativa]
                  304449
Seq. No.
                  pmx700088244.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2494266
BLAST score
                   423
                   6.0e-42
E value
                   98
Match length
% identity
                   85
                  GTP-BINDING PROTEIN LEPA >gi 1653961_dbj_BAA18871_ (D90917)
NCBI Description
                  LepA [Synechocystis sp.]
Seq. No.
                   304450
                   pmx700088273.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3334320
                   188
BLAST score
                   4.0e-15
E value
Match length
                   46
% identity
                   96
                   40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                   ribosome-associated protein p40 [Glycine max]
Seq. No.
                   304451
                   pmx700088304.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2980805
BLAST score
                   479
E value
                   2.0e-48
Match length
                   110
% identity
                   83
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

304452

Seq. ID pmx700088351.h1

Method BLAŞTX



```
q4539302
 NCBI GI
 BLAST score
                   312
                   5.0e-29
 E value
Match length
                   91
                   62
 % identity
                   (AL049480) putative protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   304453
                   pmx700088359.h1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3108347
 BLAST score
                   216
 E value
                   7.0e-18
Match length
                   53
                   75
 % identity
                   (AF061517) putative copper/zinc superoxide dismutase copper
 NCBI Description
                   chaperone [Arabidopsis thaliana]
                   304454
 Seq. No.
                   pmx700088364.h1
 Seq. ID
 Method
                   BLASTX
                   g3522956
NCBI GI
                   142
 BLAST score
 E value
                   5.0e-09
 Match length
                   41
                   63
 % identity
                    (AC004411) putative pectinacetylesterase precursor
 NCBI Description
                    [Arabidopsis thaliana]
                   304455
 Seq. No.
                   pmx700088390.h1
 Seq. ID
 Method
                   BLASTX
                   g2245074
 NCBI GI
 BLAST score
                   189
                   1.0e-14
 E value
 Match length
                    67
 % identity
                   55
                   (Z97343) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    304456
                   pmx700088394.h1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g2961389
 BLAST score
                    259
 E value
                    7.0e-23
 Match length
                   72
                    62
 % identity
 NCBI Description
                    (AL022141) purple acid phosphatase like protein
                    [Arabidopsis thaliana] >gi_4006925_emb CAB16853.1_ (Z99708)
                   purple acid phosphatase like protein [Arabidopsis thaliana]
 Seq. No.
                    304457
                    pmx700088410.h1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4249380
 BLAST score
                    145
```

43079

3.0e-09

E value



Match length 37

% identity

(AC005966) ESTs gb Z37637, gb AA042498 and gb AA042269 come NCBI Description from this gene. [Arabidopsis thaliana]

304458 Seq. No.

pmx700088421.h1 Seq. ID

Method BLASTX q3924612 NCBI GI 298 BLAST score 3.0e-27 E value Match length 73 % identity 78

(AF069442) mitochondrial elongation factor Tu [Arabidopsis NCBI Description

thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial

elongation factor Tu [Arabidopsis thaliana]

304459 Seq. No.

pmx700088469.h1 Seq. ID

Method BLASTX NCBI GI g1911627 BLAST score 263 3.0e-23 E value Match length 92 % identity 55

NCBI Description beta-galactosidase [dogs, spleen, Peptide Partial, 667 aa]

304460 Seq. No.

pmx700088474.h1 Seq. ID

Method BLASTX g3608154 NCBI GI BLAST score 142 5.0e-09 E value Match length 57

% identity 51

(AC005314) unknown protein [Arabidopsis thaliana] NCBI Description

304461 Seq. No.

pmx700088483.h1 Seq. ID

Method BLASTX NCBI GI a3953470 BLAST score 361 1.0e-34 E value Match length 96 % identity 68

NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]

304462 Seq. No.

Seq. ID pmx700088507.h1

Method BLASTX NCBI GI q2352795 BLAST score 508 E value 5.0e-52 Match length 103 % identity 99

(AF007793) retinoblastoma-related protein 1 [Zea mays] NCBI Description



```
304463
Seq. No.
Seq. ID
                  pmx700088556.h1
                  BLASTX
Method
                  q4454012
NCBI GI
                  393
BLAST score
                  2.0e-38
E value
Match length
                  103
% identity
                  70
                  (AL035396) Pollen-specific protein precursor like
NCBI Description
                   [Arabidopsis thaliana]
                  304464
Seq. No.
                  pmx700088577.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885342
                  154
BLAST score
E value
                  1.0e-14
                  89
Match length
                  53
% identity
NCBI Description (AC005623) putative DNA polymerase [Arabidopsis thaliana]
                  304465
Seq. No.
                  pmx700088578.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4467098
BLAST score
                   225
                   1.0e-18
E value
                   56
Match length
                   73
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   304466
Seq. No.
                   pmx700088585.hl
Seq. ID
Method
                   BLASTN
                   g2773153
NCBI GI
BLAST score
                   113
E value
                   8.0e-57
                   161
Match length
                   93
% identity
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
                   304467
Seq. No.
Seq. ID
                   pmx700088634.hl
Method
                   BLASTX
NCBI GI
                   g1628482
BLAST score
                   172
E value
                   2.0e-12
Match length
                   77
                   10
% identity
NCBI Description (X97570) embryogenesis transmembrane protein [Zea mays]
```

Method BLASTX NCBI GI g4539351 BLAST score 224

E value 1.0e-18
Match length 63
% identity 71

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 304469

Seq. ID pmx700088685.h1

Method BLASTX
NCBI GI g3746059
BLAST score 153
E value 3.0e-10
Match length 41
% identity 66

NCBI Description (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis

thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative

cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 304470

Seq. ID pmx700088708.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 304471

Seq. ID pmx700088724.h1

Method BLASTX
NCBI GI g4582448
BLAST score 299
E value 2.0e-27
Match length 84
% identity 71

NCBI Description (AC007071) putative preprotein translocase SecY subunit

[Arabidopsis thaliana]

Seq. No. 304472

Seq. ID pmx700088804.h1

Method BLASTX
NCBI GI g3687231
BLAST score 153
E value 8.0e-21
Match length 103
% identity 52

NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304473

Seq. ID pmx700088844.h1

Method BLASTN
NCBI GI g499011
BLAST score 38
E value 5.0e-12
Match length 62
% identity 90

NCBI Description S.vulgare SoAc1 mRNA

```
304474
Seq. No.
                  pmx700088873.h1
Seq. ID
Method
                  BLASTN
                  g1698581
NCBI GI
                  65
BLAST score
                  3.0e-28
E value
Match length
                  177
                  85
% identity
                  Oryza sativa integral membrane protein (OsNramp3) mRNA,
NCBI Description
                  partial cds
                  304475
Seq. No.
                  pmx700088887.h1
Seq. ID
Method
                  BLASTN
                  g3450841
NCBI GI
                   62
BLAST score
                  2.0e-26
E value
                  160
Match length
                  86
% identity
                  Oryza sativa mitogen activated protein kinase kinase (MEK1)
NCBI Description
                  mRNA, complete cds
                   304476
Seq. No.
                  pmx700088926.h1
Seq. ID
                  BLASTX
Method
                   g3281861
NCBI GI
                   206
BLAST score
                   3.0e-21
E value
                   90
Match length
% identity
                   52
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   304477
Seq. No.
                   pmx700088961.h1
Seq. ID
Method
                   BLASTX
                   g4185499
NCBI GI
                   145
BLAST score
E value
                   3.0e-09
Match length
                   54
                   52
% identity
                   (AF096095) fertilization-independent seed 2 protein
NCBI Description
                   [Arabidopsis thaliana] >gi 4185501 (AF096096)
                   fertilization-independent seed 2 protein [Arabidopsis
                   thaliana]
                   304478
Seq. No.
                   pmx700088971.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1871187
BLAST score
                   264
                   3.0e-23
E value
Match length
                   100
                   57
% identity
                  (U90439) unknown protein [Arabidopsis thaliana]
NCBI Description
```

43083

304479

Seq. No.

E value

Match length

4.0e-40

102



```
pmx700089011.h1
Seq. ID
                  BLASTX
Method
                  g2852632
NCBI GI
                  172
BLAST score
                  2.0e-12
E value
                  84
Match length
                  37
% identity
NCBI Description (AF007152) unknown [Homo sapiens]
                  304480
Seq. No.
                  pmx700089036.h1
Seq. ID
Method
                  BLASTX
                  g3785989
NCBI GI
BLAST score
                  312
                  8.0e-29
E value
                  105
Match length
                  59
% identity
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
                  304481
                  pmx700089077.h1
Seq. ID
                  BLASTX
Method
                  g1076777
NCBI GI
                  159
BLAST score
                  6.0e-11
E value
                  34
Match length
                  91
% identity
NCBI Description protein H2A - wheat >gi_536890_dbj_BAA07277_ (D38088)
                  protein H2A [Triticum aestivum]
                  304482
Seq. No.
                  pmx700089079.h1
Seq. ID
                  BLASTX
Method
                  g1653300
NCBI GI
BLAST score
                  182
                  1.0e-13
E value
                  96
Match length
% identity
                  40
NCBI Description (D90912) hypothetical protein [Synechocystis sp.]
                  304483
Seq. No.
                  pmx700089093.h1
Seq. ID
                  BLASTX
Method
                  q730456
NCBI GI
BLAST score
                  324
                  3.0e-30
E value
                  64
Match length
                  94
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
Seq. No.
                  304484
Seq. ID
                  pmx700089114.h1
Method
                  BLASTX
NCBI GI
                  g4544454
BLAST score
                  362
```



% identity (AC006592) putative DNAJ protein [Arabidopsis thaliana] NCBI Description 304485 Seq. No. pmx700089116.h1 Seq. ID Method BLASTX NCBI GI g3913525 BLAST score 243 7.0e-21E value 92 Match length 63 % identity DNA POLYMERASE DELTA CATALYTIC CHAIN >gi_2895198 (AF020193) NCBI Description DNA polymerase delta [Glycine max] Seq. No. 304486 pmx700089141.h1 Seq. ID BLASTX Method NCBI GI g4115377 BLAST score 270 9.0e-24E value 105 Match length 49 % identity (AC005967) unknown protein [Arabidopsis thaliana] NCBI Description 304487 Seq. No. pmx700089148.h1 Seq. ID Method BLASTX g1076669 NCBI GI BLAST score 272 E value 4.0e-24 Match length 59 85 % identity NADH dehydrogenase (EC 1.6.99.3) - potato NCBI Description >gi_668987_emb_CAA59063_ (X84320) NADH dehydrogenase [Solanum tuberosum] 304488 Seq. No. pmx700089159.h1 Seq. ID Method BLASTX NCBI GI q2827631 254 BLAST score 4.0e-22 E value Match length 65 69 % identity NCBI Description (AL021636) putative protein [Arabidopsis thaliana] 304489 Seq. No. pmx700089173.h1 Seq. ID Method BLASTX NCBI GI q3540201 BLAST score 268

E value 9.0e-24 Match length 81 62 % identity

NCBI Description (AC004260) Putative nuclear protein [Arabidopsis thaliana]

304490 Seq. No.

```
Seq. ID
                   pmx700089188.h1
Method
                   BLASTX
                   q3298547
NCBI GI
BLAST score
                   325
                   2.0e-30
E value
Match length
                   96
% identity
                   69
NCBI Description
                   (AC004681) putative condensin protein [Arabidopsis
                   thaliana]
Seq. No.
                   304491
Seq. ID
                   pmx700089208.h1
Method
                   BLASTX
NCBI GI
                   g2969887
BLAST score
                   223
E value
                   2.0e-18
Match length
                   76
% identity
                   54
                   (Y16766) sucrose/H+ symporter [Daucus carota]
NCBI Description
                   >gi 2969889 emb CAA76368 (Y16767) sucrose/H+ symporter
                   [Daucus carota]
Seq. No.
                   304492
Seq. ID
                   pmx700089211.h1
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   36
E value
                   7.0e-11
Match length
                   48
% identity
                   67
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   304493
Seq. ID
                   pmx700089269.h1
Method
                   BLASTX
NCBI GI
                   q2244899
BLAST score
                   184
                   6.0e-14
E value
Match length
                   83
                   47
% identity
NCBI Description
                  (Z97338) similar to UFD1 protein [Arabidopsis thaliana]
Seq. No.
                   304494
Seq. ID
                  pmx700089294.h1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2920706
BLAST score 248
E value 2.0e-21
Match length 99
% identity 49

NCBI Description (Y13568) beta-xylosidase [Emericella nidulans]

Seq. No. 304495

Seq. ID pmx700089341.h1

Method BLASTX NCBI GI g629792 BLAST score 209



```
7.0e-17
E value
                  92
Match length
                  50
% identity
                  cysteine proteinase - rice >gi_530335_emb_CAA56844_
NCBI Description
                   (X80876) cysteine protease [Oryza satīva]
                  304496
Seq. No.
                  pmx700089367.h1
Seq. ID
                  BLASTN
Method
                  g450292
NCBI GI
                   54
BLAST score
                   6.0e-22
E value
                   131
Match length
                   90
% identity
                   Zea mays alpha-tubulin mRNA, complete cds.
NCBI Description
                   >gi 452473_gb_U05258_ZMU05258 Zea mays Black Mexican Sweet
                   alpha-tubulin mRNA, complete cds
                   304497
Seq. No.
                   pmx700089368.h1
Seq. ID
Method
                   BLASTX
                   g3395584
NCBI GI
                   242
BLAST score
                   1.0e-20
E value
                   100
Match length
                   50
% identity
                   (AL031179) importin beta subunit [Schizosaccharomyces
NCBI Description
                   pombe]
                   304498
Seq. No.
                   pmx700089369.h1
Seq. ID
                   BLASTN
Method
                   g3821780
NCBI GI
                   33
BLAST score
                   4.0e-09
E value
                   33
Match length
                   100
% identity
                   Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   304499
Seq. No.
                   pmx700089425.h1
 Seq. ID
                   BLASTX
Method
                   g3193324
NCBI GI
                   418
BLAST score
                   2.0e-41
E value
                   91
Match length
                   87
 % identity
                   (AF069299) contains similarity to WD domains, G-beta
 NCBI Description
                   repeats (Pfam: G-beta.hmm, score: 22.80 and 35.84)
                    [Arabidopsis thaliana]
```

Seq. No. 304500

Seq. ID pmx700089428.h1

Method BLASTX
NCBI GI g3757523
BLAST score 250
E value 1.0e-21

Match length 56 % identity

(AC005167) putative transportin [Arabidopsis thaliana] NCBI Description

Seq. No.

304501 pmx700089457.h1 Seq. ID

BLASTX Method g1706260 NCBI GI 308 BLAST score 9.0e-30 E value 90 Match length 79 % identity

CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131_pir__S59597 NCBI Description

cysteine proteinase 1 precursor - maize

>gi 643597 dbj BAA08244_ (D45402) cysteine proteinase [Zea

mays]

304502 Seq. No.

pmx700089469.hl Seq. ID

BLASTX Method g3063706 NCBI GI 225 BLAST score 7.0e-22 E value 65 Match length 80 % identity

(AL022537) putative protein [Arabidopsis thaliana] NCBI Description

304503 Seq. No.

pmx700089472.h1 Seq. ID

BLASTX Method g2245118 NCBI GI 321 BLAST score 5.0e-30 E value 88 Match length 62 % identity

(Z97343) hypothetical protein [Arabidopsis thaliana] NCBI Description

304504 Seq. No.

pmx700089473.h1 Seq. ID

Method BLASTX g4335745 NCBI GI 229 BLAST score 3.0e-19 E value 96 Match length % identity 49

(AC006284) putative hydrolase (contains an NCBI Description

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

304505 Seq. No.

pmx700089477.h1 Seq. ID

Method BLASTX g2462825 NCBI GI 279 BLAST score 5.0e-25 E value Match length 81 67 % identity



NCBI Description (AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]

Seq. No. 304506

Seq. ID pmx700089501.h1 **

Method BLASTX
NCBI GI 94220462
BLAST score 327
E value 1.0e-30
Match length 95
% identity 78

NCBI Description (AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8)

gene from Arabidopsis thaliana containing Homeobox PF_00046

and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No. 304507

Seq. ID pmx700089518.h1

Method BLASTX
NCBI GI 94220534
BLAST score 267
E value 1.0e-23
Match length 93
% identity 48

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 304508

Seq. ID pmx700089539.h1

Method BLASTX
NCBI GI g4538968
BLAST score 140
E value 9.0e-09
Match length 46
% identity 52

NCBI Description (AL049488) putative protein kinase [Arabidopsis thaliana]

Seq. No. 304509

Seq. ID pmx700089549.h1

Method BLASTX
NCBI GI g3785987
BLAST score 184
E value 7.0e-14
Match length 76
% identity 55

NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304510

Seq. ID pmx700089620.h1

Method BLASTX
NCBI GI g2146732
BLAST score 271
E value 4.0e-24
Match length 73

% identity 73
NCBI Description FK506-binding protein - Arabidopsis thaliana >gi_1373396

(U57838) rof1 [Arabidopsis thaliana]

Seq. No. 304511

```
pmx700089658.h1
Seq. ID
                  BLASTX
Method
                 - g3935148
NCBI GI
                   246
BLAST score
                   2.0e-21
E value
                   66
Match length
```

70 % identity (AC005106) T25N20.12 [Arabidopsis thaliana] NCBI Description

304512 Seq. No.

pmx700089661.h1 Seq. ID

BLASTX Method g3808101 NCBI GI BLAST score 208 5.0e-17 E value 42 Match length 100 % identity

(AJ012165) chloroplast protease [Capsicum annuum] NCBI Description

304513 Seq. No.

pmx700089678.h1 Seq. ID'

BLASTN Method g2934901 NCBI GI 53 BLAST score 2.0e-21 E value 85 Match length 91 % identity

Zea mays cpSecY (csy1) mRNA, chloroplast gene encoding NCBI Description

chloroplast protein, complete cds

304514 Seq. No.

pmx700089704.h1 Seq. ID

BLASTX Method g2826900 NCBI GI BLAST score 430 1.0e-42 E value 106 Match length % identity 81

(AB004461) DNA polymerase alpha catalytic subunit [Oryza NCBI Description

sativa]

304515 Seq. No.

pmx700089717.h1 Seq. ID

BLASTX Method NCBI GI q3641252 278 BLAST score 7.0e-25 E value 105 Match length % identity

(AF053127) leucine-rich receptor-like protein kinase [Malus NCBI Description

domestica]

304516 Seq. No.

pmx700089722.h1 Seq. ID

Method BLASTX NCBI GI g4322940 326 BLAST score



E value 2.0e-30

Match length 84 % identity 39

NCBI Description (AF096299) DNA-binding protein 2 [Nicotiana tabacum]

Seq. No. 304517

Seq. ID pmx700089732.h1

Method BLASTX
NCBI GI g4056483
BLAST score 432
E value 6.0e-43
Match length 97
% identity 86

NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304518

Seq. ID pmx700089936.h1

Method BLASTX
NCBI GI g4176557
BLAST score 291
E value 2.0e-26
Match length 97
% identity 59

NCBI Description (AL035259) conserved hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 304519

Seq. ID pmx700089949.h1

Method BLASTN
NCBI GI g1184771
BLAST score 128
E value 7.0e-66
Match length 180
% identity 95

NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC2

(gpc2) mRNA, complete cds

Seq. No. 304520

Seq. ID pmx700090048.h1

Method BLASTX
NCBI GI g3915519
BLAST score 152
E value 3.0e-13
Match length 75
% identity 53

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE C04H5.6

>gi_3873886_emb_CAB03819_ (Z81457) similar to Helicases conserved C-terminal domain; cDNA EST yk272f1.3 comes from this gene; cDNA EST yk410g7.3 comes from this gene; cDNA EST yk410g7.5 comes from this gene; cDNA EST yk316b6.3 comes from this gene; cDNA... >gi_3873945_emb_CAB03845_ (Z81462) similar to Helicases conserved C-terminal domain; cDNA EST yk272f1.3 comes from this gene; cDNA EST yk410g7.3 comes from this gene; cDNA EST yk410g7.3

gene; cDNA EST yk316b6.3 comes from this gene; cDNA

Seq. No. 304521



```
pmx700090059.h1
Seq. ID
Method
                  BLASTX
                  q3241943
NCBI GI
                  257
BLAST score
                  2.0e-22
E value
Match length
                  85
                  53
% identity
                  (AC004625) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  304522
Seq. No.
                  pmx700090068.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  146
                  2.0e-09
E value
Match length
                  44
                  50
% identity
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                  304523
Seq. No.
                  pmx700090073.h1
Seq. ID
                  BLASTX
Method
                  g1072251
NCBI GI
BLAST score
                  165
E value
                  6.0e-12
                  77
Match length
% identity
                   48
                  (U40953) Similar to thymidine diphosphoglucose
NCBI Description
                   4,6-dehydratase; coded for by C. elegans cDNA CEESG39R
                   [Caenorhabditis elegans]
                   304524
Seq. No.
                   pmx700090115.h1
Seq. ID
Method
                  BLASTX
                  g135398
NCBI GI
BLAST score
                   361
E value
                  1.0e-34
Match length
                   66
% identity
                   98
NCBI Description
                  TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1
                   chain - maize >gi_22147_emb_CAA33734_ (X15704)
                   alphal-tubulin [Zea mays]
Seq. No.
                   304525
Seq. ID
                   pmx700090141.h1
Method
                  BLASTX
NCBI GI
                   q4191789
BLAST score
                   224
E value
                   1.0e-18
Match length
                   86
% identity
NCBI Description
                   (AC005917) putative transmembrane transport protein
                   [Arabidopsis thaliana]
```

Seq. No. 304526

Seq. ID pmx700090155.h1

BLASTX Method



q3913240 NCBI GI BLAST score 171 2.0e-12 E value Match length 42 % identity 86 NCBI Description

MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR

(MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D) >gi 2239151 emb CAA71128 (Y10022) CHLD magnesium chelatase

subunit [Nicotiana tabacum]

304527 Seq. No.

Seq. ID pmx700090209.h1

BLASTN Method NCBI GI q483411 BLAST score 77 E value 2.0e-35 Match length 120 97 % identity

NCBI Description Zea Mays calmodulin-binding protein mRNA, 3'end

Seq. No. 304528

Seq. ID pmx700090212.h1

Method BLASTX NCBI GI g3482920 BLAST score 216 1.0e-28 E value 95 Match length

% identity 67

(AC003970) Hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 304529

Seq. ID pmx700090216.h1

Method BLASTX NCBI GI q3540184 BLAST score 382 E value 4.0e-37 Match length 105 59 % identity

NCBI Description (AC004122) Similar to endoxylanases [Arabidopsis thaliana]

Seq. No. 304530

Seq. ID pmx700090219.h1

Method BLASTX NCBI GI g4455190 BLAST score 162 E value 3.0e-11 Match length 47 72 % identity

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 304531

Seq. ID pmx700090391.h1

BLASTX Method NCBI GI g1899188 BLAST score 141 E value 3.0e-09

Match length 42



```
% identity
NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]
                  304532
Seq. No.
                  pmx700090533.h1
Seq. ID
Method
                  BLASTX
                  q2662343
NCBI GI
BLAST score
                  446
                  9.0e-45
E value
                  85
Match length
                  100
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  304533
                  pmx700090575.h1
Seq. ID
                  BLASTX
Method
                  g4455338
NCBI GI
                  466
BLAST score
                  5.0e-47
E value
                  97
Match length
                  85
% identity
                  (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                  304534
Seq. No.
                  pmx700090579.h1
Seq. ID
Method
                  BLASTX
                  g3702323
NCBI GI
                  357
BLAST score
                  3.0e-34
E value
Match length
                  99
                  70
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  304535
Seq. No.
                  pmx700090584.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4490314
                  278
BLAST score
                   6.0e-25
E value
Match length
                   94
% identity
                   61
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                   304536
                   pmx700090596.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4049341
BLAST score
                   219
                   5.0e-18
E value
Match length
                   95
                   43
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
                   304537
Seq. No.
                   pmx700090611.h1
Seq. ID
```

43094

BLASTN

g22322

Method NCBI GI



```
BLAST score
E value
                  5.0e-55
                  207
Match length
                  89
% identity
                  Z.mays mRNA for H2B histone (clone cH2B214)
NCBI Description
                  304538
Seq. No.
                  pmx700090615.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2345154
BLAST score
                  339
                  4.0e-32
E value
Match length
                  65
% identity
                  98
                  (AF015522) ribsomal protein S4 [Zea mays]
NCBI Description
                  304539
Seq. No.
                  pmx700090625.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2351580
BLAST score
                  163
E value
                  8.0e-22
Match length
                  57
% identity
                  95
NCBI Description
                  (U82433) thymidine diphospho-glucose 4-6-dehydratase
                  homolog [Prunus armeniaca]
                  304540
Seq. No.
                  pmx700090688.h1
Seq. ID
Method
                  BLASTX
                  g4206209
NCBI GI
BLAST score
                  514
                  1.0e-52
E value
Match length
                  100
% identity
                  95
NCBI Description
                  (AF071527) putative glucan synthase component [Arabidopsis
                  thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative
                  glucan synthase component [Arabidopsis thaliana]
Seq. No.
                  304541
Seq. ID
                  pmx700090836.h1
Method
                  BLASTX
NCBI GI
                  q3163946
BLAST score
                  487
E value
                  2.0e-49
Match length
                  92
                  100
% identity
NCBI Description
                  (AJ005599) alpha-tubulin 1 [Eleusine indica]
```

Seq. No. 304542

pmx700090851.h1 Seq. ID

Method BLASTX g2493647 NCBI GI BLAST score 140 E value 4.0e-09 Match length 41 % identity 68



NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60

KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi_2129458_pir__S71760 chaperonin 60 alpha chain Chlamydomonas reinhardtii >gi_603913 (L27472) chaperonin

alpha-like subunit [Chlamydomonas reinhardtii]

Seq. No. 304543

Seq. ID pmx700090856.h1

Method BLASTX
NCBI GI g4455158
BLAST score 212
E value 3.0e-17
Match length 79

% identity 56

NCBI Description (AL021687) kinase-like protein [Arabidopsis thaliana]

Seq. No. 304544

Seq. ID pmx700090858.h1

Method BLASTX
NCBI GI g3128195
BLAST score 169
E value 5.0e-15
Match length 72
% identity 61

NCBI Description (AC004521) putative phosphoribosyl pyrophosphate synthetase

[Arabidopsis thaliana] >gi_3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis

thaliana]

Seq. No. 304545

Seq. ID pmx700090859.h1

Method BLASTX
NCBI GI g1203832
BLAST score 202
E value 4.0e-29
Match length 82
% identity 83

NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII

[Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No. 304546

Seq. ID pmx700090860.h1

Method BLASTX
NCBI GI g3242659
BLAST score 139
E value 9.0e-09
Match length 26
% identity 92

NCBI Description (AB015599) spermidine synthase [Coffea arabica]

Seq. No. 304547

Seq. ID pmx700090861.h1

Method BLASTX
NCBI GI g2388571
BLAST score 142
E value 2.0e-18

% identity

87

```
Match length
% identity
                   64
NCBI Description
                   (AC000098) Strong similarity to Arabidopsis peroxidase
                  ATPEROX7A (gb X98321). [Arabidopsis thaliana] >gi 2738254
                   (U97684) peroxidase precursor [Arabidopsis thaliana]
Seq. No.
                  304548
                  pmx700090864.h1
Seq. ID
Method
                  {\tt BLASTX}
NCBI GI
                  g459895
BLAST score
                  223
E value
                  5.0e-34
Match length
                  76
% identity
                  100
NCBI Description
                  (L29418) sus1 gene product [Zea mays]
                  304549
Seq. No.
Seq. ID
                  pmx700090871.h1
Method
                  BLASTX
NCBI GI
                  q3334320
BLAST score
                  182
E value
                  8.0e-14
Match length
                  50
                  74
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN SA (P40) >qi 2444420 (AF020553)
                  ribosome-associated protein p40 [Glycine max]
Seq. No.
                  304550
Seq. ID
                  pmx700090878.h1
Method
                  BLASTX
NCBI GI
                  q1666234
BLAST score
                  183
E value
                  6.0e-14
Match length
                  34
                  100
% identity
NCBI Description
                  (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin
                  [Pisum sativum]
                  304551
Seq. No.
Seq. ID
                  pmx700090886.h1
Method
                  BLASTX
                  g3080414
NCBI GI
BLAST score
                  153
E value
                  2.0e-10
Match length
                  31
% identity
                  87
NCBI Description
                  (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                  304552
Seq. ID
                  pmx700090891.h1
Method
                  BLASTN
NCBI GI
                  g22429
BLAST score
                  46
E value
                  6.0e-17
Match length
                  94
```

NCBI Description Maize pseudo-Gpa1 pseudogene for glyceraldehyde-3-phosphate



dehydrogenase subunit A

```
Seq. No.
                  304553
                  pmx700090895.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1177022
BLAST score
                  142
                  1.0e-16
E value
                  54
Match length
                  81
% identity
NCBI Description HYPOTHETICAL PROTEIN KIAA0052
                  304554
Seq. No.
Seq. ID
                  pmx700090919.h1
Method
                  BLASTX
                  g2244834
NCBI GI
BLAST score
                  253
                  6.0e-22
E value
Match length
                  102
% identity
                  62
                 (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  304555
                  pmx700090921.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220485
BLAST score
                  325
E value
                  2.0e-30
Match length
                  110
% identity
                  55
                  (AC006069) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                  thaliana]
                  304556
Seq. No.
                  pmx700090926.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2494124
BLAST score
                  257
                  2.0e-22
E value
Match length
                  108
% identity
                  53
                  (AC002376) Similar to Saccharomyces CHL12 (gb Z49259).
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  304557
                  pmx700090932.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3250687
BLAST score
                  241
E value
                  2.0e-20
Match length
                  106
                  42
% identity
NCBI Description
                  (AL024486) putative LTR retrotransposon (fragment)
                   [Arabidopsis thaliana]
```

43098

304558

pmx700090933.h1

Seq. No.

Seq. ID



```
Method
NCBI GI
                  q4115918
BLAST score
                  142
                  3.0e-09
E value
                  30
Match length
                  90
% identity
NCBI Description
                  (AF118222) similar to nascent polypeptide associated
                  complex alpha chain [Arabidopsis thaliana]
```

304559 Seq. No. pmx700090942.h1 Seq. ID

Method BLASTN NCBI GI q3821780 36 BLAST score 7.0e-11 E value Match length 36 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

304560 Seq. No.

pmx700090964.h1 Seq. ID

Method BLASTX NCBI GI q120558 BLAST score 244 7.0e-21 E value Match length 82 % identity 32

FEMALE STERILE HOMEOTIC PROTEIN (FRAGILE-CHORION MEMBRANE NCBI Description

PROTEIN) >gi_280611_pir__A43742 female sterile homeotic

protein, 205K - fruit fly (Drosophila melanogaster) >gi 157453 (M23221) 7.6 kb fsh membrane protein [Drosophila

melanogaster]

Seq. No. 304561

Seq. ID pmx700090969.h1

Method BLASTX NCBI GI q3560531 BLAST score 244 E value 7.0e-21 Match length 64 % identity

(AF042332) cycloartenol-C24-methyltransferase [Oryza sativa NCBI Description

subsp. japonica]

Seq. No. 304562

Seq. ID pmx700091065.h1

Method BLASTX NCBI GI g3928084 BLAST score 202 E value 2.0e-16 Match length 71 % identity 59

(AC005770) retrotransposon-like protein [Arabidopsis NCBI Description

thaliana]

304563 Seq. No.

Seq. ID pmx700091079.h1



```
Method
                   BLASTX
NCBI GI
                   q1709358
BLAST score
                   214
E value
                   9.0e-18
Match length
                   56
% identity
                   70
NCBI Description
                  NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE
                   PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir__$48859
                   nucleoside triphosphatase - garden pea
                   >gi_2129890_pir__S65147 nucleoside triphosphatase
                  precursor, chromatin-associated - garden pea
                   >gi_563612_emb_CAA83655 (Z32743) nucleoside triphosphatase
                   [Pisum satīvum] >gi_4519173_dbj_BAA75506.1_ (AB022319)
                  nucleoside triphosphatase (NTPase) [Pisum sativum]
Seq. No.
                   304564
Seq. ID
                  pmx700091090.h1
Method
                  BLASTX
NCBI GI
                  g2827084
BLAST score
                  231
E value
                   9.0e-20
Match length
                  51
% identity
                  (AF020273) malate dehydrogenase precursor [Medicago sativa]
NCBI Description
Seq. No.
                  304565
Seq. ID
                  pmx700091127.h1
Method
                  BLASTX
NCBI GI
                  g2262159
BLAST score
                  236
E value
                  1.0e-24
Match length
                  76
% identity
                  78
NCBI Description
                   (AC002329) predicted protein similar to S.pombe protein
                  C5H10.03 [Arabidopsis thaliana]
Seq. No.
                  304566
Seq. ID
                  pmx700091137.h1
Method
                  BLASTX
NCBI GI
                  g3337367
BLAST score
                  235
E value
                  7.0e-20
Match length
                  89
                  49
% identity
NCBI Description
                  (AC004481) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  304567
Seq. ID
                  pmx700091145.h1
Method
                  BLASTX
NCBI GI
                  g2245128
```

NCBI GI g224512
BLAST score 154
E value 2.0e-10
Match length 46
% identity 65

NCBI Description (Z97344) peroxidase [Arabidopsis thaliana]

Seq. No. 304568



```
Seq. ID
                  pmx700091201.h1
Method
                  BLASTX
                  g4263722
NCBI GI
BLAST score
                  172
                  2.0e-12
E value
Match length
                  39
% identity
                  85
NCBI Description
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
                  304569
Seq. No.
                  pmx700091214.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3892057
BLAST score
                  439
E value
                  8.0e-44
Match length
                  98
% identity
                  85
NCBI Description
                  (AC002330) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  304570
Seq. ID
                  pmx700091218.h1
Method
                  BLASTX
NCBI GI
                  g2618721
BLAST score
                  208
E value
                  3.0e-25
Match length
                  77
% identity
                  79
NCBI Description
                  (U49072) IAA16 [Arabidopsis thaliana]
Seq. No.
                  304571
Seq. ID
                  pmx700091232.h1
Method
                  BLASTX
NCBI GI
                  g1237102
BLAST score
                  438
E value
                  1.0e-43
Match length
                  101
% identity
                  87
NCBI Description
                  (L40358) calmodulin-binding protein [Arabidopsis thaliana]
                  >gi 1589171 prf 2210340A calmodulin-binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  304572
                  pmx700091239.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1203832
BLAST score
                  258
```

E value 9.0e-24 Match length 65 % identity 92

NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII

[Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan

exohydrolase [Hordeum vulgare]

Seq. No. 304573

Seq. ID pmx700091258.h1

Method BLASTX NCBI GI g2102691



```
BLAST score
                  8.0e-09
E value
Match length
                  77
% identity
                  35
                  (U64817) fructokinase [Lycopersicon esculentum]
NCBI Description
                  304574
Seq. No.
                  pmx700091293.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231505
BLAST score
                  308
                  1.0e-28
E value
Match length
                  74
% identity
                  97
                  ACTIN 101 >gi 100419 pir__S20093 actin - potato
NCBI Description
                  >gi 21534 emb CAA39281 (X55752) actin [Solanum tuberosum]
                  304575
Seq. No.
                  pmx700091303.h1
Seq. ID
Method
                  BLASTX
                  g3093294
NCBI GI
BLAST score
                  290
                  2.0e-26
E value
Match length
                  99
% identity
                  62
NCBI Description (Y12782) putative villin [Arabidopsis thaliana]
                  304576
Seq. No.
Seq. ID
                  pmx700091314.hl
Method
                  BLASTX
NCBI GI
                  g1076755
BLAST score
                  311
                  8.0e-29
E value
                  96
Match length
% identity
                  67
                  protein kinase - rice >gi_450300 (L27821) protein kinase
NCBI Description
                  [Oryza sativa]
Seq. No.
                  304577
                  pmx700091318.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885341
BLAST score
                  162
E value
                  2.0e-11
Match length
                  90
% identity
                  34
NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]
Seq. No.
                  304578
                  pmx700091341.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1351136
BLAST score
                  373
```

E value 4.0e-36 Match length 91 % identity 78

NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)



>gi_514946 (L22296) UDP-glucose:D-fructose
2-glucosyl-transferase [Zea mays] >gi_533252 (L33244)
sucrose synthase 2 [Zea mays]

Seq. No. 304579

Seq. ID pmx700091420.h1

Method BLASTN
NCBI GI g2511540
BLAST score 36
E value 8.0e-11
Match length 56

NCBI Description Oryza sativa DNA-binding protein GBP16 (Rgbp16) mRNA,

complete cds

Seq. No. 304580

% identity

Seq. ID pmx700091442.h1

91

Method BLASTX
NCBI GI g1706947
BLAST score 432
E value 3.0e-52
Match length 109
% identity 95

NCBI Description (U43528) RAD51 homolog AtRad51 [Arabidopsis thaliana]

>gi_1706949 (U43652) AtRAD51 [Arabidopsis thaliana]
>gi_2388778_emb_CAA04529_ (AJ001100) Rad51-like protein

[Arabidopsis thaliana]

Seq. No. 304581

Seq. ID pmx700091459.h1

Method BLASTX
NCBI GI g2558654
BLAST score 305
E value 2.0e-31
Match length 112
% identity 61

NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No. 304582

Seq. ID pmx700091516.h1

Method BLASTX
NCBI GI g3776025
BLAST score 169
E value 2.0e-12
Match length 42
% identity 74

NCBI Description (AJ010474) RNA helicase [Arabidopsis thaliana]

Seq. No. 304583

Seq. ID pmx700091522.h1

Method BLASTX
NCBI GI g3289002
BLAST score 191
E value 1.0e-14
Match length 112
% identity 32

NCBI Description (AF073522) CRP1 [Zea mays]

```
Seq. No.
                  304584
                  pmx700091525.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3242447
BLAST score
                  208
E value
                  1.0e-16
Match length
                  48
                  79
% identity
                  (AB003131) endonuclease [Zinnia elegans]
NCBI Description
                  304585
Seq. No.
                  pmx700091545.hl
Seq. ID
                  BLASTX
Method
                  g4581164
NCBI GI
BLAST score
                  306
                  4.0e-28
E value
Match length
                  106
% identity
                  52
NCBI Description
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
                  304586
Seq. No.
                  pmx700091557.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3033401
                  394
BLAST score
                  2.0e-38
E value
Match length
                  110
% identity
                  65
NCBI Description
                  (AC004238) putative potassium transporter [Arabidopsis
                  thaliana]
                  304587
Seq. No.
                  pmx700091558.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g584825
BLAST score
                  214
                  2.0e-17
E value
Match length
                  94
% identity
                  44
                  B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
NCBI Description
                  >gi_297889_emb_CAA51078 (X72385) B2 protein [Daucus
                  carota]
Seq. No.
                  304588
                  pmx700091584.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1172586
BLAST score
                  225
E value
                  4.0e-19
Match length
                  69
% identity
                  55
NCBI Description
                  POLYPHENOL OXIDASE A1 PRECURSOR (PPO) (CATECHOL OXIDASE)
```

Seq. No. 304589

faba]

>gi_22029 emb CAA77764 (Z11702) polyphenol oxidase [Vicia



```
Seq. ID
                   pmx700091620.h1
Method
                   BLASTX
NCBI GI
                   q1729868
BLAST score
                   154
E value
                   3.0e-10
Match length
                   74
% identity
                   49
NCBI Description
                   PROBABLE T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA)
                   (CCT-BETA) >gi 1177337 emb CAA93213 (Z69239) unknown
                   [Schizosaccharomyces pombe]
Seq. No.
                   304590
Seq. ID
                   pmx700091673.h1
                   BLASTX
Method
NCBI GI
                   q3218550
BLAST score
                   200
E value
                   9.0e-16
Match length
                   52
% identity
                   69
NCBI Description
                  (AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]
Seq. No.
                   304591
Seq. ID
                   pmx700091693.h1
Method
                   BLASTX
NCBI GI
                   g2781345
BLAST score
                   168
E value
                   5.0e-12
Match length
                   51
% identity
                   47
NCBI Description
                   (AC003113) F2401.2 [Arabidopsis thaliana]
Seq. No.
                   304592
Seq. ID
                   pmx700091695.h1
Method
                   BLASTX
NCBI GI
                   g2244813
BLAST score
                   260
E value
                   8.0e-23
Match length
                   91
% identity
                   54
NCBI Description
                   (Z97336) acylaminoacyl-peptidase homolog [Arabidopsis
                   thaliana]
Seq. No.
                   304593
Seq. ID
                  pmx700091717.h1
Method
                  BLASTN
NCBI GI
                  g1669667
BLAST score
                  60
E value
                  1.0e-25
Match length
                  112
% identity
                  90
NCBI Description Forsythia x intermedia mRNA for EF-1-alpha
```

Seq. No. 304594 Seq. ID

pmx700091828.h1

Method BLASTX NCBI GI g3212852 BLAST score 223

E value

Match length

NCBI Description

% identity

3.0e-57

108

```
E value
                   2.0e-18
Match length
                   109
 % identity
                   49
NCBI Description
                   (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                   304595
Seq. ID
                   pmx700091846.hl
Method
                   BLASTX
NCBI GI
                   g4539005
BLAST score
                   164
E value
                   2.0e-11
Match length
                   95
% identity
                   39
NCBI Description
                   (AL049481) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                   304596
Seq. ID
                   pmx700091860.h1
Method
                   BLASTX
NCBI GI
                   g3063706
BLAST score
                   204
E value
                   4.0e-16
Match length
                   81
% identity
                   52
NCBI Description
                   (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                   304597
Seq. ID
                   pmx700091880.h1
Method
                   BLASTX
NCBI GI
                   g2827516
BLAST score
                   325
E value
                   3.0e-30
Match length
                   87
% identity
                   71
NCBI Description
                   (AL021633) DNA topoisomerase like- protein [Arabidopsis
                   thaliana]
Seq. No.
                   304598
Seq. ID
                   pmx700091902.hl
Method
                  BLASTX
NCBI GI
                  g4585972
BLAST score
                   216
E value
                  5.0e-18
Match length
                  55
% identity
                  78
NCBI Description
                  (AC005287) Putative ATPase [Arabidopsis thaliana]
Seq. No.
                  304599
Seq. ID
                  pmx700091912.h1
Method
                  BLASTX
NCBI GI
                  g4325368
BLAST score
                  539
```

43106

E=2.6e-226, N=1) [Arabidopsis thaliana]

(AF128396) Arabidopsis thaliana flavin-type blue-light photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2,



```
304600
Seq. No.
Seq. ID
                   pmx700091979.h1
Method
                   BLASTX
NCBI GI
                   g417154
BLAST score
                   331
E value
                   3.0e-31
Match length
                   64
% identity
                   98
NCBI Description
                   HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                   304601
Seq. ID
                   pwf700321614.h1
Method
                   BLASTX
NCBI GI
                   q136125
BLAST score
                   219
                   5.0e-18
E value
Match length
                   88
% identity
                   49
NCBI Description
                  PUTATIVE AC TRANSPOSASE (ORFA) >gi_22113_emb_CAA29005
                   (X05424) ORFa [Zea mays]
Seq. No.
                   304602
Seq. ID
                   pwf700321639.h1
Method
                   BLASTX
                   q4263522
NCBI GI
BLAST score
                   192
E value
                   6.0e-15
Match length
                   63
% identity
                   52
                  (AC004044) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   304603
Seq. No.
Seq. ID
                   pwf700321661.h1
Method
                   BLASTX
NCBI GI
                   g4508083
BLAST score
                   185
E value
                   5.0e-14
Match length
                   87
% identity
                  51
NCBI Description
                  (AC005882) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  304604
Seq. ID
                  pwf700321669.h1
Method
                  BLASTX
NCBI GI
                  g4115536
BLAST score
                  245
E value
                  5.0e-21
Match length
                  84
```

% identity 48 NCBI Description (A

NCBI Description (AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna

mungo]
304605

Seq. No.



```
Seq. ID
                  pwf700321673.h1
Method
                  BLASTX
NCBI GI
                  a2245070
BLAST score
                  142
E value
                  6.0e-09
Match length
                  104
% identity
                  41
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  304606
Seq. No.
Seq. ID
                  pwf700321683.h1
Method
                  BLASTN
                  g1657766
NCBI GI
BLAST score
                  68
                  3.0e-30
E value
Match length
                  167
% identity
                  85
NCBI Description
                  Zea mays retrotransposon Opie-2 5' LTR, primer binding
                  site, gag gene, pol gene, complete cds, polypurine tract
                  and 3' LTR
                  304607
Seq. No.
Seq. ID
                  pwf700321685.h1
Method
                  BLASTX
NCBI GI
                  g2511715
BLAST score
                  248
                  2.0e-21
E value
Match length
                  63
% identity
                  67
NCBI Description
                  (AF019380) putative phosphatidylinositol-4-phosphate
                  5-kinase [Arabidopsis thaliana]
Seq. No.
                  304608
Seq. ID
                  pwf700321691.h1
Method
                  BLASTX
NCBI GI
                  q3377509
BLAST score
                  260
E value
                  4.0e-23
Match length
                  56
% identity
                  89
                  (AF056027) auxin transport protein REH1 [Oryza sativa]
NCBI Description
Seq. No.
                  304609
Seq. ID
                  pwf700321755.h1
Method
                  BLASTX
NCBI GI
                  q4567275
BLAST score
                  225
E value
                  1.0e-18
Match length
                  73
% identity
                  59
NCBI Description
                  (AC006841) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 304610

Seq. ID pwr700448522.h1

Method BLASTX
NCBI GI g3193336
BLAST score 208



E value 7.0e-30 Match length 90 79

NCBI Description (AF069301) DBI-related protein [Homo sapiens]

Seq. No. 304611

Seq. ID pwr700448566.h1

Method BLASTX
NCBI GI g3915628
BLAST score 391
E value 3.0e-38
Match length 88
% identity 85

NCBI Description CARBOXYPEPTIDASE B PRECURSOR (PANCREAS-SPECIFIC PROTEIN)

(PASP) >gi_2960072_emb_CAA12163_ (AJ224866)

procarboxypeptidase B [Homo sapiens]

Seq. No. 304612

Seq. ID pwr700448568.h1

Method BLASTX
NCBI GI g445612
BLAST score 205
E value 2.0e-16
Match length 54
% identity 72

NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 304613

Seq. ID pwr700448580.h1

Method BLASTX
NCBI GI g1552516
BLAST score 448
E value 6.0e-45
Match length 92

% identity 93

NCBI Description (U66061) trypsinogen C [Homo sapiens]

Seq. No. 304614

Seq. ID pwr700448614.h1

Method BLASTX
NCBI GI g4505731
BLAST score 223
E value 2.0e-18
Match length 88
% identity 45

NCBI Description peroxisomal biogenesis factor 7

>gi_3122596_sp_000628_PEX7_HUMAN PEROXISOMAL TARGETING
SIGNAL 2 RECEPTOR (PTS2 RECEPTOR) (PEROXIN-7) >gi_1907315
(U76560) peroxisome targeting signal 2 receptor [Homo
sapiens] >gi_1947088 (U88871) HsPEX7 [Homo sapiens]

Seq. No. 304615

Seq. ID pwr700448619.h1

Method BLASTN
NCBI GI g4505324
BLAST score 87
E value 7.0e-42



Match length 99 % identity 97

NCBI Description Homo sapiens nuclear autoantigen of 14 kDa (N14) mRNA

>gi 2706619 emb Z96932_HSP14PROT Homo sapiens mRNA for NA14

protein

Seq. No. 304616

Seq. ID pwr700448644.h1

Method BLASTX
NCBI GI g1172836
BLAST score 372
E value 5.0e-36
Match length 70
% identity 97

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)

small ras-related protein [Nicotiana tabacum]

Seq. No. 304617

Seq. ID pwr700448652.hl

Method BLASTX
NCBI GI g126318
BLAST score 338
E value 1.0e-40
Match length 88
% identity 93

NCBI Description TRIACYLGLYCEROL LIPASE PRECURSOR (LIPASE, PANCREATIC)

>gi_418775_pir__C43357 triacylglycerol lipase (EC 3.1.1.3)
precursor, pancreatic - human >gi_190140 (M93285) lipase
[Homo sapiens] >gi_339597 (J05125) triglyceride lipase
precursor [Homo sapiens] >gi_1304379 (L24529) pancreatic

lipase [Homo sapiens]

Seq. No. 304618

Seq. ID pwr700448656.h1

Method BLASTX
NCBI GI g135449
BLAST score 282
E value 2.0e-25
Match length 69
% identity 80

NCBI Description TUBULIN BETA-1 CHAIN >gi_100932_pir__S14701 tubulin beta-1

chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1

tubulin [Zea mays]

Seq. No. 304619

Seq. ID pwr700448658.hl

Method BLASTN
NCBI GI g4505464
BLAST score 189
E value 1.0e-102
Match length 213
% identity 97

NCBI Description Homo sapiens neutral sphingomyelinase (N-SMase) activation

associated factor (NSMAF) mRNA >gi_1556398_emb_X96586_HSFAN

H.sapiens mRNA for FAN protein

Seq. No. 304620

Seq. No.

304625



```
Seq. ID
                  pwr700448681.h1
Method
                  BLASTX
NCBI GI
                  g4503135
BLAST score
                  187
                  1.0e-14
E value
Match length
                  38
                  89
% identity
                  chymotrypsinogen B1 >gi_117617_sp_P17538_CTRB_HUMAN
NCBI Description
                  CHYMOTRYPSINOGEN B PRECURSOR >gi_105619_pir__A31299
                  chymotrypsin (EC 3.4.21.1) precursor - human >gi_181190
                  (M24400) preprochymotrypsinogen (EC 3.4.21.1) [Homo
                  sapiens]
Seq. No.
                  304621
                  pwr700448695.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g190336
BLAST score
                  250
E value
                  1.0e-27
                  72
Match length
% identity
NCBI Description (M16630) protease E precursor [Homo sapiens]
                  304622
Seq. No.
Seq. ID
                  pwr700448717.h1
Method
                  BLASTX
NCBI GI
                  g2119106
BLAST score
                  204
E value
                  1.0e-16
Match length
                  38
                  97
% identity
NCBI Description ribosomal protein L3 - human (fragment) >gi 337580 (M90054)
                  ribosomal protein L3 [Homo sapiens]
Seq. No.
                  304623
Seq. ID
                  pwr700448720.hl
Method
                  BLASTN
NCBI GI
                  g3789719
BLAST score
                  81
E value
                  3.0e-38
Match length
                  105
% identity
                  94
NCBI Description Homo sapiens chromosome 17, clone hRPC.4_G_17, complete
                  sequence [Homo sapiens]
Seq. No.
                  304624
                  pwr700448756.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3924651
BLAST score
                  188
E value
                  1.0e-101
Match length
                  208
% identity
NCBI Description Homo sapiens clone UWGC:y14c057 from 6p21, complete
                  sequence [Homo sapiens]
```

 Seq. ID
 pwr700448801.h1

 Method
 BLASTN

 NCBI GI
 q4455461

BLAST score 105 E value 1.0e-52 Match length 109 % identity 99

NCBI Description Human DNA sequence from clone 198C21 on chromosome

Xq26.1-26.3 Contains GPC4 (glypican 4), ESTs, STSs and GSS,

complete sequence [Homo sapiens]

Seq. No. 304626

Seq. ID pwr700448844.hl

Method BLASTN
NCBI GI g2460199
BLAST score 49
E value 4.0e-19
Match length 93
% identity 89

NCBI Description Homo sapiens eukaryotic translation initiation factor 3

subunit (p42) mRNA, complete cds

Seq. No. 304627

Seq. ID pwr700448854.h1

Method BLASTN
NCBI GI g3192872
BLAST score 148
E value 7.0e-78
Match length 216
% identity 93

NCBI Description Homo sapiens putative glialblastoma cell

differentiation-related protein (GBDR1) mRNA, complete cds

Seq. No. 304628

Seq. ID pwr700448865.hl

Method BLASTX
NCBI GI g3450889
BLAST score 139
E value 6.0e-09
Match length 36
% identity 78

NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 304629

Seq. ID pwr700448884.h1

Method BLASTN
NCBI GI g182059
BLAST score 101
E value 3.0e-50
Match length 105
% identity 99

NCBI Description Human pancreatic elastase IIB mRNA, complete cds

Seq. No. 304630

Seq. ID pwr700448959.hl

Method BLASTX NCBI GI g2914706



```
BLAST score 161
E value 2.0e-11
Match length 38
% identity 79
```

NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.

304631

Seq. ID Method pwr700448983.h1

Method BLASTN
NCBI GI g643596
BLAST score 208
E value 1.0e-113
Match length 228
% identity 98

NCBI Description Corn mRNA for cysteine proteinase, clone CCP, complete cds

Seq. No.

304632

Seq. ID pwr700449047.h1

Method BLASTX
NCBI GI g123656
BLAST score 183
E value 8.0e-16
Match length 57
% identity 84

NCBI Description CHLOROPLAST ENVELOPE MEMBRANE 70 KD HEAT SHOCK-RELATED

PROTEIN >gi_285407_pir__A42582 heat shock protein SCE70 - spinach >gi_21338_emb_CAA43711_ (X61491) 70 kDa heat shock

protein [Spinacia oleracea]

Seq. No. 304633

Seq. ID pwr700449253.h1

Method BLASTX
NCBI GI g232033
BLAST score 297
E value 3.0e-27
Match length 67
% identity 87

NCBI Description ELONGATION FACTOR 1 BETA' >gi_479830_pir__S35501

translation elongation factor eEF-1 beta chain - wheat >gi_218341_dbj_BAA02436_ (D13147) elongation factor 1 beta'

[Trīticum aestīvum]

Seq. No. 304634

Seq. ID pwr700449292.h1

Method BLASTX
NCBI GI g2565436
BLAST score 167
E value 3.0e-12
Match length 36
% identity 94

NCBI Description (AF028842) DegP protease precursor [Arabidopsis thaliana]

Seq. No.

304635

Seq. ID pwr700449331.h1

Method BLASTX NCBI GI g3341443 BLAST score 143

```
4.0e-09
E value
Match length
                  42
% identity
                  60
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                  304636
Seq. No.
                  pwr700449361.hl
Seq. ID
                  BLASTX
Method
                  g3004564
NCBI GI
BLAST score
                  151
                  2.0e-10
E value
Match length
                  40
                   65
% identity
                   (AC003673) putative receptor Ser/Thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   304637
Seq. No.
                  pwr700449368.hl
Seq. ID
Method
                  BLASTN
                   q2431768
NCBI GI
BLAST score
                   56
                   4.0e-23
E value
                   96
Match length
                   90
% identity
                  Zea mays acidic ribosomal protein Pla (rppla) mRNA,
NCBI Description
                   complete cds
                   304638
Seq. No.
Seq. ID
                   pwr700449391.hl
Method
                   BLASTX
                   q399888
NCBI GI
BLAST score
                   166
                   4.0e-12
E value
Match length
                   34
                   97
% identity
                   HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN
NCBI Description
                   (HLA-DR ANTIGENS ASSOCIATED INVARIANT CHAIN) (P33) (CD74
                   ANTIGEN)
Seq. No.
                   304639
                   pwr700449419.h1
Seq. ID
Method
                   BLASTX
                   q3335060
NCBI GI
                   223
BLAST score
                   1.0e-18
E value
                   77
Match length
                   61
% identity
```

(AF025842) plasma membrane-type calcium ATPase [Arabidopsis NCBI Description

thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No. 304640

pwr700449588.hl Seq. ID

BLASTX Method g67366 NCBI GI 244 BLAST score 3.0e-21 E value



Match length 48 % identity 90

NCBI Description alpha-amylase (EC 3.2.1.1) precursor, salivary - human >gi_224980_prf__1205234A amylase alpha [Homo sapiens]

Seq. No. 304641

Seq. ID pwr700449604.h1

Method BLASTN
NCBI GI g3252819
BLAST score 86
E value 6.0e-41
Match length 155
% identity 99

NCBI Description Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5,

complete sequence [Homo sapiens]

Seq. No. 304642

Seq. ID pwr700449646.h1

Method BLASTN
NCBI GI g4322262
BLAST score 49
E value 4.0e-19
Match length 101

Match length 101 % identity 87

NCBI Description Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete

cds

Seq. No. 304643

Seq. ID pwr700449658.h1

Method BLASTN
NCBI GI g4507024
BLAST score 108
E value 2.0e-54
Match length 108
% identity 100

NCBI Description Homo sapiens solute carrier family 4, sodium bicarbonate

cotransporter, member 4 (SLC4A4) mRNA, and translated products >gi_2281471_gb_AF007216_AF007216 Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds

Seq. No. 304644

Seq. ID pwr700449678.h1

Method BLASTX
NCBI GI g3915628
BLAST score 145
E value 1.0e-18
Match length 54
% identity 91

NCBI Description CARBOXYPEPTIDASE B PRECURSOR (PANCREAS-SPECIFIC PROTEIN)

(PASP) >gi_2960072_emb_CAA12163_ (AJ224866)

procarboxypeptidase B [Homo sapiens]

Seq. No. 304645

Seq. ID pwr700449681.h1

Method BLASTN NCBI GI 94503090

BLAST score 93



E value 3.0e-45 Match length 123 % identity 95

NCBI Description Homo sapiens casein kinase 1, delta (CSNK1D) mRNA

>gi_881618_gb_U29171_HSU29171 Human casein kinase I delta
mRNA, complete cds >gi_1375405_gb_G27155_G27155 human STS

SHGC-31593

Seq. No. 304646

Seq. ID pwr700449719.h2

Method BLASTX
NCBI GI g3171910
BLAST score 365
E value 3.0e-35
Match length 76
% identity 91

NCBI Description (AJ001014) RAMP1 [Homo sapiens]

Seq. No. 304647

Seq. ID pwr700449749.h2

Method BLASTN
NCBI GI g165703
BLAST score 52
E value 1.0e-20
Match length 170

% identity 84
NCBI Description Rabbit smooth muscle myosin light chain kinase mRNA,

complete CDS

Seq. No. 304648

Seq. ID pwr700449783.h2

Method BLASTN
NCBI GI g505472
BLAST score 122
E value 1.0e-62
Match length 122
% identity 100

NCBI Description H.sapiens mRNA for ribosomal protein L31

Seq. No. 304649

Seq. ID pwr700449790.h2

Method BLASTX
NCBI GI g1545871
BLAST score 343
E value 8.0e-33
Match length 67
% identity 97

NCBI Description (U66607) cyclin type B-like [Zea mays] >gi_1545873 (U66608)

cyclin type B-like [Zea mays]

Seq. No. 304650

Seq. ID pwr700449849.h2

Method BLASTN
NCBI GI g4512253
BLAST score 231
E value 1.0e-127
Match length 274

```
% identity
                  Homo sapiens gene for JKTBP2, JKTBP1, complete cds
NCBI Description
                  304651
Seq. No.
                  pwr700449873.h2
Seq. ID
                  BLASTX
Method
                  q2582800
NCBI GI
                  242
BLAST score
                  7.0e-21
E value
Match length
                  74
% identity
                  66
                  (Y11607) protein phosphatase 2C [Medicago sativa]
NCBI Description
                  304652
Seq. No.
Seq. ID
                  pwr700449886.h2
Method
                  BLASTX
                  g4325344
NCBI GI
BLAST score
                  319
                  8.0e-30
E value
Match length
                  89
% identity
                  70
                  (AF128393) similar to beta-transducins (Pfam: PF00400,
NCBI Description
                  Score=71.7, E=1.5e-17, N=6) [Arabidopsis thaliana]
                  304653
Seq. No.
Seq. ID
                  pwr700449914.h1
Method
                  BLASTX
NCBI GI
                  q2467298
BLAST score
                  210
                  5.0e-17
E value
                  56
Match length
                  77
% identity
                  (AB000888) phosphatidic acid phosphatase 2a [Homo sapiens]
NCBI Description
                  >gi 3123848 (AF014402) type-2 phosphatidic acid phosphatase
                  alpha-1 [Homo sapiens]
                  304654
Seq. No.
                  pwr700449922.h1
Seq. ID
Method
                  BLASTX
                  q1778093
NCBI GI
BLAST score
                  170
                  2.0e-12
E value
Match length
                  73
                   48
% identity
                  (U64902) putative sugar transporter; member of major
NCBI Description
                   facilitative superfamily; integral membrane protein [Beta
                  vulgaris]
```

Seq. No. 304655

Seq. ID pwr700449933.h1

Method BLASTX
NCBI GI g123620
BLAST score 474
E value 5.0e-48
Match length 92
% identity 100

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir__S14950



heat shock cognate protein 70 - tomato >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate 70 [Lycopersicon esculentum]

Seq. No. 304656

Seq. ID pwr700449968.hl

Method BLASTX
NCBI GI g4039152
BLAST score 160
E value 3.0e-11
Match length 35
% identity 77

NCBI Description (AF104221) low temperature and salt responsive protein LTI6B [Arabidopsis thaliana] >gi_4325219_gb_AAD17303_

(AF122006) hydrophobic protein [Arabidopsis thaliana]

Seq. No. 304657

Seq. ID pwr700449989.hl

Method BLASTX
NCBI GI g1351296
BLAST score 231
E value 9.0e-20
Match length 51
% identity 92

NCBI Description TROPONIN I, CARDIAC MUSCLE >gi_627953_pir__A53805 troponin

I, cardiac - mouse >gi_313105_emb_CAA80459_ (Z22784) troponin I [Mus musculus] >gi_508866 (U09181) cardiac

troponin I [Mus musculus]

Seq. No. 304658

Seq. ID pwr700450004.h2

Method BLASTX
NCBI GI g2696229
BLAST score 161
E value 5.0e-21
Match length 76
% identity 64

NCBI Description (D55712) chitinase [Oryza sativa]

Seq. No. 304659

Seq. ID pwr700450008.h2

Method BLASTX
NCBI GI g135411
BLAST score 271
E value 6.0e-36
Match length 92
% identity 95

NCBI Description TUBULIN ALPHA-2 CHAIN >gi_82732_pir__S15772 tubulin alpha-2

chain - maize >gi_22148_emb_CAA33733 (X15704)

alpha2-tubulin [Zea mays]

Seq. No. 304660

Seq. ID pwr700450044.h2

Method BLASTX
NCBI GI g3426043
BLAST score 161
E value 3.0e-11



Match length 31 84 % identity (AC005168) putative choline kinase [Arabidopsis thaliana] NCBI Description Seq. No. 304661 pwr700450066.h2 Seq. ID BLASTX Method q1332579 NCBI GI BLAST score 246 6.0e-35 E value

(X98063) polyubiquitin [Pinus sylvestris] NCBI Description

Seq. No. 304662

Match length

% identity

Seq. ID pwr700450079.h2

84

9

Method BLASTN g168436 NCBI GI BLAST score 70 3.0e-31 E value Match length 249 % identity 87

Zea mays catalase (Cat3) gene, complete cds NCBI Description

304663 Seq. No.

Seq. ID pwr700450159.hl

Method BLASTN NCBI GI g285968 BLAST score 121 5.0e-62 E value 121 Match length 100 % identity

Human mRNA for KIAA0026 gene, complete cds NCBI Description

304664 Seq. No.

pwr700450191.h1 Seq. ID

Method BLASTN g4502358 NCBI GI BLAST score 236 1.0e-130 E value Match length 268 % identity 97

Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3) NCBI Description

mRNA >gi 3021700 dbj AB005299 AB005299 Homo sapiens BAI 3

mRNA, complete cds

304665 Seq. No.

pwr700450291.h1 Seq. ID

Method BLASTX NCBI GI g3319096 BLAST score 209 E value 5.0e-31 Match length 88 78 % identity

Chain L, Hiv-1 Gp120 Core Complexed With Cd4 And A NCBI Description

Neutralizing Human Antibody



```
304666
Seq. No.
  Seq. ID
                    pwr700450316.h1
  Method
                    BLASTN
                    q2431768
  NCBI GI
  BLAST score
                    75
                    2.0e-34
  E value
  Match length
                    115
  % identity
                    91
                    Zea mays acidic ribosomal protein Pla (rppla) mRNA,
  NCBI Description
                    complete cds
                    304667
  Seq. No.
  Seq. ID
                    pwr700450354.hl
  Method
                    BLASTX
  NCBI GI
                    g1732513
  BLAST score
                    285
  E value
                    7.0e-26
  Match length
                    72
  % identity
                    74
                    (U62743) snapdragon myb protein 305 homolog [Arabidopsis
  NCBI Description
                    thaliana]
                    304668
  Seq. No.
  Seq. ID
                    pwr700450402.h1
  Method
                    BLASTX
  NCBI GI
                    g1082693
  BLAST score
                    266
                    7.0e-24
  E value
  Match length
                    50
  % identity
                    96
  NCBI Description
                    phosphotyrosyl phosphatase activator PTPA - human
                    >gi 509243 emb CAA51873 (X73478) phosphotyrosyl
                    phosphatase activator [Homo sapiens]
  Seq. No.
                    304669
  Seq. ID
                    pwr700450456.h1
  Method
                    BLASTN
  NCBI GI
                    g939784
  BLAST score
                     46
                    7.0e-17
  E value
                    74
  Match length
                    91
  % identity
  NCBI Description Zea mays MADS-box protein (ZAP1) mRNA, complete cds
  Seq. No.
                    304670
  Seq. ID
                    pwr700450484.h1
  Method
                    BLASTX
  NCBI GI
                    q4559304
  BLAST score
                    267
  E value
                     6.0e-24
  Match length
                     49
  % identity
                    100
```

NCBI Description (AF127021) T7-like RNA polymerase [Zea mays]

Seq. No.

304671

Seq. ID pwr700450486.hl

Method

BLASTX



```
NCBI GI
                  g2130149
BLAST score
                  471
                  1.0e-47
E value
Match length
                  90
                  100
% identity
                  translation elongation factor eEF-1 alpha chain - maize
NCBI Description
                  (fragment)
Seq. No.
                  304672
Seq. ID
                  pwr700450493.h1
Method
                  BLASTN
NCBI GI
                  g1503995
BLAST score
                  169
                  2.0e-90
E value
Match length
                  193
% identity
                  97
NCBI Description Human mRNA for KIAA0206 gene, partial cds
                  304673
Seq. No.
                  pwr700450495.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454470
BLAST score
                  202
E value
                  4.0e-16
Match length
                  91
% identity
                  53
                  (AC006234) putative sugar transporter [Arabidopsis
NCBI Description
                  thaliana]
                  304674
Seq. No.
                  pwr700450509.h1
Seq. ID
Method
                  BLASTN
                  q556529
NCBI GI
BLAST score
                  60
E value
                  2.0e-25
Match length
                  138
% identity
                  88
NCBI Description Mouse mRNA for arylhydrocarbon receptor, complete cds
                  304675
Seq. No.
                  pwr700450523.h1
Seq. ID
Method
                  BLASTN
                  g4218352
NCBI GI
BLAST score
                  89
E value
                  5.0e-43
Match length
                  102
                  96
% identity
NCBI Description
                  Homo sapiens chromosome 18 CpG island DNA, genomic Mse1
                  fragment, clone 18CGI1G4 , complete read
Seq. No.
                  304676
Seq. ID
                  pwr700450548.h1
Method
                  BLASTN
```

7.0e-65 Match length 140

126

q1913891

NCBI GI

E value

BLAST score

```
% identity
NCBI Description Human clone 23652 mRNA sequence
                  304677
Seq. No.
                  pwr700450616.hl
Seq. ID
                  BLASTN
Method
                  g905355
NCBI GI
BLAST score
                  39
                  1.0e-12
E value
                  39
Match length
% identity
                  100
NCBI Description Human tastin mRNA, complete cds
                  304678
Seq. No.
                  pwr700450692.h1
Seq. ID
Method
                  BLASTN
                  g340218
NCBI GI
                  125
BLAST score
                  2.0e-64
E value
Match length
                  136
% identity
                  99
NCBI Description Human vimentin gene, complete cds
                  304679
Seq. No.
                  pwr700450705.h1
Seq. ID
Method
                  BLASTN
                  g1164913
NCBI GI
BLAST score
                  42
                  6.0e-15
E value
Match length
                  54
% identity
                  94
NCBI Description Human DNA sequence from cosmid U209G1 on chromosome X
                  304680
Seq. No.
                  pwr700450707.h1
Seq. ID
Method
                  BLASTN
                  g3659494
NCBI GI
BLAST score
                  234
                  1.0e-129
E value
                   274
Match length
% identity
                   96
NCBI Description Homo sapiens chromosome 17, clone hRPK.147 L 13, complete
                  sequence [Homo sapiens]
                   304681
Seq. No.
Seq. ID
                   pwr700450829.h1
Method
                   BLASTN
NCBI GI
                   g35666
BLAST score
                   75
                   2.0e-34
E value
Match length
                   99
                   94
% identity
NCBI Description Human prolactin gene 5' region
```

43122

304682

BLASTN

pwr700450838.h1

Seq. No. Seq. ID

Method



```
g189016
NCBI GI
BLAST score
                  76
                  3.0e-35
E value
Match length
                  107
                  94
% identity
                  Human nonmuscle/smooth muscle alkali myosin light chain
NCBI Description
                  gene, complete cds
                  304683
Seq. No.
                  pwr700450849.h1
Seq. ID
                  BLASTN
Method
                  q4049267
NCBI GI
                  129
BLAST score
                  9.0e-67
E value
Match length
                  133
% identity
                  99
                  Homo sapiens putative tumor suppressor ST13 (ST13) mRNA,
NCBI Description
                   complete cds
                   304684
Seq. No.
Seq. ID
                  pwr700450855.h1
Method
                  BLASTN
                   g1915966
NCBI GI
BLAST score
                   73
                   2.0e-33
E value
Match length
                   77
% identity
                   99
                  Homo sapiens small acidic protein mRNA, complete cds
NCBI Description
                   304685
Seq. No.
                   pwr700450864.h1
Seq. ID
Method
                   BLASTN
                   q509242
NCBI GI
BLAST score
                   81
                   3.0e-38
E value
                   112
Match length
% identity
                   94
NCBI Description
                  H.sapiens hPTPA mRNA
                   304686
Seq. No.
                   pwr700450953.h1
Seq. ID
Method
                   BLASTX
                   g2492519
NCBI GI
BLAST score
                   161
                   1.0e-11
E value
Match length
                   63
% identity
                   100
                   26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
```

7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase

subunit [Spinacia oleracea]

304687 Seq. No.

pwr700450970.h1 Seq. ID

BLASTN Method g2668739 NCBI GI BLAST score 161 1.0e-85 E value



Match length 173 % identity 99

NCBI Description Zea mays translation initiation factor GOS2 (TIF) mRNA,

complete cds

Seq. No. 304688

Seq. ID pwr700450973.h1

Method BLASTN
NCBI GI g3983571
BLAST score 153
E value 6.0e-81
Match length 188
% identity 97

NCBI Description Homo sapiens PAC clone DJ0593H12 from 7p31, complete

sequence [Homo sapiens]

Seq. No. 304689

Seq. ID pwr700450992.h1

Method BLASTX
NCBI GI g4454048
BLAST score 162
E value 1.0e-11
Match length 58
% identity 53

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 304690

Seq. ID pwr700451006.h1

Method BLASTX
NCBI GI g4336424
BLAST score 437
E value 1.0e-43
Match length 87
% identity 97

NCBI Description (AF089868) cell surface glycoprotein P1H12 precursor [Homo

sapiens]

Seq. No. 304691

Seq. ID pwr700451019.h1

Method BLASTN
NCBI GI g4502900
BLAST score 216
E value 1.0e-118
Match length 236
% identity 98

NCBI Description Homo sapiens clathrin, light polypeptide (Lcb) (CLTB) mRNA

>gi_187056_gb_M20470_HUMLCTHB Human lymphocyte clathrin

light-chain B mRNA, complete cds

Seq. No. 304692

Seq. ID pwr700451045.h1

Method BLASTN
NCBI GI g6012171
BLAST score 40
E value 2.0e-13
Match length 52
% identity 94





NCBI Description Hordeum vulgare mRNA for vacuolar membrane proton-translocating inorganic pyrophosphat

Seq. No. 304693

Seq. ID pwr700451051.h1

Method BLASTX
NCBI GI g3327094
BLAST score 195
E value 2.0e-15
Match length 49
% identity 86

NCBI Description (AB014540) KIAA0640 protein [Homo sapiens]

Seq. No. 304694

Seq. ID pwr700451058.h1

Method BLASTX
NCBI GI g1171064
BLAST score 251
E value 2.0e-29
Match length 80
% identity 90

NCBI Description CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR

(MELANOMA-ASSOCIATED ANTIGEN MUC18) (MELANOMA-ASSOCIATED ANTIGEN A32) (S-ENDO 1 ENDOTHELIAL-ASSOCIATED ANTIGEN)

(CD146 ANTIGEN) (MELANOMA ADHESION MOLECULE)

>gi_2134899_pir__I38049 cell surface glycoprotein MUC18
precursor - human >gi_529724 (M28882) MUC18 glycoprotein
[Homo sapiens] >gi_530048 (M29277) MUC18 glycoprotein [Homo

sapiens] >gi_825693 emb_CAA48332 (X68264) melanoma

associated glycoprotein [Homo sapiens]

Seq. No. 304695

Seq. ID pwr700451064.h1

Method BLASTX
NCBI GI g2317902
BLAST score 268
E value 7.0e-24
Match length 85
% identity 66

NCBI Description (U89959) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304696

Seq. ID pwr700451068.h1

Method BLASTN
NCBI GI g3283923
BLAST score 109
E value 9.0e-55
Match length 149
% identity 93

NCBI Description Homo sapiens clone 24452 mRNA sequence

Seq. No. 304697

Seq. ID pwr700451124.h1

Method BLASTX
NCBI GI g1703380
BLAST score 286
E value 6.0e-26

```
Match length
                  100
% identity
                  ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)
NCBI Description
                  ADP-ribosylation factor [Oryza sativa]
                  304698
Seq. No.
                  pwr700451161.hl
Seq. ID
Method
                  BLASTX
                  g629800
NCBI GI
BLAST score
                  272
E value
                  2.0e-24
Match length
                  88
% identity
                  64
                  pir7b protein - rice >gi_498747_emb_CAA84024_ (Z34270)
NCBI Description
                  Pir7b [Oryza sativa]
                  304699
Seq. No.
Seq. ID
                  pwr700451162.hl
Method
                  BLASTX
NCBI GI
                  q3421384
BLAST score
                  198
E value
                  1.0e-15
Match length
                  62
                  52
% identity
                  (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  304700
Seq. ID
                  pwr700451232.hl
Method
                  BLASTX
NCBI GI
                  q3688598
BLAST score
                  262
                  2.0e-23
E value
Match length
                  63
                  78
% identity
NCBI Description
                  (AB009029) Cycloartenol Synthase [Panax ginseng]
```

Seq. No. 304701

Seq. ID pwr700451245.h1

Method BLASTN
NCBI GI g4589410
BLAST score 46
E value 5.0e-17
Match length 122
% identity 84

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F2015, complete sequence

Seq. No. 304702

Seq. ID pwr700451251.h1

Method BLASTN
NCBI GI g32328
BLAST score 142
E value 2.0e-74
Match length 178
% identity 96

NCBI Description Human HMG-17 gene for non-histone chromosomal protein



HMG-17

Seq. No. 304703 Seq. ID pwr700

Seq. ID pwr700451511.h1 Method BLASTX

NCBI GI g170352 BLAST score 431 E value 6.0e-43 Match length 89 % identity 17

NCBI Description (M74101) hexameric polyubiquitin [Nicotiana sylvestris]

>gi_870792 (L05361) polyubiquitin [Arabidopsis thaliana]
>gi_4115333 (L81139) ubiquitin [Pisum sativum] >gi_4115335

(L81140) ubiquitin [Pisum sativum]

Seq. No. 304704

Seq. ID pwr700451532.h1

Method BLASTN
NCBI GI g2511528
BLAST score 91
E value 3.0e-44
Match length 106
% identity 96

NCBI Description Homo sapiens E1B 19K/Bcl-2-binding protein Nip3 mRNA,

nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 304705

Seq. ID pwr700451543.h1

Method BLASTN
NCBI GI g184097
BLAST score 236
E value 1.0e-130
Match length 276
% identity 96

NCBI Description Human HIV1 tata element modulatory factor mRNA sequence

from chromosome 3

Seq. No. 304706

Seq. ID pwr700451605.h1

Method BLASTN
NCBI GI g2935593
BLAST score 234
E value 1.0e-129
Match length 277
% identity 96

NCBI Description Homo sapiens Xp22 BAC GS-602M16 (Genome Systems Human BAC

library) complete sequence [Homo sapiens]

Seq. No. 304707

Seq. ID pwr700451653.h1

Method BLASTX
NCBI GI g2149051
BLAST score 324
E value 2.0e-30
Match length 63
% identity 97

NCBI Description (U73810) small Ras-like GTP-binding protein [Arabidopsis

NCBI Description



thaliana]

```
304708
Seq. No.
Seq. ID
                  pwr700451666.h1
Method
                  BLASTX
NCBI GI
                  g3450881
BLAST score
                  225
                  8.0e-19
E value
Match length
                  85
% identity
                  64
                  (AF083269) p41-Arc [Rattus norvegicus]
NCBI Description
                  304709
Seq. No.
                  pwr700451739.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4502996
BLAST score
                   66
                  3.0e-29
E value
                  78
Match length
                   96
% identity
NCBI Description
                  Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
                  >qi 35329 emb X67318 HSPCBXA1 H.sapiens mRNA for
                  procarboxypeptidase Al >gi_1254688_gb G19989 G19989 sWSS41
                   Eric D. Green Homo sapiens STS genomic, sequence tagged
                  site [Homo sapiens]
                  304710
Seq. No.
Seq. ID
                  pwr700451824.h1
Method
                  BLASTX
NCBI GI
                  q3668069
BLAST score
                  203
                  2.0e-16
E value
Match length
                  39
% identity
                  100
                  (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
NCBI Description
                   304711
Seq. No.
Seq. ID
                   pwr700451862.h1
Method
                  BLASTX
NCBI GI
                  g4204265
BLAST score
                  165
E value
                   9.0e-12
Match length
                   61
% identity
                   51
                  (AC005223) 45643 [Arabidopsis thaliana]
NCBI Description
                   304712
Seq. No.
                   pwr700451924.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g113789
BLAST score
                   309
E value
                   6.0e-29
Match length
                   54
% identity
                   94
```

GLUCANOHYDROLASE) (ALPHA-AMYLASE CARCINOID)

ALPHA-AMYLASE 2B PRECURSOR (1,4-ALPHA-D-GLUCAN

>gi_1070489_pir__ALHU2B alpha-amylase (EC 3.2.1.1) 2B

```
precursor, pancreatic - human >gi_537512 (M24895) alpha-amylase [Homo sapiens] >gi_780137_dbj_BAA14130_
```

(D90097) alpha-amylase [Homo sapiens]

Seq. No. 304713

Seq. ID pwr700451947.h1

Method BLASTX
NCBI GI g1335217
BLAST score 203
E value 2.0e-16
Match length 43
% identity 95

NCBI Description (X00198) myc protein (aa 253-439) (17 is 2nd base in codon)

[Homo sapiens]

Seq. No. 304714

Seq. ID pwr700451962.h1

Method BLASTN
NCBI GI g1098636
BLAST score 185
E value 1.0e-100
Match length 212
% identity 97

NCBI Description Human fragile X mental retardation syndrome related protein

(FXR2) mRNA, complete cds

Seq. No. 304715

Seq. ID pwr700451986.h1

Method BLASTN
NCBI GI g1246234
BLAST score 85
E value 4.0e-40
Match length 216
% identity 85

NCBI Description Homo sapiens FSHD region DNA sequence

Seq. No. 304716

Seq. ID pwr700452061.h1

Method BLASTN
NCBI GI g220013
BLAST score 115
E value 2.0e-58
Match length 122
% identity 99

NCBI Description Homo sapiens mRNA for pancreatic protease E precursor,

complete cds

Seq. No. 304717

Seq. ID pwr700452069.h1

Method BLASTN
NCBI GI g285950
BLAST score 130
E value 3.0e-67
Match length 150
% identity 97

NCBI Description Human mRNA for KIAA0107 gene, complete cds



```
Seq. No.
                   304718
                   pwr700452085.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4502997
BLAST score
                   153
E value
                   1.0e-10
Match length
                   33
% identity
                   85
NCBI Description
                   carboxypeptidase A1 (pancreatic)
                   >gi 399196 sp P15085 CBP1 HUMAN CARBOXYPEPTIDASE A1
                   PRECURSOR >gi 345782 pir S29127 carboxypeptidase A (EC
                   3.4.17.1) CPA1 precursor - human >gi 35330 emb CAA47732
                   (X67318) carboxypeptidase a [Homo sapiens]
Seq. No.
                   304719
Seq. ID
                   pwr700452123.h1
Method
                   BLASTX
NCBI GI
                   g4503003
BLAST score
                   220
E value
                   2.0e-18
Match length
                   46
% identity
                   93
NCBI Description
                  carboxypeptidase B1 (tissue) >gi 284360 pir A42332
                   carboxypeptidase B (EC 3.4.17.2) precursor, pancreatic -
                   human >gi_189625 (M81057) procarboxypeptidase B [Homo
                   sapiens]
                   304720
Seq. No.
Seq. ID
                   pwr700452130.h1
Method
                   BLASTN
NCBI GI
                   g307165
BLAST score
                   139
E value
                   1.0e-72
Match length
                   139
% identity
                   100
NCBI Description
                  Human myeloid cell differentiation protein (MCL1) mRNA
Seq. No.
                   304721
                   pwr700452193.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4190944
BLAST score
                   103
                   2.0e-51
E value
Match length
                   107
% identity
                   99
NCBI Description
```

Homo sapiens chromosome 9, clone hRPK.465_F_21, complete sequence [Homo sapiens]

Seq. No. 304722

Seq. ID pwr700452430.h1

Method BLASTX NCBI GI q4139785 BLAST score 170 E value 1.0e-12 Match length 33 % identity 33

NCBI Description Chain B, Canine Gdp-Ran Q691 Mutant



```
Seq. No.
                   304723
Seq. ID
                  pwr700452432.h1
Method
                   BLASTX
NCBI GI
                   g4510345
BLAST score
                   163
E value
                   1.0e-11
Match length
                  70
% identity
NCBI Description
                  (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                  304724
Seq. ID
                  pwr700452442.h1
Method
                  BLASTX
NCBI GI
                   g3461814
BLAST score
                   300
E value
                   1.0e-27
Match length
                  85
% identity
NCBI Description
                  (AC004138) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  304725
Seq. ID
                  pwr700452811.h1
Method
                  BLASTX
NCBI GI
                  g3377950
BLAST score
                  177
E value
                   3.0e-13
Match length
                  50
% identity
                   58
NCBI Description
                   (AJ009830) cysteine proteinase precursor, AN11 [Ananas
                  comosus]
                  304726
Seq. No.
Seq. ID
                  pwr700452820.h1
Method
                  BLASTX
NCBI GI
                  g3426038
BLAST score
                  241
                  8.0e-21
E value
Match length
                  78
% identity
                  62
NCBI Description
                  (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                  304727
Seq. ID
                  pwr700452842.h1
Method
                  BLASTX
                  g1706956
NCBI GI
BLAST score
                  151
E value
                  2.0e-10
Match length
                  39
                  77
% identity
NCBI Description
                  (U58283) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  304728
```

Seq. ID pwr700452873.h1

Method BLASTX NCBI GI g4510345 BLAST score 159



E value 3.0e-11 Match length 43 % identity 58 NCBI Description (AC006921) unknown protein [Arabidopsis thaliana] 304729 Seq. No. pwr700452906.h1 Seq. ID Method BLASTN NCBI GI q4454564 BLAST score 238 E value 1.0e-131 Match length 250 % identity 99 NCBI Description Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds Seq. No. 304730 Seq. ID pwr700453018.h1 Method BLASTN NCBI GI q3402739 BLAST score 226 E value 1.0e-124 Match length 265 % identity 97 NCBI Description Homo sapiens chromosome 17, clone hRPK.471 L 13, complete sequence [Homo sapiens] Seq. No. 304731 Seq. ID pwr700453054.h1 Method BLASTX NCBI GI q2463634 BLAST score 306 2.0e-28 E value Match length 75 % identity NCBI Description (U81800) monocarboxylate transporter [Homo sapiens] 304732 Seq. No. Seq. ID pwr700453080.h1 Method BLASTX NCBI GI g1173286 BLAST score 165 5.0e-12 E value Match length 43 77 % identity 40S RIBOSOMAL PROTEIN S9 >gi 112274 pir S21497 ribosomal NCBI Description protein S9 - rat >gi 57143 emb CAA47013 (X66370) ribosomal

protein S9 [Rattus norvegicus]

Seq. No. 304733

Seq. ID pwr700453096.h1

Method BLASTN g529723 NCBI GI 121 BLAST score E value 6.0e-62 Match length 149 % identity 96



```
Human MUC18 glycoprotein mRNA, complete cds
NCBI Description
Seq. No.
                  304734
Seq. ID
                  pwr700453147.h1
Method
                  BLASTX
                  q2618688
NCBI GI
BLAST score
                  209
E value
                  6.0e-17
Match length
                  60
                  65
% identity
                  (AC002510) putative esterase D [Arabidopsis thaliana]
NCBI Description
                  304735
Seq. No.
Seq. ID
                  pwr700453213.h1
Method
                  BLASTX
NCBI GI
                  g123613
BLAST score
                  200
E value
                  7.0e-16
Match length
                  53
                  74
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >qi 100222 pir S14949
NCBI Description
                  heat shock cognate protein 70 - tomato
                  >gi 19256 emb CAA37970 (X54029) heat shock protein cognate
                  70 [Lycopersicon esculentum]
Seq. No.
                  304736
Seq. ID
                  pwr700453223.h1
Method
                  BLASTX
NCBI GI
                  g4502221
BLAST score
                  211
E value
                  4.0e-33
Match length
                  85
% identity
                  83
                  Rho GTPase activating protein 5 >gi 687593 (U17032) p190-B
NCBI Description
                  [Homo sapiens]
                  304737
Seq. No.
                  pwr700453245.h1
Seq. ID
                  BLASTX
Method
                  g730536
NCBI GI
BLAST score
                  428
                  1.0e-42
E value
Match length
                  85
                  98
% identity
                  60S RIBOSOMAL PROTEIN L23 >gi 310933 (L18915) 60S ribosomal
NCBI Description
                  protein subunit L17 [Nicotiana tabacum]
```

Seq. No. 304738

Seq. ID pwr700453322.h1

Method BLASTX
NCBI GI g1053047
BLAST score 298
E value 3.0e-27
Match length 59
% identity 100

NCBI Description (U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3



[Glycine max]

304739 Seq. No.

Seq. ID pwr700453330.h1

Method BLASTX NCBI GI g4506617 BLAST score 197 9.0e-16 E value 39 Match length % identity 92

NCBI Description ribosomal protein L17 >gi 132799 sp P18621 RL17 HUMAN 60S RIBOSOMAL PROTEIN L17 (L23) >gi 71281 pir R5HU22 ribosomal

protein L17 - human >gi 34199 emb CAA37793 (X53777)

putative ribosomal protein (AA 1-184) [Homo sapiens]

Seq. No. 304740

pwr700453352.h1 Seq. ID

Method BLASTX g1945502 NCBI GI 140 BLAST score 9.0e-09 E value Match length 57 % identity 47

(U13644) F56D2.5 gene product [Caenorhabditis elegans] NCBI Description

304741 Seq. No.

Seq. ID pwr700453395.h1

BLASTN Method NCBI GI q3127925 BLAST score 84 E value 5.0e-40 Match length 84 % identity 100

NCBI Description H.sapiens RNA for type VI collagen alpha3 chain

304742 Seq. No.

Seq. ID pwr700453434.h1

Method BLASTX g2662343 NCBI GI BLAST score 277 E value 1.0e-25 Match length 65 % identity 97

(D63581) EF-1 alpha [Oryza sativa] NCBI Description

304743 Seq. No.

pwr700453445.h1 Seq. ID

Method BLASTN NCBI GI g3183937 BLAST score 143 E value 6.0e-75 Match length 191 % identity 94

NCBI Description Homo sapiens partial mRNA; ID EE2-12A

304744 Seq. No.

Seq. ID pwr700453515.h1



```
BLASTX
Method
NCBI GI
                  g1806185
BLAST score
                  145
E value
                  3.0e-14
Match length
                  46
                  83
% identity
                  (Z84395) rpsN [Mycobacterium tuberculosis]
NCBI Description
                  304745
Seq. No.
                  pwr700453539.h1
Seq. ID
                  BLASTX
Method
                  g4406780
NCBI GI
                  228
BLAST score
                  2.0e-19
E value
Match length
                  48
% identity
                  90
                  (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                  304746
Seq. No.
Seq. ID
                  pwr700453606.h1
Method
                  BLASTX
NCBI GI
                  g4455222
BLAST score
                  160
E value
                  3.0e-11
Match length
                  71
% identity
                  46
                  (AL035440) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  304747
Seq. No.
                  pwr700453642.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914056
BLAST score
                  228
E value
                   4.0e-19
Match length
                   91
% identity
                  55
NCBI Description
                  DNA MISMATCH REPAIR PROTEIN MSH2 >gi_2522362 (AF002706)
                  MutS homolog 2 [Arabidopsis thaliana] >gi_2522364
                   (AF003005) MutS homolog 2 [Arabidopsis thaliana]
                   >gi 2547236 (AF026549) DNA mismatch repair protein MSH2
                   [Arabidopsis thaliana]
                   304748
Seq. No.
                  pwr700453668.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g949877
BLAST score
                  83
E value
                   6.0e-39
Match length
                  207
% identity
                  86
```

NCBI Description H.vulgare mRNA for elongation factor 1-alpha

Seq. No.

304749

Seq. ID

qmh700025735.fl

Method NCBI GI BLASTX g629561



```
BLAST score
                  190
                  1.0e-14
E value
Match length
                  88
% identity
                  38
NCBI Description
                  SRG1 protein - Arabidopsis thaliana
                  >gi 479047 emb CAA55654 (X79052) SRG1 [Arabidopsis
                  thaliana]
Seq. No.
                  304750
Seq. ID
                  qmh700025741.f1
Method
                  BLASTX
NCBI GI
                  g2117355
BLAST score
                  257
                  1.0e-22
E value
Match length
                  90
% identity
                  56
NCBI Description
                  mitochondrial processing peptidase (EC 3.4.99.41) alpha-II
                  chain precursor - potato >qi 587562 emb CAA56520 (X80236)
                  mitochondrial processing peptidase [Solanum tuberosum]
                  304751
Seq. No.
                  qmh700025752.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3242715
BLAST score
                  241
E value
                  7.0e-34
                  90
Match length
% identity
                  78
NCBI Description
                  (AC003040) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  304752
                  qmh700025776.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1752734
BLAST score
                  164
E value
                  7.0e-12
Match length
                  71
% identity
                  44
NCBI Description
                  (D78510) beta-glucan-elicitor receptor [Glycine max]
                  304753
Seq. No.
                  qmh700025791.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2746086
BLAST score
                  329
E value
                  6.0e-31
Match length
                  93
                  63
% identity
                  (AF025292) putative high-affinity potassium transporter
NCBI Description
                  [Hordeum vulgare]
Seq. No.
                  304754
```

Seq. ID qmh700025795.f1

Method BLASTX
NCBI GI g4204469
BLAST score 303
E value 6.0e-28



```
Match length
                  78
% identity
                  (AF090120) cystathionine beta-synthetase; CBS [Fugu
NCBI Description
                  rubripes]
Seq. No.
                  304755
Seq. ID
                  qmh700025808.fl
                  BLASTX
Method
NCBI GI
                  g4558672
BLAST score
                  286
E value
                  6.0e-26
Match length
                  59
                  90
% identity
NCBI Description
                  (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis
                  thaliana]
Seq. No.
                  304756
Seq. ID
                  qmh700025853.f1
Method
                  BLASTX
NCBI GI
                  g2500365
BLAST score
                  184
E value
                  6.0e-14
Match length
                  84
                  49
% identity
NCBI Description PROBABLE 60 RIBOSOMAL PROTEIN L14 (HYDROXYPROLINE RICH
                  GLYCOPROTEIN HRGP1)
Seq. No.
                  304757
Seq. ID
                  qmh700025857.f1
Method
                  BLASTX
                  g2190992
NCBI GI
BLAST score
                  164
E value
                  1.0e-11
Match length
                  57
% identity
NCBI Description
                  (AF004358) glutathione S-transferase TSI-1 [Aegilops
                  tauschii]
Seq. No.
                   304758
Seq. ID
                   qmh700025865.f1
Method
                  BLASTX
                  q4006886
NCBI GI
BLAST score
                  313
E value
                  4.0e-29
Match length
                  82
% identity
                  74
NCBI Description (299708) putative protein [Arabidopsis thaliana]
                  304759
Seq. No.
```

qmh700025866.f1 Seq. ID

Method BLASTX NCBI GI g4038594 BLAST score 250 E value 1.0e-21 Match length 73 % identity 64

NCBI Description (AJ222798) tDET1 protein [Lycopersicon esculentum]



>gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein
[Lycopersicon esculentum]

Seq. No. 304760

Seq. ID qmh700025876.f1

Method BLASTX
NCBI GI g4539301
BLAST score 275
E value 1.0e-24
Match length 68
% identity 74

NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis

thaliana]

Seq. No. 304761

Seq. ID qmh700025902.f1

Method BLASTX
NCBI GI g3522943
BLAST score 333
E value 2.0e-31
Match length 91
% identity 36

NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No. 304762

Seq. ID qmh700025931.f1

Method BLASTN
NCBI GI g3290003
BLAST score 222
E value 1.0e-122
Match length 226
% identity 100

NCBI Description Zea mays pathogenesis related protein-1 (PR-1) mRNA,

complete cds

Seq. No. 304763

Seq. ID qmh700025981.f1

Method BLASTN
NCBI GI g1816585
BLAST score 204
E value 1.0e-111
Match length 204
% identity 100

NCBI Description Zea mays LON1 protease (LON1) mRNA, complete cds

Seq. No. 304764

Seq. ID qmh700025986.f1

Method BLASTX
NCBI GI 94512670
BLAST score 153
E value 2.0e-10
Match length 81
% identity 38

NCBI Description (AC006931) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 304765

Seq. ID qmh700026004.f1



```
BLASTX
Method
                   g3695061
NCBI GI
                   379
BLAST score
                   7.0e-37
E value
                   88
Match length
                   82
% identity
                  (AF064788) rac GTPase activating protein 2 [Lotus
NCBI Description
                   japonicus]
                   304766
Seq. No.
                   qmh700026039.fl
Seq. ID
Method
                   BLASTX
                   g4063389
NCBI GI
BLAST score
                   403
                   1.0e-39
E value
                   83
Match length
                   88
% identity
                   (AF099012) QM protein [Bombyx mandarina]
NCBI Description
                   304767
Seq. No.
Seq. ID
                   qmh700026048.fl
                   BLASTX
Method
                   g2293566
NCBI GI
                   151
BLAST score
                   4.0e-10
E value
                   34
Match length
                   91
% identity
                   (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
NCBI Description
                   304768
Seq. No.
Seq. ID
                   qmh700026062.f1
                   BLASTX
Method
NCBI GI
                   q4519936
                   231
BLAST score
                   2.0e-19
E value
                   94
Match length
% identity
                   49
NCBI Description
                  (AB019186) RPR1 [Oryza sativa]
                   304769
Seq. No.
Seq. ID
                   qmh700026082.f1
Method
                   BLASTX
NCBI GI
                   q2190992
BLAST score
                   265
E value
                   2.0e-23
Match length
                   72
% identity
                   72
NCBI Description
                   (AF004358) glutathione S-transferase TSI-1 [Aegilops
                   tauschii]
Seq. No.
                   304770
                   qmh700026121.f1
Seq. ID
Method
                   BLASTN
```

NCBI GI g433040 BLAST score 81 E value 4.0e-38 Match length 105



% identity

NCBI Description Zea mays W-22 clone PREM-1A retroelement PREM-1, partial

sequence

Seq. No.

304771

Seq. ID

qmh700026162.f1

Method NCBI GI BLASTX q629641

BLAST score

377

E value Match length 1.0e-36

% identity

72 99

NCBI Description

PsHSC71.0 protein - garden pea >gi 1076530 pir S53500 HSC71.0 protein - garden pea >gi 473217 emb CAA83548

(Z32537) PsHSC71.0 [Pisum sativum]

Seq. No.

304772 Seq. ID

Method

qmh700026172.f1 BLASTX

NCBI GI

q2507056

BLAST score

314

E value

Match length

3.0e-29 92

% identity NCBI Description

61 LIPOIC ACID SYNTHETASE (LIP-SYN) (LIPOATE SYNTHASE)

>gi 1651257 dbj BAA35271 (D90703) Lipoic acid synthetase (lip-syn). [Escherichia coli] >gi_1778545 (U82598) lipoic acid synthetase [Escherichia coli] >gi 1786846 (AEO00167) lipoate synthesis, sulfur insertion? [Escherichia coli]

Seq. No.

304773

Seq. ID

qmh700026315.f1

Method

BLASTX q3451321

NCBI GI

221

BLAST score E value

2.0e-18

Match length

% identity

84 49

NCBI Description

(AL031323) putative transcription or splicing factor

[Schizosaccharomyces pombe]

Seq. No.

304774

Seq. ID

qmh700026331.f1

Method NCBI GI BLASTX g548702

BLAST score

160

E value

3.0e-11

Match length

39

% identity

67

NCBI Description

DNA-DIRECTED RNA POLYMERASE II 14.5 KD POLYPEPTIDE (RPB9)

(RPB14.5) >gi 543001 pir S41621 DNA-directed RNA

polymerase (EC 2.7.7.6) II 14.5K chain - human

>gi 397150 emb CAA80649 (Z23102) RNA Polymerase II subunit

14.5 kD [Homo sapiens] >gi_1905901 (AD001527) HUMAN DNA-DIRECTED RNA POLYMERASE II 14.5 KD SUBUNIT [Homo

sapiens]

NCBI GI

E value

BLAST score

g3242785

6.0e-44

440



```
304775
Seq. No.
Seq. ID
                  qmh700026342.f1
Method
                  BLASTX
NCBI GI
                  g1946265
BLAST score
                  356
E value
                  4.0e-34
Match length
                  66
% identity
                  91
NCBI Description
                  (Y11414) myb [Oryza sativa]
Seq. No.
                  304776
Seq. ID
                  qmh700026350.f1
Method
                  BLASTX
NCBI GI
                  q2292907
BLAST score
                  407
E value
                  4.0e-40
Match length
                  88
% identity
NCBI Description (Y10099) P-glycoprotein homologue [Hordeum vulgare]
                  304777
Seq. No.
Seq. ID
                  qmh700026358.f1
Method
                  BLASTX
NCBI GI
                  g4455274
BLAST score
                  142
                  6.0e-09
E value
Match length
                  34
% identity
NCBI Description
                  (AL035527) spliceosome associated protein-like [Arabidopsis
                  thaliana]
Seq. No.
                  304778
Seq. ID
                  qmh700026374.f1
Method
                  BLASTX
NCBI GI
                  g4335756
BLAST score
                  170
               2.0e-12
E value
                  56
Match length
% identity
NCBI Description (AC006284) putative ankyrin [Arabidopsis thaliana]
                  304779
Seq. No.
                  qmh700026417.f1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4049410
BLAST score
                  214
E value
                  9.0e-18
Match length
                  55
% identity
                  71
NCBI Description
                 (Y10225) L-ascorbate oxidase [Cucumis melo]
Seq. No.
                  304780
                  qmh700026426.f1
Seq. ID
Method
                  BLASTX
```



```
Match length
                  98
                  80
% identity
NCBI Description
                  (AF055355) respiratory burst oxidase protein C [Arabidopsis
                  thaliana]
                  304781
Seq. No.
                  qmh700026439.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1749542
BLAST score
                  414
                  7.0e-41
E value
Match length
                  98
% identity
                  81
NCBI Description
                  (D89167) similar to Saccharomyces cerevisiae
                  5-methyltetrahydropteroyltriglutamate-homocysteine
                  s-methyltransferase, SWISS-PROT Accession Number P05694
                  [Schizosaccharomyces pombe]
                  304782
Seq. No.
Seq. ID
                  qmh700026479.fl
Method
                  BLASTX
NCBI GI
                  g604479
BLAST score
                  227
E value
                  5.0e-19
Match length
                  86
% identity
                  56
NCBI Description
                  (U18422) DP2 [Homo sapiens]
Seq. No.
                  304783
Seq. ID
                  qmh700026482.f1
Method
                  BLASTX
NCBI GI
                  g3193332
BLAST score
                  163
E value
                  1.0e-11
Match length
                  38
% identity
                  82
NCBI Description
                  (AF069299) similar to Arabidopsis AT-hook protein 1
                  (GB:AJ222585) [Arabidopsis thaliana]
```

Seq. No. 304784

Seq. ID qmh700026501.fl

Method BLASTN NCBI GI g532571 BLAST score 143 E value 9.0e-75 Match length 271 % identity 88

NCBI Description Barley lipoxygenase 1 (LoxA) gene, complete cds

Seq. No. 304785

Seq. ID qmh700026514.f1

Method BLASTX NCBI GI q3152606 BLAST score 248 E value 1.0e-21 Match length 58 % identity 72



NCBI Description (AC004482) putative ring zinc finger protein [Arabidopsis thaliana]

Seq. No. 304786

Seq. ID qmh700026544.f1

Method BLASTN
NCBI GI g22144
BLAST score 39
E value 1.0e-12
Match length 62
% identity 92

NCBI Description Maize anaerobically regulated gene for fructose

bisphosphate aldolase (EC 4.1.2.13)

Seq. No. 304787

Seq. ID qmh700026554.f1

Method BLASTX
NCBI GI g729103
BLAST score 296
E value 4.0e-27
Match length 75
% identity 81

NCBI Description CHALCONE--FLAVONONE ISOMERASE >gi_542181_pir__S41570

chalcone isomerase (EC 5.5.1.6) - maize

>gi 396149 emb CAA80441 (Z22760) chalcone flavonone

isomerase [Zea mays]

Seq. No. 304788

Seq. ID qmh700026589.f1

Method BLASTX
NCBI GI g2982431
BLAST score 141
E value 6.0e-09
Match length 87
% identity 36

NCBI Description (AL022224) leucine rich repeat-like protein [Arabidopsis

thaliana]

Seq. No. 304789

Seq. ID qmh700026619.f1

Method BLASTX
NCBI GI g2996096
BLAST score 359
E value 1.0e-36
Match length 96
% identity 86

NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1

alpha [Oryza sativa]

Seq. No. 304790

Seq. ID qmh700026666.f1

Method BLASTX
NCBI GI g4510339
BLAST score 284
E value 1.0e-25
Match length 93
% identity 56



NCBI Description (AC006921) putative ABC transporter protein [Arabidopsis thaliana]

Seq. No. 304791

Seq. ID qmh700026728.f1

Method BLASTX
NCBI GI g2500107
BLAST score 348
E value 4.0e-33
Match length 78
% identity 90

NCBI Description DNA REPAIR PROTEIN RAD51 HOMOLOG >gi_1143810 (U22441)

LeRAD51 [Solanum lycopersicum]

Seq. No. 304792

Seq. ID qmh700026771.f1

Method BLASTX
NCBI GI g4539463
BLAST score 194
E value 4.0e-15
Match length 94
% identity 50

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 304793

Seq. ID qmh700026786.f1

Method BLASTX
NCBI GI g3135251
BLAST score 227
E value 5.0e-19
Match length 90
% identity 50

NCBI Description (AC003058) putative receptor protein kinase [Arabidopsis

thaliana] >gi_3176719 (AC002392) putative protein kinase

[Arabidopsis thaliana]

Seq. No. 304794

Seq. ID qmh700026878.f1

Method BLASTX
NCBI GI g1173071
BLAST score 189
E value 1.0e-18
Match length 63
% identity 80

NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 (MINOR ALLERGEN ALT A 6)

(ALT A VI) >gi_1085614_pir__S43109 acidic ribosomal protein P2 - Alternaria alternata >gi_467617_emb_CAA55066_ (X78222) minor allergen, ribosomal protein [Alternaria alternata]

Seq. No. 304795

Seq. ID qmh700026905.f1

Method BLASTX
NCBI GI g2129703
BLAST score 335
E value 2.0e-31
Match length 110
% identity 56



NCBI Description receptor kinase - Arabidopsis thaliana

>gi_2129704_pir__S71184 receptor kinase - Arabidopsis
thaliana >gi_166692 (M80238) receptor kinase [Arabidopsis

thaliana] >gi_445123_prf__1908429A receptor kinase

[Arabidopsis thaliana]

Seq. No. 304796

Seq. ID qmh700026913.f1

Method BLASTX
NCBI GI 94406766
BLAST score 171
E value 3.0e-12
Match length 72
% identity 47

NCBI Description (AC006836) putative flavonol sulfotransferase [Arabidopsis

thaliana]

Seq. No. 304797

Seq. ID qmh700026918.f1

Method BLASTX
NCBI GI g3184102
BLAST score 190
E value 2.0e-14
Match length 110
% identity 36

NCBI Description (AL023777) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 304798

Seq. ID qmh700026919.f1

Method BLASTX
NCBI GI g3763920
BLAST score 224
E value 2.0e-18
Match length 93

% identity 46

NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304799

Seq. ID qmh700026976.f1

Method BLASTX
NCBI GI g1402916
BLAST score 221
E value 3.0e-18
Match length 103
% identity 44

NCBI Description (X98319) peroxidase [Arabidopsis thaliana]

>gi 1429217 emb CAA67311 (X98775) peroxidase ATP12a

[Arabidopsis thaliana]

Seq. No. 304800

Seq. ID qmh700027079.f1

Method BLASTX
NCBI GI g2827139
BLAST score 266
E value 1.0e-23
Match length 58
% identity 84



NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

Seq. No. 304801

Seq. ID qmh700027127.f1

Method BLASTN
NCBI GI g2773153
BLAST score 35
E value 3.0e-10
Match length 43
% identity 95

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 304802

Seq. ID qmh700027137.f1

Method BLASTX
NCBI GI g4314400
BLAST score 269
E value 7.0e-24
Match length 97
% identity 51

NCBI Description (AC006232) putative selenium-binding protein [Arabidopsis

thaliana]

Seq. No. 304803

Seq. ID qmh700027205.f1

Method BLASTX
NCBI GI g100874
BLAST score 290
E value 2.0e-34
Match length 81
% identity 99

NCBI Description gene SN protein - maize >gi_22479_emb_CAA43115_ (X60706) SN

[Zea mays]

Seq. No. 304804

Seq. ID qmh700027229.f1

Method BLASTX
NCBI GI g548770
BLAST score 231
E value 2.0e-19
Match length 52
% identity 81

NCBI Description 60S RIBOSOMAL PROTEIN L3 >qi 481228 pir S38359 ribosomal

protein L3 - rice >gi_303853_dbj_BAAO2155_ (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 304805

Seq. ID qmh700027266.f1

Method BLASTX
NCBI GI g4263713
BLAST score 167
E value 6.0e-12
Match length 72



% identity 49
NCBI Description (AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304806

Seq. ID qmh700027288.f1

Method BLASTN
NCBI GI g3420038
BLAST score 166
E value 2.0e-88
Match length 257
% identity 73

NCBI Description Zea mays gypsy/Ty3-type retrotransposon Tekay, complete

sequence

Seq. No. 304807

Seq. ID qmh700027316.f1

Method BLASTX
NCBI GI g643443
BLAST score 210
E value 5.0e-17
Match length 86
% identity 49

NCBI Description (U08104) PHOG [Penicillium chrysogenum]

Seq. No. 304808

Seq. ID qmh700027322.f1

Method BLASTN
NCBI GI 9473602
BLAST score 239
E value 1.0e-132
Match length 267
% identity 97

NCBI Description Zea mays W-22 histone H2A mRNA, complete cds

Seq. No. 304809

Seq. ID qmh700027375.f1

Method BLASTX
NCBI GI g4235644
BLAST score 193
E value 3.0e-15
Match length 69
% identity 49

NCBI Description (AF119040) polyprotein [Lycopersicon esculentum]

Seq. No. 304810

Seq. ID qmh700027420.f1

Method BLASTX
NCBI GI g3860258
BLAST score 212
E value 2.0e-17
Match length 75
% identity 51

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 304811

Seq. ID qmh700027460.f1

Method BLASTX



```
q4185141
NCBI GI
BLAST score
                  156
                  6.0e-11
E value
Match length
                  43
                  98
% identity
                  (AC005724) putative calmodulin-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  304812
Seq. No.
                  qmh700027468.fl
Seq. ID
                  BLASTX
Method
                  g3420902
NCBI GI
BLAST score
                  268
E value
                  8.0e-24
Match length
                  65
                  71
% identity
                  (AF081126) ER lumen protein retaining receptor [Drosophila
NCBI Description
                  melanogaster]
                  304813
Seq. No.
                  qmh700027476.fl
Seq. ID
Method
                  BLASTX
                  g100347
NCBI GI
BLAST score
                  169
E value
                  2.0e-12
Match length
                  79
                  47
% identity
                  monosaccharide transport protein MST1 - common tobacco
NCBI Description
                  >gi 19885 emb CAA47324 (X66856) monosaccharid transporter
                   [Nicotiana tabacum]
                   304814
Seq. No.
                   qmh700027478.fl
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3522943
BLAST score
                   320
                   7.0e-30
E value
Match length
                   93
% identity
                   58
                  (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
NCBI Description
                   304815
Seq. No.
                   qmh700027480.f1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4539459
BLAST score
                   219
                   4.0e-18
E value
                   37
Match length
% identity
                  (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   304816
                   qmh700027485.fl
```

Seq. ID

Method BLASTX NCBI GI g4490330 BLAST score 289 3.0e-26 E value



Match length 90 % identity 66

NCBI Description (AL035656) splicing factor-like protein [Arabidopsis

thaliana]

Seq. No. 304817

Seq. ID qmh700027542.f1

Method BLASTN
NCBI GI g2183248
BLAST score 45
E value 3.0e-16
Match length 85
% identity 88

NCBI Description Triticum aestivum glutathione-S-transferase mRNA, complete

cds

Seq. No. 304818

Seq. ID qmh700027574.f1

Method BLASTX
NCBI GI g2499488
BLAST score 229
E value 1.0e-22
Match length 78
% identity 74

NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE

ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))

(PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)

(PPI-PFK) >gi 483547 emb CAA83682_ (Z32849)

pyrophosphate-dependent phosphofructokinase alpha subunit

[Ricinus communis]

Seq. No. 304819

Seq. ID qmh700027575.f1

Method BLASTX
NCBI GI g3170525
BLAST score 268
E value 6.0e-24
Match length 83
% identity 57

NCBI Description (AF054615) cellulase [Fragaria x ananassa]

Seq. No. 304820

Seq. ID qmh700027606.f1

Method BLASTX
NCBI GI g3157926
BLAST score 185
E value 4.0e-14
Match length 72
% identity 51

NCBI Description (AC002131) Strong similarity to extensin-like protein

gb_Z34465 from Zea mays. [Arabidopsis thaliana]

Seq. No. 304821

Seq. ID qmh700027608.f1

Method BLASTX
NCBI GI g3024018
BLAST score 332



E value 2.0e-31 Match length 65 % identity 95

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 304822

Seq. ID qmh700027638.f1

Method BLASTX
NCBI GI g2147399
BLAST score 193
E value 3.0e-15
Match length 39
% identity 100

NCBI Description gene H3.2 protein - hamster (Cricetulus sp.) (fragment)

>gi 554580 (M28265) H3.2 [Cricetulus sp.]

Seq. No. 304823

Seq. ID qmh700027647.f1

Method BLASTX
NCBI GI g3914493
BLAST score 342
E value 2.0e-32
Match length 89
% identity 72

NCBI Description PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT

(AIR CARBOXYLASE) (AIRC) >gi 3256711 dbj BAA29394

(AP000002) 177aa long hypothetical

phosphoribosylaminoimidazole carboxylase catalytic subunit

[Pyrococcus horikoshii]

Seq. No. 304824

Seq. ID qmh700027662.f1

Method BLASTX
NCBI GI g3252807
BLAST score 217
E value 8.0e-18
Match length 93
% identity 52

NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304825

Seq. ID qmh700027677.f1

Method BLASTX
NCBI GI g3785975
BLAST score 164
E value 1.0e-11
Match length 74
% identity 45

NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No. 304826

Seq. ID qmh700027690.f1

Method BLASTX NCBI GI g4539386



```
BLAST score
E value
                  1.0e-18
Match length
                  67
% identity
                  61
                   (AL035526) extensin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  304827
                  qmh700027732.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3695380
BLAST score
                  202
E value
                  3.0e-16
Match length
                  63
% identity
                  57
NCBI Description
                   (AF096370) partial CDS; contains similarity to Nicotiana
                  tabacum membrane-associated salt-inducible protein
                   (GB:U08285) [Arabidopsis thaliana]
Seq. No.
                  304828
Seq. ID
                  qmh700027741.f1
Method
                  BLASTN
NCBI GI
                  g3822035
BLAST score
                  94
E value
                  7.0e-46
Match length
                  137
% identity
                  92
NCBI Description
                  Zea mays endo-1,3-1,4-beta-D-glucanase mRNA, complete cds
Seq. No.
                  304829
                  qmh700027767.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2191146
BLAST score
                  219
                  5.0e-18
E value
Match length
                  95
% identity
                  72
NCBI Description
                  (AF007269) MAP Kinase [Arabidopsis thaliana]
Seq. No.
                  304830
Seq. ID
                  qmh700027772.f1
Method
                  BLASTX
NCBI GI
                  q4567205
BLAST score
                  261
E value
                  6.0e-23
Match length
                  95
% identity
                  57
NCBI Description
                  (AC007168) putative trehalose-6-phosphate phosphatase
                  [Arabidopsis thaliana]
```

Seq. ID qmh700027773.f1

Method BLASTX NCBI GI g2253010 BLAST score 254 E value 2.0e-24 Match length 67 % identity 77



NCBI Description (Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]

Seq. No. 304832

Seq. ID qmh700027774.f1

Method BLASTX
NCBI GI g1314711
BLAST score 280
E value 2.0e-25
Match length 62
% identity 84

NCBI Description (U54615) calcium-dependent protein kinase [Arabidopsis

thaliana] >gi_3068712 (AF049236) calcium dependent protein

kinase [Arabidopsis thaliana]

Seq. No. 304833

Seq. ID qmh700027802.f1

Method BLASTX
NCBI GI g3451474
BLAST score 201
E value 7.0e-16
Match length 85
% identity 48

NCBI Description (AL031349) conserved hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 304834

Seq. ID qmh700027805.f1

Method BLASTX
NCBI GI g2293566
BLAST score 331
E value 3.0e-31
Match length 72
% identity 90

NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No. 304835

Seq. ID qmh700027865.f1

Method BLASTN
NCBI GI g22176
BLAST score 47
E value 1.0e-17
Match length 71
% identity 92

NCBI Description Z.mays P gene

Seq. No. 304836

Seq. ID qmh700027889.f1

Method BLASTN
NCBI GI g3511235
BLAST score 63
E value 3.0e-27
Match length 173
% identity 90

NCBI Description Zea mays starch branching enzyme IIb (ae) gene, complete

cds



```
Seq. No.
                  304837
                  qmh700027946.f1
Seq. ID
Method
                  BLASTX
                  g3335372
NCBI GÍ
                  232
BLAST score
                  1.0e-19
E value
                  64
Match length
% identity
                  64
                  (AC003028) putative SRG1 protein [Arabidopsis thaliana]
NCBI Description
                  304838
Seq. No.
                  qmh700028003.fl
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112971
BLAST score
                  178
E value
                  3.0e-13
Match length
                  61
                   59
% identity
                  ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
NCBI Description
                   (GLUTAMATE OXALOACETATE TRANSAMINASE-1)
                  >gi 625210 pir XNCHDC aspartate transaminase (EC 2.6.1.1),
                   cytosolic - chicken >gi 63066 emb CAA33646 (X15636)
                   aspartate aminotransferase (AA 1 - 412) [Gallus gallus]
                   304839
Seq. No.
Seq. ID
                   qmh700028070.f1
Method
                   BLASTX
NCBI GI
                   g3647233
BLAST score
                   386
                   1.0e-37
E value
Match length
                   88
% identity
                   82
                   (AF039748) 40S ribosomal protein S4 [Dictyostelium
NCBI Description
                   discoideum]
                   304840
Seq. No.
                   qmh700028117.f1
Seq. ID
                   BLASTX
Method
                   g1805261
NCBI GI
                   333
BLAST score
                   2.0e-31
E value
Match length
                   93
                   70
% identity
                   (U75347) fatty acid synthase, alpha subunit [Emericella
NCBI Description
                   nidulans]
                   304841
Seq. No.
                   qmh700028135.fl
Seq. ID
Method
                   BLASTX
                   g2689720
NCBI GI
BLAST score
                   166
E value
                   7.0e-12
```

Match length 75 47 % identity

(AF037168) DnaJ homologue [Arabidopsis thaliana] NCBI Description

304842 Seq. No.



```
qmh700028139.fl
Seq. ID
                  BLASTX
Method
                  g4567227
NCBI GI
BLAST score
                   265
                   2.0e-23
E value
Match length
                   61
                   75
% identity
                   (AC007119) putative transport protein [Arabidopsis
NCBI Description
                  thaliana]
                   304843
Seq. No.
                   qmh700028166.f1
Seq. ID
Method
                   BLASTX
                   g4008156
NCBI GI
BLAST score
                   177
                   4.0e-13
E value
Match length
                   44
                   80
% identity
                   (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]
NCBI Description
Seq. No.
                   304844
                   qmh700028170.f1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2842493
BLAST score
                   365
E value
                   3.0e-35
Match length
                   88
% identity
                   76
                  (AL021749) predicted protein [Arabidopsis thaliana]
NCBI Description
                   304845
Seq. No.
                   qmh700028186.f1
Seq. ID
                   BLASTX
Method
                   g1729839
NCBI GI
BLAST score
                   395
                   1.0e-38
E value
                   89
Match length
                   82
% identity
                   TUBULIN ALPHA-1A CHAIN >gi_477047_pir__A47707 alpha
NCBI Description
                   1A-tubulin - slime mold (Physarum polycephalum) >gi_161214
                   (M98863) alpha tubulin [Physarum polycephalum]
                   304846
Seq. No.
                   qmh700028211.f1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3522945
BLAST score
                   223
                   2.0e-18
E value
                   89
Match length
                   40
% identity
NCBI Description
                  (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   304847
```

qmh700028219.f1 Seq. ID

Method BLASTX g1657268 NCBI GI BLAST score 311

```
E value
Match length
                  91
% identity
                   64
NCBI Description
                  (Y07701) aminopeptidase [Homo sapiens]
                  304848
Seq. No.
                  qmh700028266.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2815493
BLAST score
                  187
E value
                  1.0e-14
Match length
                   49
% identity
                   65
NCBI Description
                  SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
                   (CP-MI) >gi_1731988 emb CAA70816 (Y09603) serine
                  carboxypeptidase I, CP-MI [Hordeum vulgare]
Seq. No.
                  304849
Seq. ID
                  qmh700028331.f1
Method
                  BLASTX
NCBI GI
                  g267442
BLAST score
                  142
E value
                  5.0e-09
Match length
                  79
% identity
                  42
NCBI Description
                  HYPOTHETICAL 18.7 KD PROTEIN IN RHLE-DING INTERGENIC REGION
                   (F160) >gi 147599 (L02123) YbiA [Escherichia coli]
                  >gi_178701\overline{7} (AE000182) orf, hypothetical protein
                   [Escherichia coli] >gi 4062356 dbj BAA35458 (D90716)
                  Hypothetical 18.7 kd protein in rhlE-dinG/rarB intergenic
                  region (F160). [Escherichia coli] >gi_4062360_dbj_BAA35464
                   (D90717) Hypothetical 18.7 kd protein in rhlE-dinG/rarB
                  intergenic region (F160). [Escherichia coli]
Seq. No.
                  304850
Seq. ID
                  qmh700028339.f1
Method
                  BLASTX
                  g2292907
NCBI GI
BLAST score
                  321
E value
                  5.0e-30
Match length
                  90
% identity
                  69
NCBI Description
                  (Y10099) P-glycoprotein homologue [Hordeum vulgare]
Seq. No.
                  304851
Seq. ID
                  qmh700028377.f1
Method
                  BLASTX
NCBI GI
                  g1297187
```

% identity

BLAST score

Match length

E value

NCBI Description (U53501) similar to protein encoded by GenBank Accession Number U41815, nucleoporin 98 [Arabidopsis thaliana]

Seq. No. 304852

Seq. ID qmh700028388.f1

175

90

47

6.0e-13

43155

in.



```
Method
                  BLASTX
                  g1903357
NCBI GI
BLAST score
                  142
E value
                  5.0e-09
Match length
                  75
% identity
                  41
NCBI Description
                  (AC000104) Strong similarity to Arabidopsis 2A6
                  (gb X83096). [Arabidopsis thaliana]
Seq. No.
                  304853
Seq. ID
```

qmh700028406.fl

Method BLASTX NCBI GI g4417271 BLAST score 194 E value 5.0e-16 Match length 83 % identity 54

NCBI Description (AC007019) putative cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 304854 Seq. ID qmh700028420.fl Method BLASTX

NCBI GI g2435521 BLAST score 170 E value 4.0e-12 Match length 61 % identity 51

(AF024504) contains similarity to Nicotiana tabacum NCBI Description

membrane-associated salt-inducible protein (GB:U08285)

[Arabidopsis thaliana]

Seq. No. 304855

Seq. ID qmh700028441.fl

Method BLASTX NCBI GI g3047096 BLAST score 174 E value 5.0e-13 Match length 78 % identity 53

(AF058826) similar to eukaryotic protein kinase domains NCBI Description

(Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]

Seq. No. 304856

Seq. ID qmh700028448.fl

Method BLASTX NCBI GI g2367623 BLAST score 271 E value 5.0e-24 Match length 70 # identity 74

NCBI Description (AF016187) chaperone/heat shock protein [Emericella

nidulans]

Seq. No. 304857

Seq. ID qmh700028453.f1

Method BLASTX

NCBI GI

E value

BLAST score

q2281103

5.0e-17

210



```
NCBI GI
                   q267056
BLAST score
                   165
E value
                   5.0e-12
Match length
                   32
                   100
% identity
NCBI Description
                  SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
                   >gi 100710 pir S25526 sucrose synthase (EC 2.4.1.13) -
                   rice >gi_20374 emb_CAA78747 (Z15028) sucrose synthase
                   [Oryza sativa]
Seq. No.
                   304858
Seq. ID
                   qmh700028466.f1
Method
                   BLASTX
NCBI GI
                   g3941289
BLAST score
                   164
E value
                  1.0e-11
Match length
                  57
% identity
                   49
NCBI Description
                  (AF018093) similarity to SCAMP37 [Pisum sativum]
Seq. No.
                   304859
Seq. ID
                   qmh700028469.f1
Method
                   BLASTX
NCBI GI
                   g2244866
BLAST score
                   182
E value
                   6.0e-14
Match length
                   58
% identity
                   62
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   304860
                   qmh700028523.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3551133
BLAST score
                   381
E value
                  5.0e-37
Match length
                  97
% identity
                  77
NCBI Description
                  (AB012045) Plasma membrane aquaporin (PAQ2) [Raphanus
                  sativus]
                  304861
Seq. No.
                  qmh700028533.f1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g556409
BLAST score
                  401
E value
                  2.0e-39
Match length
                  86
% identity
                  97
NCBI Description
                  (L34551) transcriptional activator protein [Oryza sativa]
Seq. No.
                  304862
Seq. ID
                  qmh700028534.f1
Method
                  BLASTX
```



Match length 63 % identity 56

NCBI Description (AC002333) Glucan endo-1,3-beta glucosidase isolog

[Arabidopsis thaliana]

Seq. No. 304863

Seq. ID qmh700028556.f1

Method BLASTX
NCBI GI g3157950
BLAST score 164
E value 1.0e-11
Match length 58
% identity 52

NCBI Description (AC002131) Contains similarity to hypothetical protein

C18b11.05 gb Z50728 from S. pombe. EST gb H76601 comes

from this gene. [Arabidopsis thaliana]

Seq. No. 304864

Seq. ID qmh700028562.f1

Method BLASTX
NCBI GI g3461836
BLAST score 248
E value 2.0e-21
Match length 74
% identity 62

NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana]

>gi 3927841 (AC005727) putative protein kinase [Arabidopsis

thaliana]

Seq. No. 304865

Seq. ID qmh700028568.f1

Method BLASTX
NCBI GI g464365
BLAST score 216
E value 1.0e-17
Match length 60
% identity 67

NCBI Description PEROXIDASE P7 >gi_66306_pir__OPNB7 peroxidase (EC 1.11.1.7)

- turnip

Seq. No. 304866

Seq. ID qmh700028591.f1

Method BLASTX
NCBI GI g2245378
BLAST score 227
E value 5.0e-19
Match length 88
% identity 56

NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No. 304867

Seq. ID qmh700028601.f1

Method BLASTX
NCBI GI g4587990
BLAST score 146
E value 9.0e-10
Match length 43



% identity NCBI Description (AF085279) hypothetical protein [Arabidopsis thaliana] 304868 Seq. No. qmh700028614.f1 Seq. ID Method BLASTX NCBI GI g4539009 BLAST score 238 2.0e-20 E value Match length 82 56 % identity NCBI Description (AL049481) putative protein [Arabidopsis thaliana] Seq. No. 304869 qmh700028629.f1 Seq. ID Method BLASTN g809607 NCBI GI 127 BLAST score E value 3.0e-65 Match length 272 % identity 82 NCBI Description Z.mays zmc-II gene 304870 Seq. No. Seq. ID qmh700028693.f1 Method BLASTX NCBI GI g462195 BLAST score 371 6.0e-36 E value Match length 77 % identity 91 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) NCBI Description >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza satīva] 304871 Seq. No. qmh700028733.f1 Seq. ID Method BLASTX q3122914 NCBI GI BLAST score 214 7.0e-23 E value Match length 68 % identity 68 VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) NCBI Description >gi_1890130 (U89986) valyl tRNA synthetase [Arabidopsis thaliana]

Seq. No. 304872

Seq. ID qmh700028765.f1

Method BLASTX
NCBI GI g3702323
BLAST score 255
E value 2.0e-22
Match length 80
% identity 64





```
NCBI Description
                  (AC005397) unknown protein [Arabidopsis thaliana]
                  304873
Seq. No.
                  qmh700028786.fl
Seq. ID
Method
                  BLASTN
                  g2642323
NCBI GI
BLAST score
                  65
                  3.0e-28
E value
Match length
                  65
% identity
                  100
                  Zea mays profilin (PRO4) mRNA, complete cds
NCBI Description
                  304874
Seq. No.
                  qmh700028808.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1370162
BLAST score
                  202
E value
                  5.0e-16
Match length
                  64
% identity
                  66
NCBI Description
                  (X97853) RAB1A [Lotus japonicus]
                  304875
Seq. No.
                  qmh700028825.f1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g520543
BLAST score
                  68
E value
                  5.0e-30
Match length
                  96
% identity
                  93
                  Sorghum bicolor clone BADH1 betaine aldehyde dehydrogenase
NCBI Description
                  mRNA, partial cds
                  304876
Seq. No.
                  qmh700028826.f1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2911250
BLAST score
                  262
E value
                  1.0e-146
Match length
                  278
% identity
                  99
NCBI Description
                  Saccharomyces cerevisiae chromosome I left arm sequence
                  304877
Seq. No.
                  qmh700028848.f1
Seq. ID
Method
                  {\tt BLASTX}
NCBI GI
                  g1587206
BLAST score
                  228
                   4.0e-19
E value
Match length
                  67
                  63
% identity
```

Seq. ID qmh700028879.f1

NCBI Description T complex protein [Cucumis sativus]

Method BLASTN NCBI GI g1895083



```
BLAST score
E value
                  2.0e-30
Match length
                  136
% identity
                  88
NCBI Description
                  Zea mays golgi associated protein se-wap41 mRNA, complete
                  304879
Seq. No.
Seq. ID
                  qmh700028935.f1
Method
                  BLASTX
NCBI GI
                  g4455345
                  195
BLAST score
E value
                  1.0e-25
Match length
                  82
% identity
                  76
                 (AL035522) putative protein [Arabidopsis thaliana]
NCBI Description
                  304880
Seq. No.
                  qmh700028964.fl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3522943
BLAST score
                  392
E value
                  2.0e-38
Match length
                  90
% identity
                  42
NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
Seq. No.
                  304881
                  qmh700028985.fl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q488573
BLAST score
                  395
E value
                  9.0e-39
Match length
                  83
% identity
                  95
NCBI Description
                 (U09463) histone H3.2 [Medicago sativa]
                  304882
Seq. No.
                  qmh700029016.fl
Seq. ID
Method
                  BLASTN
NCBI GI
                  g288611
BLAST score
                  73
```

E value 5.0e-33 Match length 198 % identity 85

NCBI Description Z.mays PG gene for polygalacturonase

Seq. No. 304883

Seq. ID qmh700029054.fl

Method BLASTX NCBI GI g2055374 BLAST score 247 E value 2.0e-21 Match length 68 % identity

NCBI Description (U29095) serine-threonine protein kinase [Triticum

aestivum]

NCBI Description

```
Seq. No.
                   304884
Seq. ID
                   qmh700029095.f1
Method
                   BLASTX
NCBI GI
                   q2244898
BLAST score
                   247
                   5.0e-25
E value
Match length
                   76
% identity
                   74
NCBI Description
                  (Z97338) strong similarity to protein phosphatase 2A
                   regulatory charm, 74K [Arabidopsis thaliana]
Seq. No.
                   304885
Seq. ID
                   qmh700029113.fl
Method
                   BLASTX
NCBI GI
                   g126772
BLAST score
                   347
E value
                   4.0e-33
Match length
                   84
                   75
% identity
NCBI Description
                  MALATE SYNTHASE, GLYOXYSOMAL >gi 101858 pir S17774 malate
                   synthase (EC 4.1.3.2) - Neurospora crassa
                   >gi_2975_emb_CAA39994 (X56672) malate synthase [Neurospora
                   crassa]
                   304886
Seq. No.
Seq. ID
                   qmh700029134.f1
Method
                  BLASTN
                  g435312
NCBI GI
BLAST score
                   174
E value
                   3.0e-93
Match length
                  211
% identity
                   95
NCBI Description
                  Z.mays mRNA for beta-D-glucosidase
Seq. No.
                   304887
Seq. ID
                   qmh700029140.fl
Method
                  BLASTX
NCBI GI
                  q3522939
BLAST score
                  173
E value
                  1.0e-12
Match length
                   58
                  59
% identity
NCBI Description
                   (AC004411) putative squamosa-promoter binding protein
                   [Arabidopsis thaliana]
Seq. No. Seq. ID
                  304888
                  qmh700029141.f1
Method
                  BLASTX
NCBI GI
                  q1346810
BLAST score
                  281
E value
                  2.0e-25
Match length
                  86
% identity
                  69
```

(U39303) P26s4 [Drosophila melanogaster]

26S PROTEASE REGULATORY SUBUNIT 4 (P26S4) >gi 1066065



Seq. ID qmh700029191.f1

Method BLASTX
NCBI GI g2191175
BLAST score 247
E value 2.0e-21
Match length 80

% identity 62

NCBI Description (AF007270) A_IG002P16.24 gene product [Arabidopsis

thaliana]

Seq. No.

304890

Seq. ID

qmh700029209.f1

Method BLASTX
NCBI GI g1171027
BLAST score 276
E value 9.0e-25
Match length 89
% identity 57

NCBI Description MALE STERILITY PROTEIN 2 >gi_421835_pir___S33804 gene MS2

protein - Arabidopsis thaliana >gi_396835_emb_CAA52019_ (X73652) male sterility 2 (MS2) protein [Arabidopsis thaliana] >gi_448297_prf_1916413A male sterility 2 gene

[Arabidopsis thaliana]

Seq. No.

304891

Seq. ID qmh700029242.f1

Method BLASTX
NCBI GI g113621
BLAST score 228
E value 1.0e-20
Match length 66

Match length 66 % identity 85

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No.

304892

Seq. ID qmh700029306.f1

Method BLASTN
NCBI GI g4416300
BLAST score 94
E value 2.0e-45
Match length 190
% identity 87

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No.

304893

Seq. ID

qmh700029336.f1

Method BLASTN
NCBI GI g454880
BLAST score 54
E value 1.0e-21



Match length 92 % identity 90

NCBI Description Rice mRNA for WSI724 protein induced by water stress,

complete cds

Seq. No. 304894

Seq. ID qmh700029342.f1

Method BLASTX
NCBI GI g3551960
BLAST score 303
E value 6.0e-28
Match length 73
% identity 77

NCBI Description (AF082033) senescence-associated protein 15 [Hemerocallis

hybrid cultivar]

Seq. No. 304895

Seq. ID qmh700029420.f1

Method BLASTX
NCBI GI g2496730
BLAST score 222
E value 2.0e-18
Match length 89
% identity 51

NCBI Description HYPOTHETICAL PROTEIN Y40U PRECURSOR >gi 2182565 (AE000089)

Y4oU [Rhizobium sp. NGR234]

Seq. No. 304896

Seq. ID qmh700029429.f1

Method BLASTX
NCBI GI g3540219
BLAST score 215
E value 1.0e-17
Match length 83

% identity 57

NCBI Description (D87686) KIAA0017 protein [Homo sapiens]

Seq. No. 304897

Seq. ID qmh700029437.f1

Method BLASTX
NCBI GI g4056503
BLAST score 162
E value 2.0e-11
Match length 36
% identity 86

NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 304898

Seq. ID qmh700029447.f1

Method BLASTX
NCBI GI g1363485
BLAST score 152
E value 3.0e-10
Match length 38
% identity 82

NCBI Description IAA3 protein - Arabidopsis thaliana >gi_972911 (U18406)

IAA3 [Arabidopsis thaliana] >gi 1903369 gb AAB70452

% identity

94





```
(AC000104) Match to Arabidopsis IAA3 (gb_U18406). EST gb T04296 comes from this gene. [Arabidopsis thaliana]
```

```
Seq. No.
                   304899
Seq. ID
                   qmh700029448.fl
Method
                   BLASTX
NCBI GI
                   g2226329
BLAST score
                   219
E value
                   4.0e-18
Match length
                   65
% identity
                   69
NCBI Description
                  (AF001634) physical impedance induced protein [Zea mays]
Seq. No.
                   304900
Seq. ID
                   qmh700029457.f1
Method
                   BLASTX
NCBI GI
                   q1170937
BLAST score
                   155
E value
                   2.0e-10
Match length
                   31
                   97
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
Seq. No.
                   304901
Seq. ID
                   qmh700029460.f1
Method
                   BLASTX
NCBI GI
                   g2191184
BLAST score
                   314
E value
                   3.0e-29
Match length
                  91
% identity
                   67
NCBI Description
                  (AF007271) Similar to sodium/hydrogen exchanger; coded for
                  by A. thaliana cDNA T75860 [Arabidopsis thaliana]
Seq. No.
                   304902
Seq. ID
                   qmh700029464.f1
Method
                  BLASTN
NCBI GI
                  q2920838
BLAST score
                   48
E value
                   3.0e-18
Match length
                   92
% identity
                  88
NCBI Description
                  Oryza sativa fungal elicitor immediate early responsive
                   (Os-FIERG2) mRNA, complete cds
Seq. No.
                  304903
Seq. ID
                   qmh700029473.f1
Method
                  BLASTX
                                                   9,50
NCBI GI
                  q1076678
BLAST score
                  159
                  2.0e-11
E value
Match length
                  35
```

NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)



```
304904
Seq. No.
Seq. ID
                   qmh700029484.f1
Method
                   BLASTX
NCBI GI
                   g4204695
BLAST score
                   322
E value
                   3.0e-30
Match length
                   88
% identity
                   62
                   (AF117062) putative inositol polyphosphate 5-phosphatase
NCBI Description
                   At5P1 [Arabidopsis thaliana]
Seq. No.
                   304905
Seq. ID
                   qmh700029541.f1
Method
                   BLASTX
NCBI GI
                   q2492491
BLAST score
                   353
E value
                   9.0e-38
Match length
                   90
% identity
                   92
                  14-3-3 PROTEIN HOMOLOG (TH1433) >gi_806859 (U24158) 14.3.3.
NCBI Description
                  protein [Trichoderma harzianum]
                   304906
Seq. No.
Seq. ID
                   qmh700029554.f1
Method
                  BLASTN
NCBI GI
                   q4140643
BLAST score
                   53
E value
                   4.0e-21
Match length
                   57
% identity
                   98
NCBI Description
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                   complete sequence
Seq. No.
                  304907
Seq. ID
                   qmh700029575.f1
Method
                  BLASTX
NCBI GI
                  g1209711
BLAST score
                  302
E value
                  8.0e-28
Match length
                  88
% identity
                  61
NCBI Description
                  (U41293) unknown [Saccharomyces cerevisiae]
Seq. No.
                  304908
Seq. ID
                  qmh700029583.fl
Method
                  BLASTX
NCBI GI
                  g3023852
BLAST score
                  501
E value
                  4.0e-51
Match length
                  92
% identity
                  96
```

PROTEIN (CROSS-PATHWAY CONTROL WD-REPEAT PROTEIN CPC-2) >gi 1362527_pir__S57839 CPC2 protein - Neurospora crassa >gi_971566_emb_CAA57460_ (X81875) CPC2 protein [Neurospora

GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

crassa]

NCBI Description



```
304909
Seq. No.
Seq. ID
                   qmh700029614.f1
Method
                   BLASTX
NCBI GI
                   q1621465
BLAST score
                   204
E value
                   5.0e-18
Match length
                   61
% identity
NCBI Description
                  (U73105) laccase [Liriodendron tulipifera]
Seq. No.
                   304910
Seq. ID
                   qmh700029644.f1
Method
                   BLASTX
NCBI GI
                   q585661
BLAST score
                   176
E value
                   3.0e-26
Match length
                   67
% identity
                   93
NCBI Description
                  PEROXIDASE PRECURSOR >gi 287401 dbj BAA03644 (D14997)
                   peroxidase [Oryza sativa]
Seq. No.
                   304911
Seq. ID
                   qmh700029657.f1
Method
                   BLASTN
NCBI GI
                   g22614
BLAST score
                   38
                   4.0e-12
E value
Match length
                   58
                   91
% identity
NCBI Description S.vulgare pepC gene for PEP carboxylase
Seq. No.
                   304912
Seq. ID
                   qmh700029726.fl
Method
                   BLASTX
NCBI GI
                   g3688602
BLAST score
                   186
E value
                   3.0e-14
Match length
                   57
% identity
                   63
NCBI Description
                  (AB009031) Oxidosqualene Cyclase [Panax ginseng]
Seq. No.
                   304913
Seq. ID
                   qmh700029732.f1
Method
                   BLASTX
NCBI GI
                   q3790587
BLAST score
                   149
E value
                   7.0e-10
Match length
                   32
% identity
                   78
                   (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. ID qmh700029739.f1 Method BLASTX

Method BLASTX NCBI GI g2702268



```
BLAST score
E value
                  3.0e-15
Match length
                  83
                  53
% identity
NCBI Description
                  (AC003033) putative cellulase [Arabidopsis thaliana]
Seq. No.
                  304915
                  qmh700029749.fl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3004564
BLAST score
                  171
E value
                  2.0e-12
Match length
                  57
% identity
                  54
NCBI Description
                  (AC003673) putative receptor Ser/Thr protein kinase
                   [Arabidopsis thaliana]
                  304916
Seq. No.
Seq. ID
                  qmh700029757.fl
Method
                  BLASTX
                  g3420050
NCBI GI
BLAST score
                  147
E value
                  1.0e-09
Match length
                  46
% identity
                  57
NCBI Description
                  (AC004680) hypothetical protein [Arabidopsis thaliana]
                  304917
Seq. No.
                  qmh700029773.fl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911073
                  190
BLAST score
E value
                  5.0e-15
Match length
                  69
% identity
                  64
NCBI Description
                  (AL021960) putative protein [Arabidopsis thaliana]
Seq. No.
                  304918
                  qmh700029786.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4249382
BLAST score
                  271
E value
                  4.0e-24
Match length
                  62
% identity
                  77
NCBI Description
                  (AC005966) Strong similarity to gi 3337350 F13P17.3
                  putative permease from Arabidopsis thaliana BAC
                  gb_AC004481. [Arabidopsis thaliana]
Seq. No.
                  304919
```

Seq. ID qmh700029789.f1

Method BLASTX NCBI GI q4581155 BLAST score 226 E value 7.0e-19 Match length 88 % identity 55



```
NCBI Description
                  (AC006919) putative receptor kinase [Arabidopsis thaliana]
                   304920
Seq. No.
Seq. ID
                   amh700029792.f1
Method
                   BLASTN
NCBI GI
                   g532622
BLAST score
                   98
E value
                   5.0e-48
Match length
                   119
                   98
% identity
NCBI Description
                  Zea mays lipase (LIP) mRNA, complete cds
Seq. No.
                   304921
                   qmh700029840.fl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4522009
BLAST score
                   205
E value
                  2.0e-16
Match length
                   84
                   50
% identity
NCBI Description
                  (AC007069) unknown protein [Arabidopsis thaliana]
                   304922
Seq. No.
Seq. ID
                   qmh700029848.f1
                   BLASTX
Method
                   g3386611
NCBI GI
BLAST score
                   282
E value
                   2.0e-25
Match length
                   82
% identity
                   57
NCBI Description
                  (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.
                   304923
Seq. ID
                   qmh700029851.fl
Method
                   BLASTX
NCBI GI
                   g2648032
BLAST score
                   396
E value
                   1.0e-38
Match length
                   102
% identity
                   72
NCBI Description
                  (AJ001374) alpha-glucosidase [Solanum tuberosum]
Seq. No.
                   304924
Seq. ID
                   qmh700029905.fl
Method
                  BLASTX
NCBI GI
                   q3176686
BLAST score
                   301
```

NCBI GI g317668 BLAST score 301 E value 1.0e-27 Match length 66 % identity 85

NCBI Description (AC003671) Similar to high affinity potassium transporter,

HAK1 protein gb_U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 304925

Seq. ID qmh700029923.f1

Method BLASTX



```
NCBI GI
                  q2108252
BLAST score
                  231
E value
                  1.0e-19
Match length
                  81
                  28
% identity
                  (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
                  >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
                   [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
                   (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
Seq. No.
                  304926
Seq. ID
                  qmh700029945.fl
Method
                  BLASTX
NCBI GI
                  q2944404
BLAST score
                  481
E value
                  8.0e-49
Match length
                  90
                  100
% identity
NCBI Description
                  (AF049853) serine/threonine protein phosphatase type 1
                   [Neurospora crassa]
                  304927
Seq. No.
                  qmh700029947.fl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3402673
                  292
BLAST score
E value
                  8.0e-27
Match length
                  76
% identity
                  72
NCBI Description
                  (AC004697) unknown protein [Arabidopsis thaliana]
                  304928
Seq. No.
                  qmh700029964.f1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3402672
BLAST score
                  251
E value
                  8.0e-22
                  93
Match length
                  57
% identity
NCBI Description
                  (AC004697) putative white protein [Arabidopsis thaliana]
Seq. No.
                  304929
Seq. ID
                  qmh700029973.f1
Method
                  BLASTN
NCBI GI
                  g473975
BLAST score
                  44
E value
                  4.0e-16
Match length
                  92
% identity
NCBI Description
                  Rice mRNA, partial homologous to cytochrome b-5 gene
```

Seq. ID qmh700030071.fl

BLASTX Method g730662 NCBI GI BLAST score 317 E value 1.0e-29



Match length 78 % identity 77 NCBI Description 40

40S RIBOSOMAL PROTEIN S4 >gi_478316_pir__JN0871 ribosomal

protein S4 - fruit fly (Drosophila melanogaster)

>gi_440853_dbj_BAA03786_ (D16257) ribosomal protein S4

[Drosophila melanogaster]

Seq. No.

304931

Seq. ID

qmh700030130.fl

Method BLASTX
NCBI GI g2462911
BLAST score 168
E value 2.0e-12
Match length 44

% identity 66

NCBI Description (Z83832) UDP-glucose:sterol glucosyltransferase [Avena

sativa]

Seq. No.

304932

Seq. ID qmh700030142.f1

Method BLASTX
NCBI GI g626042
BLAST score 158
E value 3.0e-11
Match length 30
% identity 100

NCBI Description beta-glucosidase, root meristem (EC 3.2.1.-) precursor -

maize >gi_435313_emb_CAA52293_ (X74217) beta-glucosidase

[Zea mays]

Seq. No.

304933

Seq. ID qmh700030150.f1

Method BLASTX
NCBI GI g1076693
BLAST score 231
E value 1.0e-19
Match length 65
% identity 69

NCBI Description chitinase (EC 3.2.1.14) class I - European elder (fragment)

>gi_603882_emb_CAA87072 (Z46948) pathogenesis-related

protein PR-3 type [Sambucus nigra]

Seq. No.

304934

Seq. ID qmh700030222.f1

Method BLASTN
NCBI GI g2463566
BLAST score 39
E value 1.0e-12
Match length 79
% identity 87

NCBI Description Zea mays mRNA for squalene synthase, complete cds

Seq. No.

304935

Seq. ID qmh700030226.f1

Method BLASTX
NCBI GI g2443329
BLAST score 144

```
E value
                   3.0e-09
Match length
                  76
                  42
% identity
NCBI Description
                  (D86122) Mei2-like protein [Arabidopsis thaliana]
                  304936
Seq. No.
Seq. ID
                  qmh700030266.f1
Method
                  BLASTX
NCBI GI
                  q730373
                  273
BLAST score
E value
                  2.0e-24
Match length
                  93
% identity
                  51
                  PROTEASOME 26 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                  COMPLEX 26 KD SUBUNIT) >gi 392868 (U00790) proteasome
                  subunit [Drosophila melanogaster]
Seq. No.
                  304937
Seq. ID
                  qmh700030267.f1
Method
                  BLASTN
NCBI GI
                  g22176
BLAST score
                  47
E value
                  2.0e-17
Match length
                  87
% identity
                  45
NCBI Description Z.mays P gene
                  304938
Seq. No.
Seq. ID
                  qmh700030280.f1
Method
                  BLASTX
```

NCBI GI q4558665 BLAST score 344 E value 9.0e-33 Match length 88 % identity 69

(AC007063) putative white protein [Arabidopsis thaliana] NCBI Description

304939 Seq. No.

Seq. ID qmh700030290.f1

Method BLASTX NCBI GI q3242783 BLAST score 317 1.0e-29 E value Match length 88 % identity 66

NCBI Description (AF055354) respiratory burst oxidase protein B [Arabidopsis

thaliana]

304940 Seq. No.

Seq. ID qmh700030296.f1

Method BLASTX NCBI GI q2642154 BLAST score 252 E value 6.0e-22 Match length 86 % identity 56

NCBI Description (AC003000) unknown protein [Arabidopsis thaliana]





>gi_3790595 (AF079186) RING-H2 finger protein RHC2a
[Arabidopsis thaliana]

 Seq. No.
 304941

 Seq. ID
 qmh700030303.f1

 Method
 BLASTX

 NCBI GI
 g3355662

 BLAST score
 258

 E value
 1.0e-22

 Match length
 85

58

NCBI Description (AJ009693) ribosomal protein L9 [Podocoryne carnea]

Seq. No. 304942

% identity

 Seq. ID
 qmh700030322.f1

 Method
 BLASTX

 NCBI GI
 g4006882

 BLAST score
 145

 E value
 2.0e-09

Match length 92 % identity 42

NCBI Description (Z99707) UDP-glucuronyltransferase-like protein

[Arabidopsis thaliana]

Seq. No. 304943

Seq. ID qmh700030362.f1

Method BLASTX
NCBI GI g2673911
BLAST score 172
E value 2.0e-12
Match length 47
% identity 77

NCBI Description (AC002561) putative squamosa-promoter binding protein

[Arabidopsis thaliana]

Seq. No. 304944

Seq. ID qmh700030412.f1

Method BLASTX
NCBI GI g2065531
BLAST score 211
E value 5.0e-25
Match length 71
% identity 64

NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No. 304945

Seq. ID qmh700030435.f1

Method BLASTX
NCBI GI g548771
BLAST score 303
E value 5.0e-28
Match length 87
% identity 67

NCBI Description 60S RIBOSOMAL PROTEIN L3-2 >gi_101073_pir__S25592 ribosomal

protein L3 - fission yeast (Schizosaccharomyces pombe) >gi_5059_emb_CAA40901_ (X57734) ribosomal protein L3

[Schizosaccharomyces pombe]



```
Seq. No.
                  304946
Seq. ID
                  qmh700030470.f1
Method
                  BLASTN
NCBI GI
                  q4512215
BLAST score
                  42
E value
                  2.0e-14
Match length
                  42
% identity
                  100
NCBI Description Zea mays ZmRR1 mRNA for response regulator, complete cds
                  304947
Seq. No.
Seq. ID
                  qmh700030551.f1
Method
                  BLASTX
NCBI GI
                  g1079280
BLAST score
                  317
E value
                  1.0e-29
Match length
                  84
% identity
                  69
NCBI Description
                  chaperonin containing TCP-1 complex gamma chain - African
                  clawed frog >gi 793886 emb CAA59350 (X84990) Cctg [Xenopus
                  laevis]
Seq. No.
                  304948
Seq. ID
                  qmh700030596.f1
Method
                  BLASTX
NCBI GI
                  q1171429
BLAST score
                  160
E value
                  2.0e-11
Match length
                  65
% identity
                  52
NCBI Description (U44028) CKC [Arabidopsis thaliana]
Seq. No.
                  304949
Seq. ID
                  qmh700030618.fl
Method
                  BLASTX
NCBI GI
                  g3915112
BLAST score
                  317
E value
                  2.0e-29
Match length
                  97
% identity
                  65
                  TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
NCBI Description
                  4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)
                  >gi_642954 (U19922) cinnamic acid 4-hydroxylase [Zinnia
                  elegans]
                  304950
```

Seq. ID qmh700030651.f1

Method BLASTN NCBI GI g577818 BLAST score 112 E value 3.0e-56 Match length 194 % identity 91

NCBI Description Z.mays gene for H2B histone (gH2B4)

Seq. No. 304951

```
qmh700030653.f1
```

100

Seq. ID qmh700030653.

Method BLASTX

NCBI GI g120670

BLAST score 372

E value 5.0e-36

Match length 71

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_100879_pir__S06879 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12) C - maize

>gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]

Seq. No. 304952

% identity

Seq. ID qmh700030672.f1

Method BLASTX
NCBI GI g133844
BLAST score 358
E value 2.0e-34
Match length 80
% identity 84

NCBI Description 40S RIBOSOMAL PROTEIN S19 (S16) >gi 83720 pir JQ1349

ribosomal protein S19.e, cytosolic - Emericella nidulans >gi_168088 (M65259) ribosomal protein S16 [Emericella

nidulans]

Seq. No. 304953

Seq. ID qmh700030687.f1

Method BLASTX
NCBI GI g3548802
BLAST score 262
E value 4.0e-23
Match length 87
% identity 56

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein

[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 304954

Seg. ID rvl700453729.h1

Method BLASTX
NCBI GI 94455198
BLAST score 258
E value 1.0e-22
Match length 60
% identity 83

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 304955

Seq. ID rv1700453768.h1

Method BLASTX
NCBI GI g2618699
BLAST score 183
E value 4.0e-14
Match length 62
% identity 50

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]



```
304956
Seq. No.
                  rv1700453822.h1
Seq. ID
Method
                  BLASTX
                  g3894197
NCBI GI
                  230
BLAST score
                  1.0e-19
E value
Match length
                  55
                  76
% identity
                  (AC005662) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  304957
Seq. No.
                  rv1700453824.h1
Seq. ID
Method
                  BLASTX
                  q480450
NCBI GI
BLAST score
                  189
E value
                  8.0e-15
Match length
                  44
                  80
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                   thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                   reductoisomerase [Arabidopsis thaliana]
                  304958
Seq. No.
                   rv1700453848.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2498077
BLAST score
                   222
                  1.0e-18
E value
Match length
                   45
                  100
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                   (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase
                   [Saccharum officinarum]
                   304959
Seq. No.
Seq. ID
                   rv1700454171.h1
                   BLASTN
Method
NCBI GI
                   g2665839
BLAST score
                   81
                   5.0e-38
E value
Match length
                   145
                   89
% identity
                  Zea mays putative histone deacetylase RPD3 mRNA, complete
NCBI Description
Seq. No.
                   304960
                   rv1700454174.h1
Seq. ID
Method
                   BLASTX
```

NCBI GI g4589961 BLAST score 221 E value 3.0e-18

Match length 66 64 % identity

(AC007169) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

304961

Seq. ID

rv1700454232.h1

```
Method
NCBI GI
                  q3928097
BLAST score
                  310
E value
                  1.0e-28
                  92
Match length
                  58
% identity
NCBI Description
                  (AC005770) unknown protein, 5' partial [Arabidopsis
                  thaliana]
                  304962
Seq. No.
Seq. ID
                  rv1700454293.h1
Method
                  BLASTX
NCBI GI
                  q1899060
                  207
BLAST score
                  5.0e-24
E value
Match length
                  61
% identity
                  98
NCBI Description (U79669) endosperm C-24 sterol methyltransferase [Zea mays]
Seq. No.
                  304963
                  rv1700454369.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g577824
BLAST score
                  224
E value
                  1.0e-123
Match length
                  248
% identity
                  98
NCBI Description Z.mays gene for H2B histone (gH2B3)
                  304964
Seq. No.
                  rv1700454370.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4512698
BLAST score
                  443
E value
                  2.0e-44
Match length
                  88
% identity
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  304965
                  rv1700454476.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g577824
BLAST score
                  241
E value
                  1.0e-133
Match length
                  241
% identity
                  100
```

Seq. ID rv1700454511.h1 Method BLASTN

NCBI Description Z.mays gene for H2B histone (gH2B3)

NCBI GI g4582786
BLAST score 44
E value 6.0e-16
Match length 60
% identity 93





```
NCBI Description Zea mays mRNA for adenosine kinase, putative
                   304967
Seq. No.
Seq. ID
                   rv1700454601.h1
Method
                  BLASTX
NCBI GI
                  g2130122
BLAST score
                   153
E value
                   9.0e-21
Match length
                   62
                  89
% identity
NCBI Description
                  cyclin III - maize >gi 516548 (U10076) cyclin IIIZm [Zea
                  mays]
                   304968
Seq. No.
Seq. ID
                  rv1700454665.h1
                  BLASTX
Method
NCBI GI
                  g2496730
BLAST score
                  164
E value
                  6.0e-12
Match length
                  60
% identity
                  52
                  HYPOTHETICAL PROTEIN Y40U PRECURSOR >gi_2182565 (AE000089)
NCBI Description
                  Y4oU [Rhizobium sp. NGR234]
Seq. No.
                  304969
Seq. ID
                  rv1700454694.h1
Method
                  BLASTX
NCBI GI
                  q131772
BLAST score
                  162
E value
                  1.0e-11
Match length
                  36
% identity
                   92
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                  >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                  maize
Seq. No.
                  304970
Seq. ID
                  rv1700454731.h1
Method
                  BLASTX
NCBI GI
                  q741983
BLAST score
                  207
E value
                  6.0e-17
Match length
                  43
% identity
                  95
NCBI Description sucrose synthase: ISOTYPE=2 [Zea mays]
Seq. No.
                  304971
Seq. ID
                  rv1700454781.h1
Method
                  BLASTX
NCBI GI
                  q3236240
BLAST score
                  342
E value
                  2.0e-32
```

74 84

Match length

NCBI Description

% identity

(AC004684) unknown protein [Arabidopsis thaliana]



Seq. ID rvl700454915.h1

Method BLASTX
NCBI GI g2497953
BLAST score 201
E value 3.0e-19
Match length 57
% identity 89

NCBI Description MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM

COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum

cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No. 304973

Seq. ID rv1700454919.h1

Method BLASTX
NCBI GI g2702281
BLAST score 192
E value 6.0e-15
Match length 55
% identity 67

NCBI Description (AC003033) putative protein disulfide isomerase precursor

[Arabidopsis thaliana]

Seq. No. 304974

Seq. ID rv1700454950.h1

Method BLASTX
NCBI GI g4507033
BLAST score 148
E value 5.0e-10
Match length 28
% identity 100

NCBI Description solute carrier family 5 (sodium/glucose cotransporter),

member 2 >gi_400337_sp_P31639_SL52_HUMAN_SODIUM/GLUCOSE COTRANSPORTER 2 (NA(+)/GLUCOSE COTRANSPORTER 2) (LOW

AFFINITY SODIUM-GLUCOSE COTRANSPORTER)

>gi_1082791_pir__A56765 sodium-glucose cotransporter homolog - human >gi_338053 (M95549) sodium/glucose

cotransporter-like protein [Homo sapiens]

Seq. No. 304975

Seq. ID rv1700455027.h1

Method BLASTX
NCBI GI g4584525
BLAST score 277
E value 5.0e-25
Match length 76
% identity 67

NCBI Description (AL049607) protein phosphatase 2C-like protein [Arabidopsis

thaliana]

Seq. No. 304976

Seq. ID rvl700455104.h1

Method BLASTX
NCBI GI g1418767
BLAST score 160
E value 4.0e-11



Match length 86 % identity 42

NCBI Description (X96698) D1075-like [Homo sapiens]

Seq. No. 304977

Seq. ID rv1700455109.h1

Method BLASTX
NCBI GI g4584527
BLAST score 141
E value 6.0e-09
Match length 83
% identity 41

NCBI Description (AL049607) putative protein [Arabidopsis thaliana]

Seq. No. 304978

Seq. ID rv1700455117.h1

Method BLASTX
NCBI GI g2463509
BLAST score 162
E value 2.0e-11
Match length 37
% identity 76

NCBI Description (Y09541) pectate lyase [Zinnia elegans]

Seq. No. 304979

Seq. ID rv1700455135.h1

Method BLASTN
NCBI GI g2226328
BLAST score 114
E value 7.0e-58
Match length 122
% identity 98

NCBI Description Zea mays physical impedance induced protein (IIG1) mRNA,

complete cds

Seq. No. 304980

Seq. ID rv1700455147.h1

Method BLASTX
NCBI GI g1351974
BLAST score 270
E value 4.0e-24
Match length 55
% identity 100

NCBI Description ADP-RIBOSYLATION FACTOR >gi 1076788 pir S49325

ADP-ribosylation factor - maize >gi_1076789_pir__S53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_

(X80042) ADP-ribosylation factor [Zea mays]

Seq. No. 304981

Seq. ID rv1700455150.h1

Method BLASTX
NCBI GI g3915733
BLAST score 199
E value 5.0e-16
Match length 44
% identity 84

NCBI Description HEP27 PROTEIN (PROTEIN D)

```
Seq. No.
                  304982
Seq. ID
                  rv1700455156.h1
Method
                  BLASTX
NCBI GI
                  q1708259
BLAST score
                  152
E value
                  3.0e-10
Match length
                  29
                  100
% identity
NCBI Description
                  HIGH MOBILITY GROUP PROTEIN HMG2 (HMG-2)
                  >gi_1363146_pir__S54774 high mobility group 2 protein -
                  mouse >gi_609169_emb_CAA86727 (Z46757) high mobility group
                  2 protein [Mus musculus]
Seq. No.
                  304983
                  rv1700455214.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3687243
BLAST score
                  232
E value
                  1.0e-19
Match length
                  61
                  75
% identity
                  (AC005169) putative ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
                  304984
Seq. No.
Seq. ID
                  rv1700455473.h1
Method
                  BLASTN
NCBI GI
                  g1495424
{\tt BLAST} score
                  234
                  1.0e-129
E value
Match length
                  258
% identity
                  98
NCBI Description H.sapiens mRNA for collagenase-3 protein
                  304985
Seq. No.
                  rv1700455478.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245113
BLAST score
                  211
E value
                  2.0e-26
Match length
                  82
% identity
                  83
NCBI Description
                  (Z97343) glycerol-3-phosphate permease homolog [Arabidopsis
                  thaliana]
```

Seq. ID rv1700455534.h1

Method BLASTX
NCBI GI g2244772
BLAST score 193
E value 3.0e-15
Match length 50
% identity 74

NCBI Description (Z97335) transport protein [Arabidopsis thaliana]

Seq. No. 304987



```
rv1700455594.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q577169
BLAST score
                  217
E value
                  1.0e-119
Match length
                  257
% identity
                  Human double-stranded RNA adenosine deaminase mRNA,
NCBI Description
                  complete cds
Seq. No.
                  304988
Seq. ID
                  rv1700455745.h1
Method
                  BLASTN
                  q168486
NCBI GI
BLAST score
                  74
                  9.0e - 34
E value
                  105
Match length
% identity
                  95
NCBI Description Maize glutathione S-transferase gene (GST-I), exon 1
                  304989
Seq. No.
                  rv1700455903.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q118104
BLAST score
                  185
                  2.0e-14
E value
Match length
                  43
% identity
                  84
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
                  304990
Seq. No.
Seq. ID
                  rv1700455926.h1
Method
                  BLASTX
NCBI GI
                  q2062176
BLAST score
                  207
                   9.0e-17
E value
Match length
                  77
% identity
                  58
                  (AC001645) Myb-related transcription activator (MybSt1)
NCBI Description
                   isolog [Arabidopsis thaliana]
Seq. No.
                   304991
Seq. ID
                   rv1700455927.h1
Method
                  BLASTX
NCBI GI
                  g4580455
BLAST score
                  183
                  5.0e-14
E value
Match length
                  50
```

% identity 70

(AC006081) unknown protein [Arabidopsis thaliana] NCBI Description

304992 Seq. No.

Seq. ID rv1700455972.h1



```
BLASTX
Method
NCBI GI
                  q1109830
BLAST score
                  175
E value
                  3.0e-13
                  66
Match length
                  48
% identity
NCBI Description
                  (U41534) coded for by C. elegans cDNA CEESI42F; Similar to
                  helicases of SNF2/RAD54 family. [Caenorhabditis elegans]
                  304993
Seq. No.
                  rv1700455980.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2492636
BLAST score
                  188
E value
                  1.0e-14
Match length
                  37
                  97
% identity
                  ACONITASE (ACONITATE HYDRATASE) (CITRATE HYDRO-LYASE)
NCBI Description
                  >gi 1084317 pir S49849 aconitate hydratase (EC 4.2.1.3) -
                  muskmelon (fragment) >gi 599723 emb CAA58047 (X82840)
                  aconitase [Cucumis melo]
                  304994
Seq. No.
Seq. ID
                  rv1700456045.h1
Method
                  BLASTX
NCBI GI
                  g2316016
BLAST score
                  289
E value
                  2.0e-26
Match length
                  74
% identity
                  69
NCBI Description
                  (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
Seq. No.
                  304995
Seq. ID
                  rv1700456056.h1
Method
                  BLASTN
NCBI GI
                  g4234849
BLAST score
                  33
E value
                  4.0e-09
Match length
                  49
% identity
                  92
                  Zea mays copia-like retrotransposon Sto-30, partial
NCBI Description
                  sequence
Seq. No.
                  304996
Seq. ID
                  rv1700456058.h1
Method
                  BLASTX
NCBI GI
                  g2245070
BLAST score
                  357
E value
                  3.0e-34
Match length
                  90
```

% identity

(Z97342) hypothetical protein [Arabidopsis thaliana] NCBI Description

304997 Seq. No.

Seq. ID rv1700456124.h1

Method BLASTX NCBI GI g3236254



BLAST score E value 1.0e-21 Match length 72

58 % identity

(AC004684) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 304998

rv1700456149.h1 Seq. ID

Method BLASTX NCBI GI g2224911 BLAST score 245 E value 3.0e-21 Match length 74 % identity 69

NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus

carota]

Seq. No. 304999

rv1700456175.h1 Seq. ID

Method BLASTN NCBI GI g3851000 BLAST score 122 E value 2.0e-62 Match length 133 % identity 99

NCBI Description Zea mays pyruvate dehydrogenase E1 beta subunit isoform 2

mRNA, nuclear gene encoding mitochondrial protein, complete

Seq. No. 305000

Seq. ID rv1700456230.h1

Method BLASTN NCBI GI g1184771 BLAST score 66 E value 5.0e-29 Match length 66 % identity 100

NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC2

(gpc2) mRNA, complete cds

Seq. No. 305001

Seq. ID rv1700456256.h1

Method BLASTX NCBI GI g4557505 BLAST score 181 E value 7.0e-16 Match length 50 % identity 90

cytochrome b-245, alpha polypeptide NCBI Description

> >gi 115210 sp P13498 C24A HUMAN CYTOCHROME B-245 LIGHT CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEUTROPHIL CYTOCHROME B, 22 KD POLYPEPTIDE) (P22-PHOX) (CYTOCHROME B(558) ALPHA CHAIN) (SUPEROXIDE-GENERATING NADPH OXIDASE LIGHT CHAIN SUBUNIT) >gi 88261 pir A28201 cytochrome b-245 alpha chain

- human >gi $\overline{1}89106$ (M2 $\overline{11}86$) p22 phagocyte b-cytochrome

[Homo sapiens]



```
305002
Seq. No.
Seq. ID
                  rv1700456278.h1
Method
                  BLASTN
NCBI GI
                   q182513
BLAST score
                   50
                  9.0e-20
E value
Match length
                  102
                  89
% identity
NCBI Description Human ferritin L chain mRNA, complete cds
                  305003
Seq. No.
                  rv1700456294.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3747047
BLAST score
                   43
E value
                  2.0e-15
Match length
                  83
                   88
% identity
NCBI Description Zea mays methionine synthase mRNA, partial cds
Seq. No.
                   305004
                   rv1700456303.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4336204
BLAST score
                   68
                   3.0e-30
E value
Match length
                   68
% identity
                   100
NCBI Description
                  Zea mays cytochrome b5 reductase (NFR) mRNA, complete cds
                   305005
Seq. No.
Seq. ID
                   rv1700456426.h1
Method
                   BLASTN
NCBI GI
                   q4416300
BLAST score
                   69
E value
                   1.0e-30
Match length
                   255
                   81
% identity
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
                   305006
Seq. No.
Seq. ID
                   rv1700456470.h1
Method
                   BLASTX
NCBI GI
                   g4502169
BLAST score
                   401
E value
                   2.0e-39
Match length
                   87
% identity
                   92
```

NCBI Description UNKNOWN >gi 1314560 (U50939) amyloid precursor

> protein-binding protein 1 [Homo sapiens] >gi 3242733 (AC004638) amyloid precursor protein-binding protein 1

(APP-B1) [Homo sapiens]

Seq. No. 305007

Seq. ID rv1700456486.h1

Method BLASTX



```
NCBI GI
                    q2244754
  BLAST score
                    164
  E value
                     9.0e-22
  Match length
                     70
                     65
  % identity
                     (Z97335) heat shock transcription factor homolog
  NCBI Description
                     [Arabidopsis thaliana]
                    305008
  Seq. No.
                    rv1700456745.h1
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g2367431
  BLAST score
                    165
                     9.0e-12
  E value
  Match length
                     46
                    70
  % identity
  NCBI Description (AF000403) putative cytochrome P450 [Lotus japonicus]
                     305009
  Seq. No.
                     rv1700456827.h1
  Seq. ID
  Method
                    BLASTX
                     g2911059
  NCBI GI
  BLAST score
                     153
                     1.0e-10
  E value
                     59
  Match length
  % identity
                     56
                    (AL021961) putative protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                     305010
                     rv1700456835.h1
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     q643596
  BLAST score
                     38
  E value
                     2.0e-12
  Match length
                     46
  % identity
                     96
  NCBI Description Corn mRNA for cysteine proteinase, clone CCP, complete cds
  Seq. No.
                     305011
                     rv1700456869.h1
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g414704
  BLAST score
                     42
  E value
                     1.0e-14
  Match length
                     86
  % identity
                     88
  NCBI Description O.sativa mRNA for cytochrome b5
                     305012
  Seq. No.
  Seq. ID
                     rv1700456913.h1
  Method
                     BLASTX
  NCBI GI
                     q3461848
  BLAST score
                     150
```

E value 6.0e-10 77 Match length 49 % identity

NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]



```
305013
Seq. No.
Seq. ID
                   rv1700457067.h1
Method
                   BLASTN
NCBI GI
                   g22121
BLAST score
                   66
E value
                   3.0e-29
Match length
                   70
% identity
                   99
NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1F)
Seq. No.
                   305014
Seq. ID
                   rv1700457089.h1
Method
                   BLASTX
NCBI GI
                   q4506695
BLAST score
                   303
E value
                   5.0e-28
Match length
                   81
% identity
                   74
                   ribosomal protein S19 >gi_730640_sp_P39019_RS19_HUMAN 40S
RIBOSOMAL PROTEIN S19 >gi_2119097_pir__I52692_ribosomal
NCBI Description
                   protein S19, cytosolic - human >gi_337733 (M81757) S19
                   ribosomal protein [Homo sapiens] >gi_4210954 (AF092907)
                   ribosomal protein S19; RPS19 [Homo sapiens]
Seq. No.
                   305015
Seq. ID
                   rv1700457118.h1
Method
                   BLASTX
NCBI GI
                   g2288999
BLAST score
                   179
E value
                   8.0e-15
Match length
                   62
% identity
                   66
NCBI Description
                   (AC002335) electron transfer flavoprotein ubiquinone
                   oxidoreductase isolog [Arabidopsis thaliana]
                   305016
Seq. No.
Seq. ID
                   rv1700457120.h1
Method
                   BLASTX
NCBI GI
                   g2995953
BLAST score
                   188
E value
                   2.0e-14
Match length
                   51
% identity
                   67
NCBI Description
                   (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]
Seq. No.
                   305017
Seq. ID
                   rv1700457125.h1
Method
                   BLASTX
                   q1172836
```

Method BLASTX
NCBI GI g117283
BLAST score 340
E value 3.0e-32
Match length 66
% identity 95

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)

small ras-related protein [Nicotiana tabacum]



```
Seq. No.
                   305018
Seq. ID
                   rv1700457187.h1
Method
                   BLASTX
NCBI GI
                   g3023816
BLAST score
                   277
E value
                   6.0e-25
Match length
                   56
% identity
                   95
```

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

```
305019
Seq. No.
Seq. ID
                   rv1700457257.h1
Method
                   BLASTN
NCBI GI
                   g1524382
BLAST score
                   67
```

2.0e-29 E value Match length 130 % identity 100

NCBI Description Z.mays mRNA for EPSP-synthase

Seq. No. 305020

Seq. ID rv1700457285.h1

Method BLASTX NCBI GI g3581828 BLAST score 249 E value 1.0e-21 Match length 90 % identity 56

NCBI Description (AJ000917) O. volvulus cyclophilin 4 [Onchocerca volvulus]

Seq. No. 305021

Seq. ID rv1700457301.h1

Method BLASTN NCBI GI g3420038 BLAST score 108 E value 5.0e-54Match length 192 89 % identity

NCBI Description Zea mays gypsy/Ty3-type retrotransposon Tekay, complete

sequence

Seq. No. 305022

Seq. ID rv1700457346.h1

Method BLASTX NCBI GI g1717744 BLAST score 163 1.0e-11 E value Match length 82 % identity 45

NCBI Description TOPOISOMERASE 1-RELATED PROTEIN TRF4

>gi_1077298_pir S51882 topoisomerase I-related protein

TRF4 - yeast (Saccharomyces cerevisiae)

>gi_663237_emb_CAA88145_ (Z48149) ORF [Saccharomyces cerevisiae] >gi 950226 (U31355) Trf4p [Saccharomyces

cerevisiae] >gi_1419987_emb_CAA99134_ (Z74857) ORF YOL115w



[Saccharomyces cerevisiae]

```
305023
Seq. No.
Seq. ID
                  rv1700457423.h1
Method
                  BLASTX
NCBI GI
                  g120670
BLAST score
                  338
E value
                  4.0e-32
Match length
                  65
% identity
                  98
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_100879_pir__S06879 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) C - maize
                  >gi 295853 emb CAA33620 (X15596) GAPDH [Zea mays]
                  305024
Seq. No.
Seq. ID
                  rv1700457544.h1
Method
                  BLASTX
NCBI GI
                  g4585871
BLAST score
                  340
E value
                  3.0e-32
Match length
                  85
% identity
                  69
NCBI Description
                  (AC005850) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  305025
Seq. ID
                  rv1700457621.h1
Method
                  BLASTX
NCBI GI
                  g3421378
BLAST score
                  172
                  7.0e-13
E value
Match length
                  50
% identity
                  70
NCBI Description
                  (AF080249) kinesin-like heavy chain [Arabidopsis thaliana]
                  305026
Seq. No.
Seq. ID
                  rv1700457789.h1
Method
                  BLASTX
NCBI GI
                  q166384
BLAST score
                  174
                  7.0e-13
E value
                  71
Match length
% identity
NCBI Description
                  (M35867) histone H3 (H3-1.1) [Medicago sativa]
                  305027
Seq. No.
Seq. ID
                  rv1700457833.h1
Method
                  BLASTX
NCBI GI
                  g1084457
BLAST score
                  188
E value
                  2.0e-14
Match length
                  56
                  70
% identity
NCBI Description
                  elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_
```

Seq. No. 305028

(D23674) elongation factor 1 beta [Oryza sativa]

```
rv1700457857.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1709970
BLAST score
                   219
                   3.0e-18
E value
Match length
                   57
% identity
                  74
NCBI Description
                  60S RIBOSOMAL PROTEIN L10A
                  305029
Seq. No.
Seq. ID
                  rv1700457875.h1
Method
                  BLASTX
NCBI GI
                  g397396
BLAST score
                  219
E value
                  3.0e-18
Match length
                  87
% identity
                  59
```

NCBI Description (X66077) DNA-binding protein [Zea mays]

 Seq. No.
 305030

 Seq. ID
 rv1700457890.h1

 Method
 BLASTX

 NCBI GI
 g3738283

 BLAST score
 263

 E value
 3.0e-23

 Match length
 50

Match length 50 % identity 86

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 305031

Seq. ID rv1700457930.h1

Method BLASTX
NCBI GI g3860277
BLAST score 208
E value 8.0e-17
Match length 63
% identity 65

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi 4314394 gb AAD15604 (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 305032

Seq. ID rv1700458068.h1

Method BLASTN
NCBI GI g2921303
BLAST score 44
E value 4.0e-16
Match length 44
% identity 100

NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA,

complete cds

Seq. No. 305033

Seq. ID rv1700458196.h1

Method BLASTX
NCBI GI g3024122
BLAST score 346



E value 4.0e-33 Match length 81 % identity 84

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No. 305034

Seq. ID rv1700458208.h1

Method BLASTX
NCBI GI g340062
BLAST score 184
E value 3.0e-14
Match length 53
% identity 75

NCBI Description (M10939) pro-ubiquitin [Homo sapiens]

Seq. No. 305035

Seq. ID rv1700458216.h1

Method BLASTN
NCBI GI g1699161
BLAST score 149
E value 1.0e-78
Match length 161
% identity 98

NCBI Description RP3: ETX1, ETX1=X-linked retintis pigmentosa (RP3)

candidate gene [human, retina, Genomic/mRNA, 2221 nt]

Seq. No. 305036

Seq. ID rvl700458273.h1

Method BLASTN
NCBI GI g2286152
BLAST score 124
E value 1.0e-63
Match length 164
% identity 94

NCBI Description Zeá mays cytoplasmic malate dehydrogenase mRNA, complete

cds

Seq. No. 305037

Seq. ID rv1700458337.h1

Method BLASTX
NCBI GI 94038044
BLAST score 176
E value 4.0e-13
Match length 80
% identity 40

NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]

>gi_4406788_gb_AAD20098_ (AC006532) unknown protein

[Arabidopsis thaliana]

Seq. No. 305038

Seq. ID rv1700458384.h1

Method BLASTX
NCBI GI g129916
BLAST score 301
E value 1.0e-27



```
Match length
% identity
                  PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY
NCBI Description
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                  >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
                  305039
Seq. No.
Seq. ID
                  rv1700458465.h1
Method
                  BLASTX
NCBI GI
                  g4322323
BLAST score
                  171
E value
                  1.0e-12
Match length
                  48
% identity
                  60
NCBI Description
                  (AF080543) amino acid transporter [Nepenthes alata]
Seq. No.
                  305040
Seq. ID
                  rv1700458476.h1
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                  216
E value
                  1.0e-17
Match length
                  82
% identity
NCBI Description
                  (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  305041
Seq. ID
                  rv1700458577.h1
Method
                  BLASTX
NCBI GI
                  g1685005
BLAST score
                  148
È value
                  8.0e-10
Match length
                  45
% identity
                  53
NCBI Description
                  (U32644) immediate-early salicylate-induced
                  glucosyltransferase [Nicotiana tabacum]
                  305042
Seq. No.
```

Seq. ID

rv1700458614.h1 Method BLASTX

NCBI GI g3184073 BLAST score 144 2.0e-09 E value Match length 87 % identity 36

NCBI Description (AL023779) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 305043

Seq. ID rv1700458616.h1

Method BLASTN NCBI GI g22320 BLAST score 43 E value 1.0e-15 Match length 81 % identity 89

NCBI Description Maize H1 mRNA for H1 histone



Seq. No. 305044

Seq. ID rv1700458637.h1

Method BLASTN
NCBI GI g4507584
BLAST score 97

E value 1.0e-47 Match length 121 % identity 95

NCBI Description Homo sapiens tumor necrosis factor receptor superfamily,

member 6b, decoy (TNFRSF6B) mRNA, and translated products

>gi_4106877_gb_AF104419_AF104419 Homo sapiens decoy

receptor 3 (DcR3) mRNA, complete cds

Seq. No. 305045

Seq. ID rv1700458657.h1

Method BLASTN
NCBI GI g3327067
BLAST score 218
E value 1.0e-119
Match length 255
% identity 96

NCBI Description Homo sapiens mRNA for KIAA0627 protein, partial cds

Seq. No. 305046

Seq. ID rv1700458670.h1

Method BLASTN
NCBI GI g2245648
BLAST score 122
E value 3.0e-62
Match length 170
% identity 85

NCBI Description Zea mays discolored-1 (mutant allele dsc1-Ref::Mu1) gene,

partial sequence

Seq. No. 305047

Seq. ID rv1700458829.h1

Method BLASTX
NCBI GI g3152568
BLAST score 246
E value 3.0e-21
Match length 83
% identity 57

NCBI Description (AC002986) Similar to hypothetical protein product

gb_Z97337 from A. thaliana. EST gb_H76597 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 305048

Seq. ID rvt700548360.h1

Method BLASTN
NCBI GI g2196671
BLAST score 45
E value 3.0e-16
Match length 45
% identity 100

NCBI Description Z.mays mRNA for HMG protein



 Seq. No.
 305049

 Seq. ID
 rvt700548395.h1

 Method
 BLASTX

 NCBI GI
 g2501555

BLAST score 348 E value 3.0e-33 Match length 92 % identity 71

NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No. 305050

Seq. ID rvt700548547.h1

Method BLASTX
NCBI GI g2961390
BLAST score 245
E value 5.0e-21
Match length 89
% identity 52

NCBI Description (AL022141) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No. 305051

Seq. ID rvt700548596.h1

Method BLASTX
NCBI GI g3928142
BLAST score 183
E value 4.0e-14
Match length 42
% identity 90

NCBI Description (AJ131045) protein phosphatase [Cicer arietinum]

Seq. No. 305052

Seq. ID rvt700548660.h1

Method BLASTN
NCBI GI g2832242
BLAST score 72
E value 2.0e-32
Match length 246
% identity 83

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 305053

Seq. ID rvt700548696.h1

Method BLASTN
NCBI GI g391876
BLAST score 38
E value 4.0e-12
Match length 98
% identity 85

NCBI Description Oryza sativa mRNA for adenylate kinase-a, complete cds

Seq. No. 305054

Seq. ID rvt700548710.h1

Method BLASTX NCBI GI g3157941 BLAST score 334



E value 1.0e-31 Match length 91 % identity 66 NCBI Description (AC002131) Contains similarity to hypothetical protein gb U95973 from A. thaliana. [Arabidopsis thaliana] Seq. No. 305055 Seq. ID rvt700548716.h1 Method BLASTX NCBI GI q3292822 BLAST score 153 E value 3.0e-10 Match length 94 40 % identity NCBI Description (AL031018) putative protein [Arabidopsis thaliana] Seq. No. 305056 Seq. ID rvt700548720.h1 Method BLASTX NCBI GI g123620 BLAST score 473 E value 6.0e-48 Match length 92 % identity 100 HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950 NCBI Description heat shock cognate protein 70 - tomato >gi_19258_emb_CAA37971 (X54030) heat shock protein cognate 70 [Lycopersicon esculentum] Seq. No. 305057 Seq. ID rvt700548757.h1 Method BLASTX NCBI GI q100484 BLAST score 322 E value 3.0e-30 Match length 89 % identity 63 NCBI Description hypothetical protein - garden snapdragon Seq. No. 305058 Seq. ID rvt700548796.h1 Method BLASTX NCBI GI g2982289 BLAST score 340 E value 1.0e-40 Match length 89 % identity 90 NCBI Description (AF051229) 60S ribosomal protein L17 [Picea mariana]

Seq. No. 305059

Seq. ID rvt700548872.h1

Method BLASTX NCBI GI g1362162 BLAST score 235 6.0e-20 E value Match length 58 % identity 71





NCBI Description beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No. 305060

Seq. ID rvt700549014.h1

Method BLASTN
NCBI GI g168398
BLAST score 191
E value 1.0e-103
Match length 210
% identity 98

NCBI Description Zea mays auxin-binding protein (abp4) gene, exons 1-5 and

complete cds

Seq. No. 305061

Seq. ID rvt700549030.h1

Method BLASTX
NCBI GI g2109293
BLAST score 188
E value 2.0e-14
Match length 40
% identity 82

NCBI Description (U97568) serine/threonine protein kinase [Arabidopsis

thalianal

Seq. No. 305062

Seq. ID rvt700549031.h1

Method BLASTX
NCBI GI g4263722
BLAST score 456
E value 8.0e-46
Match length 96
% identity 89

NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No. 305063

Seq. ID rvt700549056.h1

Method BLASTN
NCBI GI g3309177
BLAST score 73
E value 6.0e-33
Match length 201
% identity 89

NCBI Description Zea mays starch branching enzyme I (sbel) gene, complete

cds

Seq. No. 305064

Seq. ID rvt700549071.h1

Method BLASTX
NCBI GI g2497820
BLAST score 341
E value 2.0e-32
Match length 70
% identity 91

NCBI Description DNA REPLICATION LICENSING FACTOR MCM3 HOMOLOG (REPLICATION

ORIGIN ACTIVATOR) (ROA PROTEIN) >gi_1076823_pir__S52247 probable replication origin activator protein ROA - maize

```
(fragment) >gi_609290_emb_CAA82556_ (Z29368) ROA protein
                  [Zea mays]
                  305065
Seq. No.
                  rvt700549171.h1
Seq. ID
                  BLASTX
Method
                  g4079800
NCBI GI
BLAST score
                  237
                  3.0e-20
E value
Match length
                  47
% identity
                  96
                  (AF052503) S-phase-specific ribosomal protein [Oryza
NCBI Description
                  sativa]
                  305066
Seq. No.
                  rvt700549191.h1
Seq. ID
Method
                  BLASTX
                  q2613143
NCBI GI
BLAST score
                  254
E value
                  2.0e-22
Match length
                  61
                  87
% identity
NCBI Description (AF030548) tubulin [Oryza sativa]
Seq. No.
                  305067
                  rvt700549201.h1
Seq. ID
Method
                  BLASTX
                  g2760345
NCBI GI
BLAST score
                  392
                  2.0e-38
E value
Match length
                  91
                  26
% identity
NCBI Description (U84967) ubiquitin [Arabidopsis thaliana]
Seq. No.
                  305068
                  rvt700549255.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22324
BLAST score
                  80
E value
                  3.0e-37
Match length
                  144
                  89
% identity
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)
Seq. No.
                  305069
                  rvt700549267.h1
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4587615
BLAST score 171
E value 2.0e-12
Match length 73
% identity 47

NCBI Description (AC006951) putative acyl-CoA synthetase [Arabidopsis

thaliana]

305070 -

Seq. No.

Seq. ID rvt700549270.h1

```
Method BLASTX
NCBI GI g4587584
BLAST score 367
E value 2.0e-35
Match length 80
% identity 90
```

NCBI Description (AC007232) unknown protein [Arabidopsis thaliana]

Seq. No. 305071

Seq. ID rvt700549271.h1

Method BLASTX
NCBI GI g3025329
BLAST score 226
E value 6.0e-19
Match length 78
% identity 59

NCBI Description HYPOTHETICAL 25.4 KD PROTEIN F53F4.3 IN CHROMOSOME V

>gi_3877534_emb_CAB01212_ (Z77663) Similarity to S.pombe
hypothetical proteinSPAC4G9.01 (TR:E223656) [Caenorhabditis

elegans]

Seq. No. 305072

Seq. ID rvt700549272.h1

Method BLASTX
NCBI GI g729230
BLAST score 238
E value 2.0e-20
Match length 60
% identity 82

NCBI Description CHROMOSOME SEGREGATION PROTEIN CUT3 >gi_1076872_pir__S51622

cut3 protein - fission yeast (Schizosaccharomyces pombe)

>gi 603501_dbj_BAA06454_ (D30788) cut3 protein

[Schizosaccharomyces pombe]

Seq. No. 305073

Seq. ID rvt700549277.h1

Method BLASTX
NCBI GI g4262148
BLAST score 366
E value 2.0e-35
Match length 84
% identity 81

NCBI Description (AC005275) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 305074

Seq. ID rvt700549286.h1

Method BLASTN
NCBI GI g2286152
BLAST score 88
E value 3.0e-42
Match length 132
% identity 92

NCBI Description Zea mays cytoplasmic malate dehydrogenase mRNA, complete

cds

Seq. No. 305075



```
Seq. ID
                   rvt700549337.h1
 Method
                   BLASTX
                   q4585972
 NCBI GI
 BLAST score
                   262
 E value
                   4.0e-23
 Match length
                   87
 % identity
                   59
                   (AC005287) Putative ATPase [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   305076
 Seq. ID
                   rvt700549395.h1
 Method
                   BLASTX
NCBI GI
                   q4646206
 BLAST score
                   224
                   1.0e-18
 E value
 Match length
                   75
                   55
 % identity
 NCBI Description
                    (AC007230) Contains similarity to gb D13630 KIAA0005 gene
                   from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360,
                   gb_T20468, gb_T45191 and gb_AI100459 come from this gene.
                    [Arabidopsis thaliana]
                   305077
 Seq. No.
 Seq. ID
                   rvt700549396.h1
 Method
                   BLASTX
 NCBI GI
                   q2317901
 BLAST score
                   367
 E value
                   2.0e-35
 Match length
                   103
 % identity
                   68
 NCBI Description
                   (U89959) Similar to vesicle transport protein, PIR
                   Accession Number A55931 [Arabidopsis thaliana]
 Seq. No.
                   305078
 Seq. ID
                   rvt700549405.hl
 Method
                   BLASTX
                   g2245378
 NCBI GI
 BLAST score
                   309
 E value
                   1.0e-28
 Match length
                   84
                   70
 % identity
                   (U83245) auxin response factor 1 [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   305079
 Seq. ID
                   rvt700549416.h1
 Method
                   BLASTX
 NCBI GI
                   g1071913
 BLAST score
                   378
                   9.0e-37
 E value
                   86
 Match length
 % identity
                   cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
 NCBI Description
                    - spinach >gi 1066153 dbj BAA07177 (D37963) cysteine
                   synthase [Spinacia oleracea]
```

Seq. No. 305080

Seq. ID rvt700549473.h1

```
Method BLASTX
NCBI GI 94539397
BLAST score 194
E value 1.0e-19
Match length 60
% identity 82
```

NCBI Description (AL035526) cellulose synthase-like protein [Arabidopsis thaliana]

Seq. No. 305081

Seq. ID rvt700549495.h1

Method BLASTX
NCBI GI g2052383
BLAST score 270
E value 4.0e-24
Match length 55
% identity 84

NCBI Description (U66345) calreticulin [Arabidopsis thaliana]

Seq. No. 305082

Seq. ID rvt700549501.h1

Method BLASTX
NCBI GI g1834317
BLAST score 137
E value 9.0e-09
Match length 38
% identity 68

NCBI Description (D82024) DNA topoisomerase II [Dictyostelium discoideum]

Seq. No. 305083

Seq. ID rvt700549510.h1

Method BLASTX
NCBI GI g4585972
BLAST score 156
E value 1.0e-10
Match length 54
% identity 56

NCBI Description (AC005287) Putative ATPase [Arabidopsis thaliana]

Seq. No. 305084

Seq. ID rvt700549516.h1

Method BLASTX
NCBI GI g3935138
BLAST score 252
E value 6.0e-22
Match length 82
% identity 49

NCBI Description (AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No. 305085

Seq. ID rvt700549549.h1

Method BLASTX
NCBI GI g3342800
BLAST score 254
E value 6.0e-29
Match length 92
% identity 80



NCBI Description (AF061837) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No. 305086

Seq. ID rvt700549643.h1

Method BLASTX
NCBI GI g559713
BLAST score 195
E value 4.0e-22
Match length 70
% identity 73

NCBI Description (D38552) The ha1539 protein is related to cyclophilin.

[Homo sapiens]

Seq. No. 305087

Seq. ID rvt700549728.h1

Method BLASTN
NCBI GI g1617470
BLAST score 96
E value 5.0e-47
Match length 144
% identity 92

NCBI Description Z.diploperennis DNA for Grandel-4 retrotransposon

Seq. No. 305088

Seq. ID rvt700549736.hl

Method BLASTX
NCBI GI g3176714
BLAST score 210
E value 3.0e-17
Match length 49
% identity 76

NCBI Description (AC002392) putative tRNA-splicing endonuclease positive

effector [Arabidopsis thaliana]

Seq. No. 305089

Seq. ID rvt700549787.h1

Method BLASTX
NCBI GI g2980789
BLAST score 247
E value 2.0e-21
Match length 91
% identity 55

NCBI Description (AL022197) hypothetical protein [Arabidopsis thaliana]

Seq. No. 305090

Seq. ID rvt700549792.h1

Method BLASTX
NCBI GI g4263831
BLAST score 209
E value 6.0e-17
Match length 88
% identity 48

NCBI Description (AC006067) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 305091



rvt700549881.h1 Seq. ID BLASTX Method g3878119 NCBI GI 152 BLAST score 2.0e-10 E value Match length 51 % identity 53 (Z49068) similar to GTP-binding protein; cDNA EST NCBI Description EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL: D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353 Seq. No. 305092 Seq. ID rvt700549892.h1 Method BLASTX NCBI GI g3860277 BLAST score 226 E value 7.0e-19 68 Match length 71 % identity (AC005824) putative ribosomal protein L10 [Arabidopsis NCBI Description thaliana] >gi 4314394 gb AAD15604 (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana] Seq. No. 305093 Seq. ID rvt700549916.h1 Method BLASTX NCBI GI q4204310 BLAST score 351 E value 2.0e-33 Match length 93 75 % identity (AC003027) lcl prt seq No definition line found NCBI Description [Arabidopsis thaliana] 305094 Seq. No. Seq. ID rvt700549925.h1 Method BLASTX g3882239 NCBI GI BLAST score 146 2.0e-09 E value 57 Match length % identity 49 (AB018302) KIAA0759 protein [Homo sapiens] NCBI Description

305095 Seq. No.

Seq. ID rvt700549990.h1

Method BLASTX NCBI GI g2689631 BLAST score 252 5.0e-22 E value 52 Match length 90 % identity

(AF022389) ADP-ribosylation factor [Vigna unguiculata] NCBI Description

Seq. No. 305096



```
rvt700550008.h1
Seq. ID
                  BLASTX
Method
                  g1350677
NCBI GI
                  165
BLAST score
                  5.0e-12
E value
                  40
Match length
                  82
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L19
                  305097
Seq. No.
                  rvt700550092.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171978
BLAST score
                  245
                  3.0e-21
E value
                  81
Match length
                  59
% identity
                  POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                   (PABP 2) >gi 304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)
                  poly(A)-binding protein [Arabidopsis thaliana]
                  305098
Seq. No.
                  rvt700550155.h1
Seq. ID
Method
                  BLASTX
                  g4204309
NCBI GI
                  192
BLAST score
                   3.0e-15
E value
Match length
                  63
                  59
% identity
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   305099
Seq. No.
                   rvt700550176.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q399854
BLAST score
                   168
                   4.0e-12
E value
Match length
                   74
% identity
                   58
                  HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize
NCBI Description
                  >gi 22325 emb CAA40565 (X57313) H2B histone [Zea mays]
Seq. No.
                   305100
Seq. ID
                   rvt700550177.h1
Method
                   BLASTX
NCBI GI
                   q2244865
BLAST score
                   145
                   2.0e-09
E value
Match length
                   77
```

43 % identity

(Z97337) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 305101

rvt700550237.h1 Seq. ID

Method BLASTX

```
q1491710
NCBI GI
BLAST score
                   220
                   3.0e-18
E value
Match length
                   71
                   56
% identity
                   (X96506) alpha subunit; forms heterodimer with NC2
NCBI Description
                  alpha/Dr1 [Homo sapiens]
                   305102
Seq. No.
                   rvt700550261.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g481477
BLAST score
                   313
E value
                   4.0e-29
Match length
                   63
                   17
% identity
                  ubiquitin precursor - rice >gi_416038_emb_CAA53665
NCBI Description
                   (X76064) polyubiquitin [Oryza sativa] >gi 1574944 (U37687)
                   polyubiquitin [Oryza sativa]
                   305103
Seq. No.
                   rvt700550275.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2231702
BLAST score
                   240
E value
                   1.0e-20
Match length
                   61
                   77
% identity
                  (U92086) clathrin assembly protein AP19 homolog
NCBI Description
                   [Arabidopsis thaliana] >gi_3080409_emb_CAA18728.1_
                   (AL022604) clathrin assembly protein AP19 homolog
                   [Arabidopsis thaliana]
Seq. No.
                   305104
                   rvt700550282.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4206306
BLAST score
                   273
                   2.0e-24
E value
Match length
                   55
% identity
                   91
NCBI Description
                  (AF049110) prpol [Zea mays]
                   305105
Seq. No.
Seq. ID
                   rvt700550301.hl
Method
                   BLASTX
NCBI GI
                   q2191144
```

Method BLASTX
NCBI GI g2191144
BLAST score 225
E value 9.0e-19
Match length 90
% identity 54

NCBI Description (AF007269) A_IG002N01.24 gene product [Arabidopsis

thaliana]

Seq. No. 305106

Seq. ID rvt700550386.h1

Method BLASTX



```
q2052383
NCBI GI
BLAST score
                   361
                   9.0e-35
E value
                   69
Match length
                   88
% identity
                  (U66345) calreticulin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   305107
                   rvt700550434.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3122853
BLAST score
                   200
E value
                   7.0e-16
                   68
Match length
                   51
% identity
                   WD-REPEAT PROTEIN SAZD >gi 1082863 pir A49367 transducin
NCBI Description
                   homolog sazD - human >gi_4\overline{1}4536 (U\overline{0}260\overline{9}) transducin-like
                   protein [Homo sapiens]
                   305108
Seq. No.
                   rvt700550449.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3482933
BLAST score
                   161
E value
                   3.0e-11
Match length
                   46
% identity
                   65
                   (AC003970) Similar to cdc2 protein kinases [Arabidopsis
NCBI Description
                   thaliana]
                   305109
Seq. No.
                   rvt700550457.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2924653
BLAST score
                   60
E value
                   3.0e-25
Match length
                   189
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MDA7, complete sequence [Arabidopsis thaliana]
                   305110
Seq. No.
                   rvt700550509.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3913426
BLAST score
                   161
E value
                   1.0e-19
Match length
                   71
% identity
                   75
                   S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
```

(SAMDC) >qi 1532048 emb CAA69074 (Y07766)

S-adenosylmethionine decarboxylase [Oryza sativa]

305111 Seq. No.

rvt700550520.h1 Seq. ID

BLASTX Method NCBI GI g4539660



```
BLAST score
                   2.0e-11
E value
Match length
                  85
                   40
% identity
                  (AF061282) polyprotein [Sorghum bicolor]
NCBI Description
                  305112
Seq. No.
                  rvt700550537.h1
Seq. ID
                                                   , 🌣
Method
                  BLASTX
                   g4490739
NCBI GI
                   168
BLAST score
                   4.0e-12
E value
                   55
Match length
                   56
% identity
                  (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                   305113
Seq. No.
                   rvt700550563.h1
Seq. ID
                   BLASTX
Method
                   g2149640
NCBI GI
                   282
BLAST score
                   2.0e-25
E value
                   91
Match length
                   53
% identity
                  (U91995) Argonaute protein [Arabidopsis thaliana]
NCBI Description
                   305114
Seq. No.
                   rvt700550837.h1
Seq. ID
Method
                   BLASTX
                   g1707928
NCBI GI
BLAST score
                   323
                   3.0e-30
E value
                   94
Match length
                   94
% identity
                  GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 2
NCBI Description
                   PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
                   PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE
                   ADENYL TRANSFERASE) >gi_1076806_pir__S49439
                   glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
                   maize >gi_558365_emb_CAA86227_ (Z38111) ADP-glucose
                   pyrophosphorylase [Zea mays]
                   305115
Seq. No.
                   rvt700550890.h1
Seq. ID
Method
                   BLASTN
                   g22103
NCBI GI
BLAST score
                   45
                   3.0e-16
E value
                   125
Match length
% identity
                   84
```

NCBI Description Zea mays A2 gene

305116 Seq. No.

Seq. ID rvt700550936.h1

BLASTX Method NCBI GI g2501102 BLAST score 149



```
E value
Match length
                    47
  % identity
                    SYNTAXIN-RELATED PROTEIN KNOLLE >gi 1184165 (U39451)
  NCBI Description
                    syntaxin-related [Arabidopsis thaliana] >gi 1184167
                     (U39452) syntaxin-related [Arabidopsis thaliana]
                    >gi_3063443 (AC003981) F22013.4 [Arabidopsis thaliana]
                    >gi_1587182_prf__2206310A syntaxin-related protein
                     [Arabidopsis thaliana]
  Seq. No.
                    305117
  Seq. ID
                    rvt700551021.h1
  Method
                    BLASTX
  NCBI GI
                    q3152581
  BLAST score
                    145
  E value
                    2.0e-09
  Match length
                    38
  % identity
                    63
                    (AC002986) Similar to E. coli sulfurtransferase (rhodanese)
  NCBI Description
                    gb_AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come
                    from this gene. [Arabidopsis thaliana]
  Seq. No.
                    305118
  Seq. ID
                    rvt700551035.hl
  Method
                    BLASTX
                    q4539452
  NCBI GI
  BLAST score
                    344
  E value
                    1.0e-32
  Match length
                    93
  % identity
                    68
  NCBI Description
                     (AL049500) putative phosphoribosylanthranilate transferase
                     [Arabidopsis thaliana]
  Seq. No.
                    305119
  Seq. ID
                    rvt700551251.h1
  Method
                    BLASTN
  NCBI GI
                    q168492
```

BLAST score 52 E value 2.0e-20 Match length 52 % identity 100

NCBI Description Corn histone H3 (H3C3) gene, complete cds

Seq. No. 305120

Seq. ID rvt700551261.h1

Method BLASTX NCBI GI g2894534 BLAST score 328 E value 5.0e-31 Match length 64 % identity 95

NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 305121

Seq. ID rvt700551269.h1

BLASTX Method NCBI GI g3668086

```
150
BLAST score
                  5.0e-10
E value
                  42
Match length
% identity
                  64
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                  305122
Seq. No.
                  rvt700551304.hl
Seq. ID
                  BLASTX
Method
                  g4538903
NCBI GI
                  303
BLAST score
                   6.0e-28
E value
                   63
Match length
```

% identity (AL049482) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. rvt700551311.h1 Seq. ID BLASTX Method q4539665 NCBI GI 343

86

305123

BLAST score 1.0e-32 E value Match length 83 % identity 69

(AF061282) polyprotein [Sorghum bicolor] NCBI Description

305124 Seq. No.

rvt700551320.hl Seq. ID

Method BLASTX g2160185 NCBI GI 386 BLAST score 1.0e-37 E value 90 Match length 76 % identity

(ACO00132) Similar to S. pombe ISP4 (gb_D83992). NCBI Description

[Arabidopsis thaliana]

305125 Seq. No.

rvt700551346.h1 Seq. ID

BLASTX Method NCBI GI q3935149 BLAST score 171 1.0e-12 E value Match length 89 39 % identity

(AC005106) T25N20.13 [Arabidopsis thaliana] NCBI Description

305126 Seq. No.

rvt700551357.h1 Seq. ID

Method BLASTX NCBI GI q2661179 BLAST score 333 E value 2.0e-31 Match length 88 70 % identity

NCBI Description (U80984) AtZW10 [Arabidopsis thaliana]



```
305127
Seq. No.
                  rvt700551387.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g507844
BLAST score
                  44
                  1.0e-15
E value
Match length
                  80
                  89
% identity
                  Zea mays A188 retrotransposon gag gene, complete cds
NCBI Description
                   305128
Seq. No.
                   rvt700551396.h1
Seq. ID
Method
                  BLASTX
                   g3548810
NCBI GI
BLAST score
                   230
E value
                   3.0e-22
Match length
                   88
% identity
                   57
                  (AC005313) putative chloroplast nucleoid DNA binding
NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   305129
                   rvt700551414.hl
Seq. ID
                   BLASTX
Method
                   g3228517
NCBI GI
BLAST score
                   213
E value
                   2.0e-17
Match length
                   74
                   58
% identity
                   (AF007788) ETTIN [Arabidopsis thaliana]
NCBI Description
                   305130
Seq. No.
                   rvt700551436.h1
Seq. ID
                   BLASTX
Method
                   g3702121
NCBI GI
                   298
BLAST score
                   2.0e-27
E value
                   83
Match length
                   67
% identity
                   (AJ011681) retinoblastoma-related protein [Chenopodium
NCBI Description
                   rubrum]
                   305131
Seq. No.
                   rvt700551539.h1
Seq. ID
                   BLASTX
Method
                   g3738329
NCBI GI
                   242
BLAST score
                   5.0e-34
E value
                   89
Match length
                   86
% identity
                  (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
```

305132 Seq. No. rvt700551555.hl Seq. ID

BLASTN Method NCBI GI g2104907

BLAST score 46

```
E value 4.0e-17
Match length 74
% identity 92
```

NCBI Description Z.mays mRNA for potassium channel

Seq. No. 305133

Seq. ID rvt700551689.h1

Method BLASTN
NCBI GI g4416300
BLAST score 34
E value 9.0e-10
Match length 58
% identity 90

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 305134

Seq. ID rvt700551725.h1

Method BLASTX
NCBI GI g4206197
BLAST score 402
E value 2.0e-39
Match length 92
% identity 83

NCBI Description (AF071527) putative pre-mRNA splicing factor [Arabidopsis

thaliana]

Seq. No. 305135

Seq. ID rvt700551730.h1

Method BLASTX
NCBI GI 94314358
BLAST score 267
E value 1.0e-23
Match length 71
% identity 73

NCBI Description (AC006340) putative kinesin heavy chain protein

[Arabidopsis thaliana]

Seq. No. 305136

Seq. ID rvt700551735.h1

Method BLASTN
NCBI GI g22484
BLAST score 56
E value 4.0e-23
Match length 56
% identity 100

NCBI Description Z.mays RNA for superoxide dismutase Sod4A

Seq. No.

305137

Seq. ID rvt700551738.hl

Method BLASTX
NCBI GI g2342679
BLAST score 225
E value 9.0e-19
Match length 78
% identity 53

NCBI Description (AC000106) Similar to Vicia sativa ENBP1 (gb_X95995).



[Arabidopsis thaliana]

```
Seq. No.
                  305138
Seq. ID
                  rvt700551761.hl
Method
                  BLASTX
NCBI GI
                  q2832661
BLAST score
                  152
E value
                  2.0e-10
Match length
                  69
                  59
% identity
                  (AL021710) pherophorin - like protein [Arabidopsis
NCBI Description
                  thaliana]
                  305139
Seq. No.
Seq. ID
                  rvt700551779.h1
Method
                  BLASTX
NCBI GI
                  g3915826
BLAST score
                  239
E value
                   2.0e-20
Match length
                   58
                   84
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
                   305140
Seq. No.
Seq. ID
                   rvt700551783.h1
Method
                   BLASTX
NCBI GI
                   q4056502
BLAST score
                   221
E value
                   2.0e-18
Match length
                   70
% identity
                   63
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
                   305141
Seq. No.
                   rvt700551785.h1
Seq. ID
                   BLASTX
Method
                   g1169528
NCBI GI
                   259
BLAST score
                   5.0e-26
E value
Match length
                   75
% identity
                   91
                   ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973)
                   enolase [Zea mays]
                   305142
Seq. No.
                   rvt700551802.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2911072
BLAST score
                   222
                   2.0e-18
E value
                   70
Match length
% identity
                   63
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 305143
Seq. ID rvt700551852.h1

```
BLASTX
Method
                    g283051
NCBI GI
                    262
BLAST score
                    4.0e-23
E value
                    72
Match length
                    67
% identity
                   RNA-directed DNA polymerase (EC 2.7.7.49) - maize
NCBI Description
                    transposon (fragment)
                    305144
Seq. No.
                    rvt700551976.h1
Seq. ID
                    BLASTX
Method
                    g1431629
NCBI GI
BLAST score
                    354
                    6.0e - 34
E value
Match length
                    88
                    69
% identity
                    (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                    305145
Seq. No.
                    rvt700551979.hl
Seq. ID
                    BLASTX
Method
                    q134598
NCBI GI
                    244
BLAST score
                    5.0e-21
E value
Match length
                    47
                    100
% identity
                    SUPEROXIDE DISMUTASE-4AP (CU-ZN)
NCBI Description
                    305146
Seq. No.
                    rvt700552009.h1
Seq. ID
                    BLASTX
Method
                    g115577
NCBI GI
                    297
BLAST score
                    2.0e-41
E value
Match length
                    92
% identity
                    98
                    PHOSPHOENOLPYRUVATE CARBOXYLASE, HOUSEKEEPING ISOZYME
NCBI Description
                    (PEPCASE) >gi_348536_pir_S28614 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - sugarcane hybrid H32-8560
                    >qi 169844 (M86661) phosphoenolpyruvate carboxylase
                    [Saccharum sp.]
                    305147
 Seq. No.
                    rvt700552018.h1
 Seq. ID
Method
                    BLASTN
NCBI GI
                    g609289
 BLAST score
                    59
                    7.0e-25
 E value
Match length
                    145
 % identity
                    93
                    Z.mays cultivar (LG11) ROA mRNA for replication origin
 NCBI Description
                    activator protein
```

305148 Seq. No.

rvt700552033.h1 Seq. ID

Method BLASTX

BLAST score

Match length

E value

166

45

7.0e-12

```
g3868800
NCBI GI
                  278
BLAST score
                  6.0e-25
E value
Match length
                  86
% identity
                  62
                  (AB013603) topoisomerase III beta [Mus musculus]
NCBI Description
                  305149
Seq. No.
Seq. ID
                  rvt700552070.h1
Method
                  BLASTX
NCBI GI
                  g2583120
BLAST score
                  156
E value
                   2.0e-13
Match length
                  82
                   51
% identity
                   (AC002387) putative receptor-like protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   305150
Seq. No.
Seq. ID
                   rvt700552086.hl
                   BLASTX
Method
NCBI GI
                   q4056502
BLAST score
                   175
                   6.0e-21
E value
                   80
Match length
% identity
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
                   305151
Seq. No.
                   rvt700552118.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076634
BLAST score
                   251
                   8.0e-22
E value
Match length
                   92
% identity
                   51
                   protein-serine/threonine kinase NPK15 - common tobacco
NCBI Description
                   >gi_505146_dbj_BAA06538_ (D31737) protein-serine/threonine
                   kinase [Nicotiana tabacum]
                   305152
Seq. No.
                   rvt700552168.hl
Seq. ID
                   BLASTX
Method
                   g2842485
NCBI GI
                   162
BLAST score
                   2.0e-11
E value
Match length
                   42
                   67
% identity
                  (AL021749) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   305153
Seq. No.
                   rvt700552188.h1
Seq. ID
Method
                   BLASTX
                   g3319355
NCBI GI
```



% identity (AF077407) similar to chaperonin containing TCP-1 complex NCBI Description gamma chain [Arabidopsis thaliana] 305154 Seq. No. rvt700552217.h1 Seq. ID BLASTX Method g2497539 NCBI GI 138 BLAST score 8.0e-09 E value 37 Match length 81 % identity NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703 (M64736) ATP:pyruvate phosphotransferase [Ricinus communis] 305155 Seq. No. rvt700552236.h1 Seq. ID BLASTX Method q3645898 NCBI GI 514 BLAST score 1.0e-52 E value 95 Match length 98 % identity (U68408) in-frame stop codon; possibly a post-transposition NCBI Description mutation [Zea mays] 305156 Seq. No. rvt700552275.h1 Seq. ID BLASTN Method g1617470 NCBI GI BLAST score 94 2.0e-45 E value 153 Match length 14 % identity NCBI Description Z.diploperennis DNA for Grandel-4 retrotransposon 305157 Seq. No. rvt700552293.h1 Seq. ID BLASTX Method g4038056 NCBI GI BLAST score 153 6.0e-19 E value 93 Match length 53 % identity (AC005897) putative transposon [Arabidopsis thaliana] NCBI Description

305158 Seq. No.

rvt700552318.h1 Seq. ID

BLASTX Method q1845197 NCBI GI BLAST score 163 2.0e-11 E value 31 Match length 100 % identity

(Y08298) HMGc2 [Zea mays] NCBI Description

305159 Seq. No.

```
rvt700552369.h1
Seq. ID
                  BLASTX
Method
                  g3914899
NCBI GI
                  350
BLAST score
                  2.0e-33
E value
                  67
Match length
                  100
% identity
                  40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal
NCBI Description
                  protein S4 type I [Zea mays]
                  305160
Seq. No.
                  rvt700552370.h1
Seq. ID
                  BLASTX
Method
                  g2129472
NCBI GI
BLAST score
                  252
                  5.0e-22
E value
                  90
Match length
                   62
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
NCBI Description
                  precursor - Scotch pine >gi_1100225 (L32561)
                   glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
                   305161
Seq. No.
                   rvt700552417.h1
Seq. ID
                   BLASTN
Method
                   q3694836
NCBI GI
                   158
BLAST score
                   6.0e-84
E value
                   166
Match length
                   99
% identity
                   Zea mays centromeric retrotransposon-like repeat CentA,
NCBI Description
                   complete sequence
                   305162
Seq. No.
                   rvt700552434.h1
Seq. ID
                   BLASTX
Method
                   g1363528
NCBI GI
BLAST score
                   164
                   7.0e-12
E value
                   32
Match length
% identity
                   94
                   gag protein - maize >gi_507845 (U11059) gag gene product
NCBI Description
                   [Zea mays]
                   305163
Seq. No.
                   rvt700552495.h1
Seq. ID
                   BLASTN
Method
                   g829147
NCBI GI
BLAST score
                   35
                   2.0e-10
E value
Match length
                   39
                   97
% identity
NCBI Description Z.mays gene for cyclophilin
```

Method BLASTX

Seq. No.

Seq. ID

305164

rvt700552571.h1



```
g4104931
NCBI GI
                    154
BLAST score
                    9.0e-11
E value
Match length
                    33
% identity
                    85
                    (AF042196) auxin response factor 8 [Arabidopsis thaliana]
NCBI Description
                    305165
Seq. No.
                    rvt700552629.hl
Seq. ID
                    BLASTN
Method
                    q886739
NCBI GI
                    59
BLAST score
                    6.0e-25
E value
                    150
Match length
                    88
% identity
NCBI Description Z.mays histone H4 gene
                    305166
Seq. No.
Seq. ID
                    rvt700552686.h1
                    BLASTX
Method
                    g4506613
NCBI GI
BLAST score
                    165
                    8.0e-12
E value
                    52
Match length
% identity
                    69
                    ribosomal protein L22 >gi_464628_sp_P35268_RL22_HUMAN 60S
NCBI Description
                    RIBOSOMAL PROTEIN L22 (EPSTEIN-BARR VIRUS SMALL RNA
                    ASSOCIATED PROTEIN) (EBER ASSOCIATED PROTEIN) (EAP)
                     (HEPARIN BINDING PROTEIN HBP15) >gi_542841_pir__JC2120
                    heparin-binding protein 15 - human >gi_31062_emb_CAA42007_(X59357) Epstein-Barr virus small RNA associated protein [Homo sapiens] >gi_409070_dbj_BAA04545_ (D17652) HBp15/L22
                     [Homo sapiens]
                     305167
Seq. No.
                     rvt700552687.h1
Seq. ID
                    BLASTX
Method
                     g629592
NCBI GI
                     204
BLAST score
                     2.0e-16
E value
                     51
Match length
                     75
% identity
NCBI Description hypothetical protein - rape
                     305168
Seq. No.
                     rvt700552725.h1
Seq. ID
                     BLASTX
Method
                     q2959712
NCBI GI
BLAST score
                     220
                     1.0e-34
E value
Match length
                     89
                     79
 % identity
 NCBI Description (AF052206) cyclophilin 1 [Chlamydomonas reinhardtii]
```

305169

Seq. No. rvt700552790.h1 Seq. ID

BLASTX Method



q118104 NCBI GI BLAST score 332 E value 2.0e-31 72 Match length 90 % identity

PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) NCBI Description

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408 pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -

maize >gi_168461 (M55021) cyclophilin [Zea mays]

>gi 829148 emb_CAA48638_ (X68678) cyclophilin [Zea mays]

305170 Seq. No.

rvt700552817.hl Seq. ID

Method BLASTN g4416300 NCBI GI 87 BLAST score 1.0e-41 E value 135 Match length 91 % identity

Zea mays chromosome 4 22 kDa zein-associated intercluster NCBI Description

region, complete sequence

305171 Seq. No.

rvt700552831.hl Seq. ID

Method BLASTX NCBI GI g4008156 152 BLAST score 3.0e-10 E value Match length 33 85 % identity

NCBI Description (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]

305172 Seq. No.

rvt700552839.h1 Seq. ID BLASTN Method

NCBI GI q4416300 BLAST score 38 E value 4.0e-12 80 Match length % identity 89

Zea mays chromosome 4 22 kDa zein-associated intercluster NCBI Description

region, complete sequence

305173 Seq. No.

rvt700552840.h1 Seq. ID

Method BLASTX NCBI GI g553075 BLAST score 278 E value 4.0e-25 Match length 74 % identity

NCBI Description (L08591) alcohol dehydrogenase 1 [Zea mays]

Seq. No. 305174

rvt700552843.h1 Seq. ID

BLASTN Method g3851000 NCBI GI



```
BLAST score
E value
                  1.0e-100
                  189
Match length
                  99
% identity
                  Zea mays pyruvate dehydrogenase El beta subunit isoform 2
NCBI Description
                  mRNA, nuclear gene encoding mitochondrial protein, complete
                  305175
Seq. No.
                  rvt700552927.h1
Seq. ID
                  BLASTX
Method
                  g4138592
NCBI GI
                   222
BLAST score
                   2.0e-18
E value
                   69
Match length
                   58
% identity
                  (AJ005840) thioredoxin M [Triticum aestivum]
NCBI Description
                   305176
Seq. No.
                   rvt700552941.h1
Seq. ID
                   BLASTX
Method
                   g2262105
NCBI GI
                   215
BLAST score
                   7.0e-18
E value
Match length .
                   61
                   62
% identity
                   (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
                   305177
Seq. No.
                   rvt700552946.hl
Seq. ID
                   BLASTX
Method
                   g3831440
NCBI GI
                   269
BLAST score
                   6.0e-26
E value
Match length
                   90
                   57
% identity
                   (AC005819) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   >gi_4415946_gb_AAD20176_ (AC006418) putative cytochrome
                   P450 [Arabidopsis thaliana]
                   305178
Seq. No.
                   rvt700553055.h1
Seq. ID
                   BLASTX
Method
                   q2196672
NCBI GI
BLAST score
                   378
                   1.0e-36
E value
                   74
Match length
                   97
% identity
NCBI Description
                  (Y08807) HMGd1 [Zea mays]
```

Seq. No. 305179

Seq. ID rvt700553067.h1

Method BLASTX
NCBI GI g516554
BLAST score 221
E value 1.0e-18
Match length 49

% identity

99

NCBI Déscription (AJ224327) aquaporin [Oryza sativa]



```
% identity
NCBI Description (U10079) cyclin IaZm [Zea mays]
                  305180
Seq. No.
                  rvt700553155.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1532168
                  218
BLAST score
                  3.0e-18
E value
                  59
Match length
                  69
% identity
                  (U63815) localized according to blastn similarity to EST
NCBI Description
                  sequences; therefore, the coding span corresponds only to
                  an area of similarity since the initation codon and stop
                  codon could not be precisely determined [Arabidopsis
                  thaliana]
                  305181
Seq. No.
                  rvt700553163.h1
Seq. ID
                  BLASTN
Method
                  g3132824
NCBI GI
                  39
BLAST score
                  6.0e-13
E value
                  39
Match length
                  100
% identity
                  Zea mays putative cytosine-5 DNA methyltransferase (ZMET1)
NCBI Description
                  gene, complete cds
                  305182
Seq. No.
                  rvt700553171.h1
Seq. ID
                  BLASTX
Method
                  g3764029
NCBI GI
                  141
BLAST score
                   2.0e-14
E value
Match length
                   64
                   58
% identity
NCBI Description (AB001995) Tellp [Schizosaccharomyces pombe]
                   305183
Seq. No.
                   rvt700553173.h1
Seq. ID
                   BLASTX
Method
                   g3080374
NCBI GI
                   143
BLAST score
                                    ×
                   3.0e-09
E value
Match length
                   84
                   28
% identity
NCBI Description (AL022580) putative protein [Arabidopsis thaliana]
                   305184
Seq. No.
                   rvt700553229.h1
Seq. ID
Method
                   BLASTX
                   q2894534
NCBI GI
                   403
BLAST score
                   1.0e-39
E value
Match length
                   77
```



```
Seq. No.
                      305185
   Seq. ID
                      rvt700553309.h1
   Method
                      BLASTX
   NCBI GI
                      g3122914
                      245
   BLAST score
   E value
                      2.0e-21
   Match length
                      51
                      90
% identity
   NCBI Description
                      VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)
                      >gi_1890130 (U89986) valyl tRNA synthetase [Arabidopsis
                      thaliana]
                      305186
   Seq. No.
                      rvt700553328.hl
    Seq. ID
   Method
                      BLASTX
                      g2673914
   NCBI GI
   BLAST score
                      173
                      1.0e-12
   E value
   Match length
                      50
    % identity
                      56
   NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]
    Seq. No.
                      305187
                      rvt700553367.hl
    Seq. ID
    Method
                      BLASTN
                      q500854
    NCBI GI
                      72
    BLAST score
    E value
                      1.0e-32
                      133
    Match length
                      89
    % identity
    NCBI Description Maize dissociation element DNA
    Seq. No.
                      305188
    Seq. ID
                      rvt700553369.h1
    Method
                      BLASTX
    NCBI GI
                      q121982
    BLAST score
                      176
    E value
                      4.0e-13
    Match length
                      35
    % identity
                      97
    NCBI Description HISTONE H2A.2.2
    Seq. No.
                      305189
                      rvt700553380.h1
    Seq. ID
                      BLASTX
    Method
    NCBI GI
                      g2384671
    BLAST score
                      324
                      2.0e-30
    E value
                      77
    Match length
    % identity
                      81
                      (AF012657) putative potassium transporter AtKT2p
    NCBI Description
                       [Arabidopsis thaliana]
```

305190 Seq. No. Seq. ID rvt700553383.h1

BLASTX Method



```
g3327389
NCBI GI
                  143
BLAST score
                  3.0e-09
E value
Match length
                   35
                   83
% identity
                   (AC004483) putative DNA replication licensing factor, mcm5
NCBI Description
                   [Arabidopsis thaliana]
                   305191
Seq. No.
                   rvt700553419.h1
Seq. ID
                   BLASTX
Method
                   g4539660
NCBI GI
                   362
BLAST score
                   9.0e-35
E value
                   97
Match length
                   72
% identity
                   (AF061282) polyprotein [Sorghum bicolor]
NCBI Description
                   305192
Seq. No.
                   rvt700553434.h1
Seq. ID
Method
                   BLASTX
                   q4587599
NCBI GI
BLAST score
                   273
                   1.0e-30
E value
Match length
                   89
                   78
% identity
                   (AC006951) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   305193
                   rvt700553455.h1
Seq. ID
                   BLASTN
Method
                   g22245
NCBI GI
                   40
BLAST score
                   3.0e-13
E value
                   132
Match length
                   83
% identity
                   Zea mays DNA for cin4 element (showing homology to reverse
NCBI Description
                   transcriptase)
                   305194
Seq. No.
                   rvt700553466.hl
Seq. ID
                   BLASTN
Method
                   g1707641
NCBI GI
                   78
BLAST score
                   3.0e-36
E value
                   102
Match length
                   94
% identity
                   O.sativa mRNA for leucine rich repeat receptor-like kinase
NCBI Description
                   305195
Seq. No.
                   sem700930108.h1
Seq. ID
                   BLASTX
Method
                   q2104313
NCBI GI
                   188
BLAST score
E value
                   2.0e-14
Match length
                    77
```

51

% identity



```
(Z95388) hypothetical protein Rv2165c [Mycobacterium
 NCBI Description
                      tuberculosis]
                      305196
  Seq. No.
                      sem700930139.hl
  Seq. ID
                      BLASTX
 Method
                      g2654192
 NCBI GI
 BLAST score
                      235
                      5.0e-20
  E value
                      85
  Match length
  % identity
                      58
                     (AF035177) GTP-binding protein [Oncorhynchus tshawytsha]
  NCBI Description
                      305197
  Seq. No.
                      sem700930156.hl
  Seq. ID
  Method
                      BLASTX
  NCBI GI
                      q2194123
  BLAST score
                      175
                      6.0e-13
  E value
                      48
  Match length
  % identity
                      (AC002062) Similar to Secale chloroplast ribosomal protein
  NCBI Description
                      L12 (gb_SCL121A). EST gb_H36579 comes from this gene.
                      [Arabidopsis thaliana]
                      305198
  Seq. No.
                      sem700930201.h1
  Seq. ID
                      BLASTX
  Method
                      q464524
  NCBI GI
  BLAST score
                      245
                      4.0e-21
  E value
                      58
  Match length
  % identity
                      83
                      RAS-RELATED PROTEIN RAB-1A >gi_345404_pir__S32206 RAB1 protein - great pond snail >gi_481217_pir__S38339 rab1 protein - great pond snail >gi_288934_emb_CAA51233_
  NCBI Description
54
                       (X72688) RAB1 [Lymnaea stagnalis]
                       305199
  Seq. No.
                       sem700930240.hl
  Seq. ID
                      BLASTN
  Method
                       g2292903
  NCBI GI
                       135
  BLAST score
                       3.0e-70
  E value
                       170
  Match length
                       96
  % identity
  NCBI Description H.sapiens GalNAc-T1 gene, 3'UTR
                       305200
   Seq. No.
                       sem700930246.h1
   Seq. ID
                       BLASTX
  Method
                       a3242709
  NCBI GI
   BLAST score
                       149
                       2.0e-10
   E value
                       61
  Match length
   % identity
                       64
   NCBI Description (AC003040) putative guanine nucleotide-binding protein
```

Seq. No. Seq. ID



[Arabidopsis thaliana]

```
305201
Seq. No.
                  sz1700184945.h1
Seq. ID
Method
                  BLASTX
                  q531389
NCBI GI
                  158
BLAST score
                  4.0e-13
E value
                  58
Match length
% identity
                  66
                  (U12626) copia-like retrotransposon Hopscotch polyprotein
NCBI Description
                   [Zea mays]
                  305202
Seq. No.
Seq. ID
                  tbg700930477.hl
Method
                  BLASTX
                  g4309759
NCBI GI
BLAST score
                  276
                  7.0e-25
E value
Match length
                  82
                  71
% identity
                   (AC006217) unknown protein with Src homology 3 (SH3) domain
NCBI Description
                  profile (PDOC50002) [Arabidopsis thaliana]
                   305203
Seq. No.
Seq. ID
                   tfd700569115.h1
Method
                   BLASTX
NCBI GI
                   g2160170
BLAST score
                   313
                   4.0e-29
E value
Match length
                   90
% identity
                   72
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   305204
Seq. No.
                   tfd700569125.h1
Seq. ID
Method
                   BLASTN
                   g257040
NCBI GI
                   157
BLAST score
                   4.0e-83
E value
                   278
Match length
% identity
                   20
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
                   305205
Seq. No.
                   tfd700569133.h1
Seq. ID
                   BLASTX
Method
                   g4115534
NCBI GI
                   155
BLAST score
                   7.0e-11
E value
Match length
                   43
% identity
                   60
                   (AB012114) UDP-glycose:flavonoid glycosyltransferase [Vigna
NCBI Description
                   mungo]
                   305206
```

tfd700569138.h1



```
BLASTX
Method
                  g3687224
NCBI GI
                  223
BLAST score
                  1.0e-18
E value
Match length
                  63
                  71
% identity
                   (AC005169) putative N-acetyl-gamma-glutamyl-phosphate
NCBI Description
                  reductase [Arabidopsis thaliana]
                  305207
Seq. No.
                  tfd700569151.hl
Seq. ID
                  BLASTX
Method
                  q122022
NCBI GI
                  297
BLAST score
E value
                   3.0e-27
Match length
                   69
                   90
% identity
                  HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat
NCBI Description
                   >gi 21801_emb_CAA42530_ (X59873) histone H2B [Triticum
                   aestivum]
                   305208
Seq. No.
                   tfd700569152.h1
Seq. ID
                   BLASTX
Method
                   g2316016
NCBI GI
BLAST score
                   323
                  -3.0e-30
E value
Match length
                   93
                   70
% identity
                  (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
NCBI Description
                   305209
Seq. No.
                   tfd700569274.h2
Seq. ID
                   BLASTX
Method
                   g1170619
NCBI GI
                   155
BLAST score
                   8.0e-21
E value
                   76
Match length
                   75
% identity
                  KINESIN-LIKE PROTEIN A >gi 479594 pir S34830
NCBI Description
                   kinesin-related protein katA - Arabidopsis thaliana
                   >gi_303502_dbj_BAA01972_ (D11371) kinesin-like motor
                   protein heavy chain [Arabidopsis thaliana]
                   >gi 2911084_emb_CAA17546.1_ (AL021960) kinesin-related
                   protein katA [Arabidopsis thaliana]
                   305210
Seq. No.
                   tfd700569304.h1
 Seq. ID
                   BLASTX
Method
                   g514324
NCBI GI
                   302
BLAST score
                   7.0e-28
 E value
Match length
                   85
                   72
 % identity
                   (L34773) RNA polymerase subunit [Arabidopsis thaliana]
 NCBI Description
                   >gi 2462755 (AC002292) RNA polymerase subunit (isoform B)
```

[Arabidopsis thaliana] >gi_1586550_prf__2204246B RNA



polymerase [Arabidopsis thaliana]

```
305211
Seq. No.
                  tfd700569444.h2
Seq. ID
                  BLASTX
Method
                  g1256259
NCBI GI
BLAST score
                  142
                  3.0e-09
E value
                  33
Match length
                  79
% identity
                  (U50900) voltage-dependent anion channel protein [Spinacia
NCBI Description
                  oleracea]
                  305212
Seq. No.
                  tfd700569445.h2
Seq. ID
                  BLASTX
Method
                  g3860272
NCBI GI
                  293
BLAST score
                  7.0e-27
E value
                   68
Match length
                  79
% identity
                   (AC005824) putative suppressor protein [Arabidopsis
NCBI Description
                  thaliana] >gi 4314399 gb_AAD15609_ (AC006232) putative skd1
                  protein [Arabidopsis thaliana]
Seq. No.
                   305213
                   tfd700569460.h2
Seq. ID
                   BLASTX
Method
                   g3281853
NCBI GI
BLAST score
                   176
                   3.0e-13
E value
                   44
Match length
                   77
% identity
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   305214
Seq. No.
                   tfd700569478.h2
Seq. ID
                   BLASTN
Method
                   q4416300
NCBI GI
BLAST score
                   193
                   1.0e-104
E value
                   234
Match length
                   95
% identity
                   Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
                   305215
Seq. No.
                   tfd700569481.h2
Seq. ID
Method
                   BLASTX
                   q4455356
NCBI GI
BLAST score
                   325
                   1.0e-30
E value
                   78
Match length
                   77
% identity
                  (AL035524) putative protein [Arabidopsis thaliana]
```

Seq. No. 305216

NCBI Description

```
tfd700569585.h1
Seq. ID
Method
                  BLASTN
                  q1262139
NCBI GI
BLAST score
                  207
                  1.0e-113
E value
Match length
                  324
                  99
% identity
NCBI Description S.cerevisiae 130kb DNA fragment from chromosome XV
                  305217
Seq. No.
                  tfd700569850.h1
Seq. ID
                  BLASTX
Method
                  g4107276
NCBI GI
BLAST score
                  332
                  4.0e-31
E value
                  112
Match length
                  58
% identity
                  (X98506) acetyl-CoA synthetase [Solanum tuberosum]
NCBI Description
                  305218
Seq. No.
                  tfd700569943.h1
Seq. ID
                  BLASTN
Method
                  g3449327
NCBI GI
BLAST score
                  33
E value
                  2.0e-09
Match length
                  69
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCA23, complete sequence [Arabidopsis thaliana]
                  305219
Seq. No.
                  tfd700569967.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352081
                  256
BLAST score
E value
                  1.0e-22
Match length
                   60
                   77
% identity
                  BETA-GLUCOSIDASE, CHLOROPLAST PRECURSOR (GENTIOBIASE)
NCBI Description
                   (CELLOBIASE) (BETA-D-GLUCOSIDE GLUCOHYDROLASE) >gi_799377
                   (U25157) beta-D-glucosidase [Zea mays] >gi 1399390 (U44773)
                  beta-D-glucosidase [Zea mays] >gi_4096602 (U33816)
                  beta-D-glucosidase [Zea mays]
                   305220
Seq. No.
                   tfd700570071.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g567121
```

Method BLASTX
NCBI GI g567121
BLAST score 244
E value 3.0e-21
Match length 57
% identity 88

NCBI Description (M34024) immunoglobulin heavy chain [Homo sapiens]

Seq. No. 305221

Seq. ID tfd700570091.h1

Method BLASTN

E value

Match length

% identity

3.0e-20

105



```
g3970933
NCBI GI
                  102
BLAST score
                  2.0e-50
E value
                  164
Match length
                  92
% identity
                  Homo sapiens chromosome 19, cosmid F6697, complete sequence
NCBI Description
                  [Homo sapiens]
                  305222
Seq. No.
                  tfd700570104.h1
Seq. ID
                  BLASTN
Method
                  g13595
NCBI GI
                  46
BLAST score
                  4.0e-17
E value
Match length
                  46
                  100
% identity
NCBI Description Yeast mitochondrial transfer RNA-Ile(gau)
                  305223
Seq. No.
                  tfd700570125.h1
Seq. ID
Method
                  BLASTX
                  g2688830
NCBI GI
                  222
BLAST score
                  2.0e-18
E value
Match length
                   62
                  76
% identity
                  (AF000952) putative sugar transporter [Prunus armeniaca]
NCBI Description
                   305224
Seq. No.
                   tfd700570129.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g478685
BLAST score
                   162
                   3.0e-16
E value
Match length
                   103
                   60
% identity
                   inter-alpha-trypsin inhibitor heavy chain H1 precursor -
NCBI Description
                   human
Seq. No.
                   305225
Seq. ID
                   tfd700570148.h1
                   BLASTX
Method
                   g4406808
NCBI GI
                   184
BLAST score
E value
                   8.0e-14
                   40
Match length
% identity
                   (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
                   305226
Seq. No.
                   tfd700570183.h1
Seq. ID
Method
                   BLASTX
                   q4455323
NCBI GI
BLAST score
                   239
```



NCBI Description (AL035525) aminopeptidase-like protein [Arabidopsis

thaliana]

Seq. No. 305227

Seq. ID tfd700570218.h1

Method BLASTN
NCBI GI g2393736
BLAST score 133
E value 9.0e-69
Match length 144
% identity 98

NCBI Description Human BAC clone GS025M02 from 7q21-q22, complete sequence

[Homo sapiens]

Seq. No. 305228

Seq. ID tfd700570278.h1

Method BLASTX
NCBI GI g3935157
BLAST score 164
E value 1.0e-11
Match length 29
% identity 90

NCBI Description (AC005106) T25N20.21 [Arabidopsis thaliana]

Seq. No. 305229

Seq. ID tfd700570445.h1

Method BLASTX
NCBI GI g4559380
BLAST score 159
E value 3.0e-15
Match length 88
% identity 52

NCBI Description (AC006526) putative auxin-responsive GH3 protein

[Arabidopsis thaliana]

Seq. No. 305230

Seq. ID tfd700570492.h1

Method BLASTX
NCBI GI g4063736
BLAST score 336
E value 1.0e-31
Match length 97
% identity 72

NCBI Description (AC006258) cyclin 3a [Arabidopsis thaliana]

Seq. No. 305231

Seq. ID tfd700570538.h1

Method BLASTX
NCBI GI g82734
BLAST score 360
E value 2.0e-34
Match length 72
% identity 30

NCBI Description ubiquitin precursor - maize (fragment)

>gi_226763_prf__1604470A poly-ubiquitin [Zea mays]

Seq. No. 305232



```
Seq. ID
                  tfd700570539.h1
Method
                  BLASTX .
NCBI GI
                  q3746071
BLAST score
                  225
                  2.0e-20
E value
Match length
% identity
                  54
                  (AC005311) putative GTP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  305233
Seq. No.
Seq. ID
                  tfd700570583.hl
Method
                  BLASTX
NCBI GI
                  q119150
                  307
BLAST score
                  2.0e-28
E value
Match length
                  95
                  73
% identity
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi_82081_pir__S10507 translation elongation factor eEF-1
                  alpha chain - tomato >gi_19273_emb_CAA32618 (X14449) EF
                  1-alpha (AA 1-448) [Lycopersicon esculentum]
                  >gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha
                  [Lycopersicon esculentum]
Seq. No.
                  305234
                  tfd700570618.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629839
                  230
BLAST score
                  2.0e-19
E value
Match length
                  43
% identity
NCBI Description beta-6 tubulin - maize >gi_416147 (L10633) beta-6 tubulin
                  [Zea mays]
Seq. No.
                  305235
Seq. ID
                  tfd700570694.h1
Method
                  BLASTX
NCBI GI
                  q2149051
BLAST score
                  285
                  6.0e-26
E value
Match length
                  75
% identity
                  73
NCBI Description
                  (U73810) small Ras-like GTP-binding protein [Arabidopsis
                  thaliana]
                  305236
Seq. No.
Seq. ID
                  tfd700570713.h1
Method
                  BLASTX
NCBI GI
                  g3702966
BLAST score
                  324
```

Method BLASTX
NCBI GI g3702966
BLAST score 324
E value 3.0e-37
Match length 109
% identity 76

NCBI Description (AF079486) rac GTP binding protein Arac8 [Arabidopsis

thaliana]

Seq. ID

NCBI GI

Method



```
Seq. No.
                   305237
Seq. ID
                   tfd700570736.h1
Method
                  BLASTX
NCBI GI
                  g3925233
BLAST score
                  381
E value
                  7.0e-37
Match length
                  92
% identity
NCBI Description
                  (AF037034) putative peroxidase P7X [Zea mays]
                  305238
Seq. No.
                  tfd700570751.hl
Seq. ID
Method
                  BLASTX
                  g2459446
NCBI GI
BLAST score
                  197
                   2.0e-15
E value
Match length
                  91
% identity
                   45
                  (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
                   305239
Seq. No.
Seq. ID
                   tfd700570814.h1
Method
                  BLASTX
NCBI GI
                  q1332579
BLAST score
                   144
E value
                   4.0e-22
Match length
                  87
% identity
                   9
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                   305240
Seq. No.
Seq. ID
                   tfd700570830.h1
                  BLASTX
Method
NCBI GI
                   g134598
BLAST score
                   232
E value
                   2.0e-19
Match length
                   46
                   93
% identity
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)
Seq. No.
                   305241
Seq. ID
                   tfd700570883.hl
Method
                   BLASTN
NCBI GI
                   q806807
BLAST score
                   34
E value
                   3.0e-10
Match length
                   62
% identity
                   89
NCBI Description
                  Pisum sativum chaperonin precursor mRNA, chloroplast gene
                   encoding chloroplast protein, complete cds
Seq. No.
                   305242
```

tfd700570915.h1

BLASTN

g4505120



```
BLAST score
E value
                  7.0e-69
                  190
Match length
                  94
% identity
                  Homo sapiens methyl-CpG binding domain protein 4 (MBD4)
NCBI Description
                  mRNA, and translated products
                  >gi 3800808 gb AF072250 AF072250 Homo sapiens methyl-CpG
                  binding protein MBD4 (MBD4) mRNA, complete cds
                  305243
Seq. No.
                  tfd700570940.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q111159
BLAST score
                  167
E value
                  3.0e-12
                  36
Match length
                  81
% identity
NCBI Description TPA-induced protein 11B - mouse
Seq. No.
                  305244
                  tfd700570943.h1
Seq. ID
Method
                  BLASTN
                  g3820976
NCBI GI
BLAST score
                  42
E value
                  1.0e-14
Match length
                  54
                  94
% identity
                  Human DNA sequence from clone 101G11 on chromosome 22q12.
NCBI Description
                  Contains an ACO2 (Mitochondrial Aconitate Hydratase
                  (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene,
                  ESTs, STSs, GSSs and a putative CpG island, complet
                  305245
Seq. No.
                  tfd700570972.h1
Seq. ID
Method
                  BLASTX
                  g1184776
NCBI GI
BLAST score
                  152
E value
                  7.0e-19
Match length
                  53
                  91
% identity
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
Seq. No.
                  305246
Seq. ID
                  tfd700571011.h1
Method
                  BLASTX
NCBI GI
                  g2465923
                  174
BLAST score
                  7.0e-13
E value
```

Match length 78 % identity 47

(AF024648) receptor-like serine/threonine kinase NCBI Description

[Arabidopsis thaliana]

Seq. No. 305247

Seq. ID tfd700571046.h1

BLASTX Method



```
q4079800
NCBI GI
BLAST score
                  390
E value
                  6.0e-38
Match length
                  81
                  93
% identity
                  (AF052503) S-phase-specific ribosomal protein [Oryza
NCBI Description
                  sativa]
                  305248
Seq. No.
                  tfd700571087.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512667
BLAST score
                  218
E value
                  1.0e-21
                  79
Match length
                  66
% identity
                  (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
                  305249
Seq. No.
                  tfd700571161.h1
Seq. ID
Method
                  BLASTX
                  g4468984
NCBI GI
BLAST score
                  169
E value
                  5.0e-12
Match length
                  52
% identity
                  56
                  (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
                  305250
Seq. No.
                  tfd700571163.h1
Seq. ID
Method
                  BLASTX
                  g3080416
NCBI GI
BLAST score
                  189
                  2.0e-14
E value
Match length
                  92
                   45
% identity
NCBI Description
                  (AL022604) UDP-galactose transporter-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   305251
                   tfd700571164.h1
Seq. ID
Method
                  BLASTN
                  g3309085
NCBI GI
BLAST score
                  37
E value
                   2.0e-11
Match length
                   65
% identity
                  Arabidopsis thaliana calcineurin B-like protein 3 (CBL3)
NCBI Description
                  mRNA, complete cds
Seq. No.
                   305252
Seq. ID
                   tfd700571220.h1
Method
                  BLASTN
```

Seq. ID tfd7005712
Method BLASTN
NCBI GI g902585
BLAST score 40
E value 8.0e-14

60

Match length



```
% identity
                  Zea mays clone MubG9 ubiquitin gene, complete cds
NCBI Description
                  305253
Seq. No.
                  tfd700571240.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2997729
BLAST score
                  153
                  3.0e-18
E value
Match length
                  74
```

% identity 72 (AF054511) ribosomal protein S7 [Yarrowia lipolytica] NCBI Description

305254 Seq. No.

tfd700571249.h1 Seq. ID

Method BLASTN q4003386 NCBI GI BLAST score 211 1.0e-115 E value 250 Match length 96 % identity

Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of NCBI Description

hepatocellular colorectal and non-small cell lung cancer,

segment 9/11

Seq. No. 305255

tfd700571272.h1 Seq. ID

Method BLASTX NCBI GI q2190544 427 BLAST score 2.0e-42 E value Match length 91 90 % identity

(ACO01229) Similar to Saccharomyces hypothetical protein NCBI Description

P9642.2 (gb_U40828). [Arabidopsis thaliana]

Seq. No. 305256

Seq. ID tfd700571330.h1

Method BLASTX NCBI GI q3892057 BLAST score 233 E value 1.0e-19 Match length 58 74 % identity

NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No. 305257

Seq. ID tfd700571337.hl

Method BLASTN g507844 NCBI GI 89 BLAST score 2.0e-42 E value Match length 297 % identity 86

NCBI Description Zea mays A188 retrotransposon gag gene, complete cds

Seq. No. 305258

BLAST score

264

```
tfd700571368.hl
Seq. ID
Method
                  BLASTN
                  q3366585
NCBI GI
                  107
BLAST score
                  1.0e-53
E value
Match length
                  139
                  94
% identity
                  Homo sapiens chromosome 17, clone hRPK.1064_E_11, complete
NCBI Description
                  sequence [Homo sapiens]
                  305259
Seq. No.
                  tfd700571433.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3643608
BLAST score
                  176
                  8.0e-13
E value
                  96
Match length
                  40
% identity
                  (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  305260
Seq. No.
                  tfd700571448.hl
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3241922
                  39
BLAST score
E value
                  1.0e-12
Match length
                  67
                  90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MLM24, complete sequence [Arabidopsis thaliana]
                  305261
Seq. No.
                  tfd700571519.h1
Seq. ID
Method
                  BLASTN
                  g398154
NCBI GI
BLAST score
                  67
E value
                   2.0e-29
                   187
Match length
% identity
                   86
                  Rattus norvegicus mRNA for 14-3-3 protein eta-subtype,
NCBI Description
                   complete cds
                   305262
Seq. No.
Seq. ID
                   tfd700571545.h1
Method
                  BLASTN
NCBI GI
                   q535242
BLAST score
                   38
E value
                   4.0e-12
Match length
                   141
                   94
% identity
NCBI Description O.sativa L. (Indica cv.IR24) U3 snRNA gene promoter
                   305263
Seq. No.
                   tfd700571572.h1
Seq. ID
Method
                   BLASTX
                   g91856
NCBI GI
```

```
2.0e-23
E value
Match length
                   55
                   93
% identity
NCBI Description
                   tubulin beta-2 chain - mouse (fragment)
                   305264
Seq. No.
                   tfd700571615.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760325
                   260
BLAST score
                   1.0e-22
E value
                   110
Match length
                   55
% identity
                   (AC002130) F1N21.10 [Arabidopsis thaliana]
NCBI Description
                   305265
Seq. No.
                   tfd700571647.hl
Seq. ID
                   BLASTX
Method
                   g4502131
NCBI GI
BLAST score
                   274
                   2.0e-24
E value
                   116
Match length
% identity
                   67
                   amyloid beta (A4) precursor protein-binding, family B,
NCBI Description
                   member 1 (Fe65) >gi_2734083 (L77864) stat-like protein [Homo sapiens] >gi_3924936 (AF029234) Fe65 protein [Homo
                   sapiens]
                   305266
Seq. No.
                   tfd700571671.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4191791
BLAST score
                   240
                   3.0e-21
E value
Match length
                   109
                    46
% identity
                    (AC005917) putative sf21 {Helianthus annuus} protein
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    305267
                    tfd700571676.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                    q510473
                    282
BLAST score
E value
                    6.0e-29
                    78
Match length
% identity
                    11
NCBI Description
                   (X74405) polyubiquitin [Artemia franciscana]
Seq. No.
                    305268
                    tfd700571692.hl
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2120736
BLAST score
                    143
E value
                    6.0e-13
Match length
                    113
% identity
                    43
```



```
X-Pro dipeptidyl-peptidase (EC 3.4.14.11) - Xanthomonas
NCBI Description
                  maltophilia >gi 1753197 dbj BAA11872 (D83263) dipeptidyl
                  peptidase IV [Stenotrophomonas maltophilia]
Seq. No.
                  305269
                  tfd700571720.h1
Seq. ID
Method
                  BLASTX
                  g629844
NCBI GI
BLAST score
                  270
                  5.0e-24
E value
Match length
                  99
```

NCBI Description heat shock protein hsp70-5 - maize (fragment)

>gi 498775 emb CAA55184 (X78415) heat shock protein 70 kDa

[Zea mays]

Seq. No. 305270

% identity

tfd700571722.h1 Seq. ID

59

Method BLASTX NCBI GI g3212869 BLAST score 287 E value 5.0e-30 Match length 81 % identity 77

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 305271

tfd700571739.h1 Seq. ID

Method BLASTN g2623247 NCBI GI BLAST score 44 E value 1.0e-15 Match length 167 % identity 82

Zea mays SU1 isoamylase (sugary1) gene, complete cds NCBI Description

Seq. No. 305272

Seq. ID tfd700571752.hl

Method BLASTN NCBI GI q310099 BLAST score 197 E value 1.0e-107 Match length 277 % identity 94

NCBI Description Rattus norvegicus developmentally regulated protein mRNA,

complete cds

Seq. No. 305273

Seq. ID tfd700571786.h1

Method BLASTX NCBI GI g1169544 BLAST score 390 E value 4.0e-38 Match length 95 % identity 80

ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein NCBI Description

- Arabidopsis thaliana >gi 497629 dbj BAA04506 (D17582)

BLAST score

Match length

E value

% identity

157

29 97

7.0e-11



ERD1 protein [Arabidopsis thaliana]

```
Seq. No.
                  305274
                  tfd700571859.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3790154
BLAST score
                  126
E value
                  7.0e-65
Match length
                  165
                  94
% identity
NCBI Description
                  Human DNA sequence from clone 67K17 on chromosome
                  6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV
                  type 1 Enhancer-binding Protein 2, and a possible
                  pseudogene in an intron of this gene. Contains STSs and
                  GSSs
                  305275
Seq. No.
Seq. ID
                  tfd700571873.h1
Method
                  BLASTX
                  g4105798
NCBI GI
BLAST score
                  248
                  2.0e-21
E value
Match length
                  67
% identity
                  60
                  (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                  305276
Seq. No.
                  tfd700571883.h1
Seq. ID
Method
                  BLASTX
                  q4218011
NCBI GI
BLAST score
                  250
                  1.0e-21
E value
Match length
                   87
% identity
                   55
                   (AC006135) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  >gi_4309721_gb_AAD15491_ (AC006439) putative
                   serine/threonine protein kinase [Arabidopsis thaliana]
                   305277
Seq. No.
Seq. ID
                   tfd700571888.h1
Method
                  BLASTX
NCBI GI
                   g1184774
BLAST score
                   511
E value
                   3.0e-52
Match length
                   99
                   97
% identity
                   (U45856) cytosolic qlyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC3 [Zea mays]
Seq. No.
                   305278
Seq. ID
                   tfd700571918.h1
Method
                  BLASTX
NCBI GI
                   g2624417
```

% identity

91



```
(AJ002959) Ubiquitin carrier protein [Zea mays]
NCBI Description
                  305279
Seq. No.
Seq. ID
                  tfd700571924.h1
Method
                  BLASTX
                  g2511533
NCBI GI
BLAST score
                  446
                  1.0e-44
E value
                  111
Match length
                  78
% identity
                  (AF008121) alpha-tubulin 2 [Eleusine indica]
NCBI Description
                  305280
Seq. No.
                  tfd700571973.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4587519
BLAST score
                  373
                  5.0e-36
E value
Match length
                  101
                  79
% identity
                  (AC007060) Strong similarity to F19I3.7 gi_3033380 putative
NCBI Description
                  coatomer epsilon subunit from Arabidopsis thaliana BAC
                  gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555,
                  gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g
Seq. No.
                  305281
                  tfd700572005.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q294544
BLAST score
                  115
E value
                  2.0e-58
Match length
                  119
                  99
% identity
NCBI Description
                  Rattus norvegicus eukaryotic initiation factor 5 (eIF-5)
                  mRNA, complete cds
Seq. No.
                  305282
                  tfd700572044.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2499317
BLAST score
                  162
                   1.0e-11
E value
Match length
                  37
% identity
                  NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (COMPLEX
NCBI Description
                   I-13KD-B) (CI-13KD-B) (B13) >gi 1398908 dbj BAA13045
                   (D86215) NADH:ubiquinone oxidoreductase [Rattus norvegicus]
Seq. No.
                   305283
Seq. ID
                  tfd700572088.h1
Method
                  BLASTN
NCBI GI
                  g854734
BLAST score
                   71
                   5.0e-32
E value
Match length
                  123
```

43238

NCBI Description Rattus norvegicus casein kinase 1 gamma 2 isoform mRNA,

Match length

NCBI Description

% identity

78

49



complete cds

```
Seq. No.
                  305284
Seq. ID
                  tfd700572120.h1
Method
                  BLASTX
NCBI GI
                  g119355
BLAST score
                  210
E value
                  7.0e-17
Match length
                  46
                  91
% identity
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                  >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
                  4.2.1.11) - maize >gi 22273 emb CAA39454 (X55981) enolase
                  [Zea mays]
Seq. No.
                  305285
Seq. ID
                  tfd700572124.h1
Method
                  BLASTX
                  g399854
NCBI GI
BLAST score
                  310
E value
                  1.0e-28
Match length
                  96
% identity
                  68
NCBI Description
                  HISTONE H2B.2 >gi_283042_pir__S28049 histone H2B - maize
                  >gi 22325 emb CAA40565 (X57313) H2B histone [Zea mays]
                  305286
Seq. No.
Seq. ID
                  tfd700572151.h1
Method
                  BLASTN
                  g179725
NCBI GI
BLAST score
                  174
E value
                  3.0e-93
Match length
                  282
% identity
                  90
NCBI Description
                  Human complement component C9 mRNA, complete cds
                  305287
Seq. No.
Seq. ID
                  tfd700572169.h1
Method
                  BLASTX
NCBI GI
                  q3482932
BLAST score
                  356
E value
                  5.0e-34
Match length
                  104
% identity
                  64
NCBI Description
                  (AC003970) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  305288
Seq. ID
                  tfd700572171.hl
Method
                  BLASTX
NCBI GI
                  g2224810
BLAST score
                  190
                  2.0e-14
E value
```

(Z97022) cysteine proteinase [Hordeum vulgare]



```
Seq. No.
                   305289
Seq. ID
                   tfd700572295.h1
Method
                   BLASTX
NCBI GI
                   g1350733
BLAST score
                   138
E value
                   4.0e-11
Match length
                   55
% identity
                   71
NCBI Description
                   60S RIBOSOMAL PROTEIN L36 >gi_543316_pir__S41338 ribosomal
                   protein L36 - mouse >gi_443802 emb_CAA53502 (X75895)
                   ribosomal protein L36 [Mus musculus]
Seq. No.
                   305290
Seq. ID
                   tfd700572310.h1
Method
                   BLASTX
NCBI GI
                   a3080524
BLAST score
                   231
E value
                   3.0e-19
Match length
                   83
                   52
% identity
NCBI Description
                  (AL022599) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                   305291
Seq. ID
                   tfd700572315.h1
Method
                   BLASTX
NCBI GI
                   q3599966
BLAST score
                   202
E value
                   1.0e-18
Match length
                   96
                   49
% identity
NCBI Description
                  (AF026852) h-scol [Homo sapiens]
Seq. No.
                   305292
Seq. ID
                   tfd700572336.h1
Method
                   BLASTX
NCBI GI
                   q3334133
BLAST score
                   159
E value
                   1.0e-12
Match length
                   69
% identity
                   59
                  CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi 1432145
NCBI Description
                   (U61231) cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   305293
Seq. ID
                   tfd700572368.h1
Method
                  BLASTX
NCBI GI
                  q4006924
BLAST score
                  193
E value
                   5.0e-15
Match length
                  75
% identity
```

NCBI Description (Z99708) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No. Seq. ID

305294

Method

tfd700572379.h1 BLASTX



```
- NCBI GI
                    q2982311
 BLAST score
                    145
 E value
                    3.0e-09
 Match length
                    37
                    73
  % identity
 NCBI Description
                    (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea
                    mariana]
 Seq. No.
                    305295
 Seq. ID
                    tfd700572388.h1
 Method
                    BLASTX
 NCBI GI
                    q1666173
 BLAST score
                    137
 E value
                    9.0e-09
 Match length
                    41
  % identity
                    66
 NCBI Description
                    (Y09106) transcription factor [Nicotiana plumbaginifolia]
                    305296
 Seq. No.
 Seq. ID
                    tfd700572420.h1
 Method
                    BLASTX
 NCBI GI
                    q2832617
 BLAST score
                    214
                    3.0e-17
 E value
 Match length
                    40
 % identity
                    90
 NCBI Description
                    (AL021711) putative protein [Arabidopsis thaliana]
 Seq. No.
                    305297
 Seq. ID
                    tfd700572477.h1
 Method
                    BLASTX
 NCBI GI
                    g2911052
 BLAST score
                    304
 E value
                    6.0e-28
 Match length
                    88
 % identity
                    70
 NCBI Description
                   (AL021961) putative protein [Arabidopsis thaliana]
 Seq. No.
                    305298
 Seq. ID
                    tfd700572494.h1
 Method
                    BLASTX
 NCBI GI
                    g2618721
 BLAST score
                    231
 E value
                    1.0e-19
 Match length
                    55
                    75
 % identity
 NCBI Description
                    (U49072) IAA16 [Arabidopsis thaliana]
 Seq. No.
                    305299
 Seq. ID
                    tfd700572551.h1
 Method
                    BLASTX
 NCBI GI
                    q1924940
 BLAST score
                    363
 E value
                    8.0e-35
 Match length
                    72
 % identity
                    97
 NCBI Description (X98411) myosin-IE [Homo sapiens]
```



```
Seq. No.
                     305300
 Seq. ID
                     tfd700572652.h1
 Method
                     BLASTX
 NCBI GI
                     g3378650
 BLAST score
                     254
 E value
                     5.0e-22
 Match length
                     84
 % identity
                     62
 NCBI Description
                    (X97606) abscisic acid activated [Medicago sativa]
 Seq. No.
                     305301
 Seq. ID
                     tfd700572706.h1
 Method
                     BLASTX
 NCBI GI
                     q2668744
 BLAST score
                     248
 E value
                     2.0e-21
 Match length
                     60
 % identity
 NCBI Description
                    (AF034946) ubiquitin conjugating enzyme [Zea mays]
Seq. No.
                     305302
 Seq. ID
                     tfd700572732.h1
 Method
                     BLASTX
 NCBI GI
                     g127243
 BLAST score
                     226
 E value
                     6.0e-19
 Match length
                     86
 % identity
                     50
 NCBI Description
                     AUTONOMOUS TRANSPOSABLE ELEMENT EN-1 MOSAIC PROTEIN
                     (SUPPRESSOR-MUTATOR SYSTEM PROTEIN) (SPM)
                     >gi_320621_pir__ S28365 gene 1 protein - maize transposon
En-1 >gi_168640 (M25427) mosaic protein [Zea mays]
>gi_225007_prf__ 1206239C gene 1 [Zea mays]
 Seq. No.
                     305303
 Seq. ID
                     tfd700572757.h1
 Method
                     BLASTX
 NCBI GI
                     q3776559
 BLAST score
                     189
                     2.0e-14
 E value
Match length
                     87
 % identity
                     52
 NCBI Description
                     (AC005388) Strong similarity to gene F14J9.26 gi 3482933
                     cdc2 protein kinase homolog from A. thaliana BAC
                     gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this
                     gene. [Arabidopsis thaliana]
```

Seq. No. 305304

Seq. ID tfd700572820.h2

Method BLASTX
NCBI GI g1350930
BLAST score 414
E value 5.0e-41
Match length 82
% identity 99

NCBI Description 40S RIBOSOMAL PROTEIN S13

Seq. ID Method

```
Seq. No.
                  305305
Seq. ID
                  tfd700572827.h2
Method
                  BLASTX
NCBI GI
                  q99889
BLAST score
                  239
E value
                  1.0e-20
Match length
                  59
% identity
                  73
NCBI Description beta-conglycinin alpha chain precursor - soybean
Seq. No.
                  305306
Seq. ID
                  tfd700572832.h2
Method
                  BLASTX
NCBI GI
                  a3063442
BLAST score
                  138
E value
                  7.0e-09
Match length
                  69
% identity
                  43
NCBI Description
                  (AC003981) F22013.6 [Arabidopsis thaliana]
Seq. No.
                  305307
Seq. ID
                  tfd700572856.h2
Method
                  BLASTX
NCBI GI
                  q3914136
BLAST score
                  156
                  9.0e-11
E value
Match length
                  66
% identity
                  50
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                  >gi 2632171 emb CAA05771 (AJ002958) lipid transfer protein
                   [Cicer arietinum]
Seq. No.
                  305308
Seq. ID
                  tfd700572876.h2
Method
                  BLASTX
NCBI GI
                  g2267006
BLAST score
                  303
E value
                  5.0e-28
Match length
                  85
% identity
                  74
NCBI Description
                  (AF006825) endosperm lumenal binding protein [Oryza sativa]
Seq. No.
                  305309
Seq. ID
                  tfd700572891.h2
Method
                  BLASTX
NCBI GI
                  g2688824
BLAST score
                  175
E value
                  7.0e-18
Match length
                  66
% identity
                  71
NCBI Description
                  (U93273) putative auxin-repressed protein [Prunus
                  armeniaca]
Seq. No.
                  305310
```

43243

tfd700572895.h2

BLASTX

```
NCBI GI
BLAST score
                  322
                  3.0e-30
E value
                  84
Match length
                  76
% identity
NCBI Description beta-conglycinin alpha chain precursor - soybean
Seq. No.
                  305311
Seq. ID
                  tfd700572947.h1
Method
                  BLASTX
NCBI GI
                  g118104
                  250
BLAST score
                  3.0e-45
E value
Match length
                  96
                  85
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi_168461 (M55021) cyclophilin [Zea mays]
                  >gi_82914\overline{8}_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
Seq. No.
                  305312
Seq. ID
                  tfd700572954.h1
Method
                  BLASTX
NCBI GI
                  g2244792
BLAST score
                  243
                  1.0e-20
E value
Match length
                  109
% identity
                  44
                  (Z97336) ankyrin homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  305313
Seq. ID
                  tfd700573052.h1
Method
                  BLASTX
NCBI GI
                  g3719211
BLAST score
                  148
                  8.0e-13
E value
                  56
Match length
                  70
% identity
NCBI Description (U97021) UIP2 [Arabidopsis thaliana]
Seq. No.
                  305314
Seq. ID
                  tfd700573078.h1
Method
                  BLASTX
NCBI GI
                  g4584342
BLAST score
                  146
E value
                  2.0e-09
Match length
                  100
```

% identity

NCBI Description (AC007127) putative ubiquitin protein [Arabidopsis

thaliana]

Seq. No.

305315

Seq. ID

tfd700573105.h1

Method BLASTX NCBI GI g2827143 BLAST score 322



E value 4.0e-30 Match length 96 % identity 64

NCBI Description (AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 305316

Seq. ID tfd700573111.h1

Method BLASTX
NCBI GI g4503817
BLAST score 243
E value 1.0e-20
Match length 112
% identity 43

NCBI Description follicular lymphoma variant translocation 1

>gi_544358 sp Q06136 FVT1 HUMAN FOLLICULAR VARIANT

TRANSLOCATION PROTEIN 1 PRECURSOR (FVT-1) >gi_481027_pir__S37652 FVT1 protein - human

>gi_296186_emb_CAA45197_ (X63657) FVT1 gene is disrupted in

a t(2;18) chromosomal translocation involving Ig kappa

gene in a follicular lymphoma [Homo sapiens]

Seq. No. 305317

Seq. ID tfd700573123.h1

Method BLASTX
NCBI GI g3355622
BLAST score 202
E value 7.0e-16
Match length 66
% identity 58

NCBI Description (AJ000238) unnamed protein product [Hordeum vulgare]

Seq. No. 305318

Seq. ID tfd700573176.h1

Method BLASTX
NCBI GI g4096786
BLAST score 218
E value 3.0e-18
Match length 67
% identity 72

NCBI Description (U39958) NADP-malic enzyme [Zea mays]

Seq. No. 305319

Seq. ID tfd700573180.h1

Method BLASTN
NCBI GI g473604
BLAST score 80
E value 2.0e-37
Match length 131
% identity 90

NCBI Description Zea mays W-22 histone H2B mRNA, complete cds

Seq. No. 305320

Seq. ID tfd700573216.h1

Method BLASTN
NCBI GI g1399389
BLAST score 127

```
E value
                  3.0e-65
Match length
                  138
% identity
                  99
                  Zea mays beta-D-glucosidase (glu1) gene, complete cds
NCBI Description
                  305321
Seq. No.
Seq. ID
                  tfd700573251.h1
Method
                  BLASTX
NCBI GI
                  g4115383
BLAST-score
                  210
                  7.0e-28
E value
Match length
                  105
% identity
                  65
NCBI Description
                  (AC005967) receptor-like protein kinase [Arabidopsis
                  thalianal
Seq. No.
                  305322
Seq. ID
                  tfd700573254.h1
Method
                  BLASTN
NCBI GI
                  q4185305
BLAST score
                  42
E value
                  2.0e-14
Match length
                  94
% identity
                  86
NCBI Description
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
Seq. No.
                  305323
Seq. ID
                  tfd700573350.h1
Method
                  BLASTN
                  g5091496
                  60
                  3.0e-25
```

NCBI GI BLAST score E value 76 Match length 95 % identity

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone P0680A03,

complete sequence

Seq. No. 305324

Seq. ID tfd700573362.h1

Method BLASTX NCBI GI g82426 BLAST score 558 E value 1.0e-57 Match length 114 % identity 46

NCBI Description ubiquitin precursor - barley (fragment)

>gi 755763 emb CAA27751 (X04133) ubiquitin polyprecursor

(171 aa) [Hordeum vulgare]

Seq. No. 305325

Seq. ID tfd700573373.h1

Method BLASTX NCBI GI g4063747 BLAST score 227



```
E value
                   1.0e-33
Match length
                   107
% identity
                   61
NCBI Description
                   (AC005851) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   305326
Seq. ID
                   tfd700573382.h1
Method
                   BLASTX
                   g1168940
NCBI GI
BLAST score
                   223
E value
                   2.0e-18
Match length
                   62
% identity
                   71
NCBI Description
                   CHORISMATE MUTASE PRECURSOR (CM-1) >gi 629509 pir S38958
                   chorismate mutase precursor - Arabidopsis thaliana
                   >gi 429153 emb CAA81286 (Z26519) chorismate mutase
                   precursor [Arabidopsis thaliana]
Seq. No.
                   305327
Seq. ID
                   tfd700573401.h2
Method
                   BLASTX
                   g3668080
NCBI GI
BLAST score
                   180
                   9.0e-14
E value
Match length
                   50
% identity
                   70
NCBI Description
                   (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                   305328
Seq. ID
                   tfd700573443.h2
Method
                   BLASTX
NCBI GI
                   g1077164
BLAST score
                   213
E value
                   2.0e-17
Match length
                   88
% identity
                   51
NCBI Description
                   SWH1 protein homolog YDL019c - yeast (Saccharomyces
                   {\tt cerevisiae)} > {\tt gi\_683678\_emb\_CAA88340\_} \ ({\tt Z48432}) \ {\tt homolog} \ {\tt of}
                   yeast SWH1 protein (X74552) [Saccharomyces cerevisiae]
                   >gi_1430988_emb_CAA98578_ (Z74067) ORF YDL019c
                   [Saccharomyces cerevisiae]
Seq. No.
                   305329
Seq. ID
                   tfd700573449.h2
Method
                   BLASTN
NCBI GI
                   q3115345
BLAST score
                   113
E value
                   6.0e-57
Match length
                   145
% identity
                   94
NCBI Description
                   Homo sapiens BAC clone RG276003 from 7q22-q31.1, complete
                   sequence [Homo sapiens]
```

Seq. No. 305330

Seq. ID

tfd700573474.h2

Method BLASTX NCBI GI g122007



```
BLAST score
E value
                  2.0e-28
Match length
                  84
% identity
                  73
                  HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
NCBI Description
                  >gi_20448_emb_CAA37828 (X53831) H2A histone protein (AA 1
                  - 149) [Petroselinum crispum]
Seq. No.
                  305331
Seq. ID
                  tfd700573482.h2
Method
                  BLASTX
NCBI GI
                  g2275219
BLAST score
                  195
```

BLAST score 195
E value 2.0e-15
Match length 53
% identity 75

NCBI Description (AC002337) unknown protein [Arabidopsis thaliana]

 Seq. No.
 305332

 Seq. ID
 tfd700573489.h2

 Method
 BLASTX

 NCBI GI
 g3617742

 BLAST score
 242

 E value
 8.0e-21

Match length 64 % identity 69

NCBI Description (AC005687) RAP2.6 [Arabidopsis thaliana]

Seq. No. 305333

Seq. ID tfd700573519.h1

Method BLASTN
NCBI GI g1335859
BLAST score 104
E value 8.0e-52
Match length 140
% identity 94

NCBI Description Rattus norvegicus 5'-AMP-activated protein kinase, gamma-1

subunit mRNA, complete cds

Seq. No. 305334

Seq. ID tfd700573608.h1

Method BLASTN
NCBI GI g57573
BLAST score 174
E value 3.0e-93
Match length 275
% identity 92

NCBI Description Rat mRNA for cytoplasmic-gamma isoform of actin

Seq. No. 305335

Seq. ID tfd700573623.h1

Method BLASTX
NCBI GI g1076800
BLAST score 271
E value 4.0e-24
Match length 53
% identity 96



NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme - maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate

peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate

peroxidase [Zea mays]

Seq. No. 305336

Seq. ID tfd700573628.h1

Method BLASTX
NCBI GI g2281088
BLAST score 160
E value 5.0e-11
Match length 63
% identity 52

NCBI Description (AC002333) indole-3-acetate beta-glucosyltransferase isolog

[Arabidopsis thaliana]

Seq. No. 305337

Seq. ID tfd700573733.h1

Method BLASTX
NCBI GI g407942
BLAST score 241
E value 9.0e-21
Match length 75
% identity 64

NCBI Description (U02496) epoxide hydrolase [Solanum tuberosum]

Seq. No. 305338

Seq. ID tfd700573783.h1

Method BLASTX
NCBI GI g480723
BLAST score 404
E value 8.0e-40
Match length 85
% identity 95

NCBI Description ADP, ATP carrier protein T1 - mouse >gi_402628_emb_CAA52616_

(X74510) adenine nucleotide carrier [Mus musculus]

Seq. No. 305339

Seq. ID tfd700573985.h1

Method BLASTX
NCBI GI g113466
BLAST score 315
E value 2.0e-29
Match length 81
% identity 75

NCBI Description ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE

NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_72020_pir_XWNC ADP,ATP carrier protein - Neurospora crassa >gi_2977_emb_CAA25104_

(X00363) ADP/ATP carrier protein [Neurospora crassa]

Seq. No. 305340

Seq. ID tfd700574004.h1

Method BLASTX NCBI GI g3746071 BLAST score 287 E value 7.0e-26 Match length 98



% identity 67
NCBI Description (AC005311) putative GTP-binding protein [Arabidopsis thaliana]

Seq. No. 305341
Seq. ID tfd700574015.h1
Method BLASTX

NCBI GI g2984334
BLAST score 204
E value 4.0e-16
Match length 99
% identity 41

NCBI Description (AE000774) hemolysin homolog protein [Aquifex aeolicus]

Seq. No. 305342

Seq. ID tfd700574064.h1

Method BLASTN
NCBI GI 94115614
BLAST score 138
E value 6.0e-72
Match length 209
% identity 91

NCBI Description Zea mays mRNA for root cap-specific glycine-rich protein,

complete cds

Seq. No. 305343

Seq. ID tfd700574158.h1

Method BLASTX
NCBI GI g2213632
BLAST score 221
E value 4.0e-28
Match length 84
% identity 62

NCBI Description (AC000103) F21J9.24 [Arabidopsis thaliana]

Seq. No. 305344

Seq. ID tfd700574213.h1

Method BLASTN
NCBI GI g3080381
BLAST score 285
E value 1.0e-159
Match length 336
% identity 96

NCBI Description Homo sapiens DNA sequence from PAC 393P12 on chromosome

Xp11.21. Contains a hypothetical protein KIAA0413

(KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269

Seq. No. 305345

Seq. ID tfd700574235.h1

Method BLASTX
NCBI GI g2673917
BLAST score 464
E value 1.0e-46
Match length 107
% identity 42

NCBI Description (AC002561) putative ATP-dependent RNA helicase [Arabidopsis



[thaliana]

```
Seq. No.
                   305346
Seq. ID
                   tfd700574258.h1
Method
                   BLASTN
NCBI GI
                   g6598538
BLAST score
                   41
E value
                   8.0e-14
Match length
                   69
                   90
% identity
NCBI Description
```

NCBI Description Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

 Seq. No.
 305347

 Seq. ID
 tfd700574334.h2

 Method
 BLASTN

 NCBI GI
 g3819386

 BLAST score
 69

BLAST score 69
E value 1.0e-30
Match length 140
% identity 89

NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0872.rev

Seq. No. 305348

Seq. ID tfd700574368.h2

Method BLASTX
NCBI GI g1076509
BLAST score 191
E value 8.0e-15
Match length 65
% identity 75

NCBI Description chloroplast RNA binding protein - kidney bean

>gi_558629_emb_CAA57551 (X82030) chloroplast RNA binding

protein [Phaseolus vulgaris]

Seq. No. 305349

Seq. ID tfd700574379.h2

Method BLASTX
NCBI GI g1076715
BLAST score 238
E value 3.0e-20
Match length 78
% identity 54

NCBI Description abscisic acid-induced protein HVA22 - barley >qi 404589

(L19119) A22 [Hordeum vulgare]

Seq. No. 305350

Seq. ID tfd700574409.h1

Method BLASTX
NCBI GI g3128228
BLAST score 351
E value 1.0e-33
Match length 75
% identity 89

NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No.

Seq. ID

305356

tfd700574477.h1

```
Seq. No.
                  305351
                  tfd700574421.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3158474
                  374
BLAST score
E value
                  3.0e-36
Match length
                  79
                  90
% identity
NCBI Description
                  (AF067184) aquaporin 1 [Samanea saman]
Seq. No.
                  305352
Seq. ID
                  tfd700574424.h1
Method
                  BLASTN
NCBI GI
                  g4097879
BLAST score
                  81
E value
                  6.0e-38
Match length
                  165
% identity
                  87
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  305353
Seq. No.
Seq. ID
                  tfd700574444.h1
Method
                  BLASTX
NCBI GI
                  g2129842
BLAST score.
                  157
E value
                  8.0e-11
Match length
                  58
% identity
                  50
                  SE60 protein - soybean >gi 509769 emb CAA79164 (Z18359)
NCBI Description
                  seed-specific low molecular weight sulfur-rich protein
                  [Glycine max]
                  305354
Seq. No.
Seq. ID
                  tfd700574456.h1
Method
                  BLASTX
NCBI GI
                  g229707
BLAST score
                  418
E value
                  2.0e-41
Match length
                  82
                  94
% identity
NCBI Description Bean pod mottle virus
Seq. No.
                  305355
Seq. ID
                  tfd700574469.hl
Method
                  BLASTX
NCBI GI
                  q541950
BLAST score
                  262
E value
                  3.0e-23
Match length
                  58
% identity
                  88
NCBI Description
                  SPCP1 protein - soybean >gi 310576 (L12257) nodulin-26
                  [Glycine max]
```

```
Method
                  BLASTX
                                               94
NCBI GI
                  g2605510
BLAST score
                  393
                  2.0e-38
E value
Match length
                  88
                  88
% identity
NCBI Description
                  (AB008678) alpha subunit of beta conglycinin [Glycine max]
                  305357
Seq. No.
                  tfd700574488.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g625537
BLAST score
                  452
E value
                  2.0e-45
Match length
                  89
                  97
% identity
                  glycinin A3B4 (plasmid pSPGL1) - Glycine soja (strain L23)
NCBI Description
                  (fragment)
Seq. No.
                  305358
                  tfd700574493.h1
Seq. ID
Method
                  BLASTX
                  g1666173
NCBI GI
BLAST score
                  265
E value
                  2.0e-23
Match length
                  74
                  74
% identity
NCBI Description
                  (Y09106) transcription factor [Nicotiana plumbaginifolia]
                  305359
Seq. No.
                  tfd700574560.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q758354
BLAST score
                  49
                  6.0e-19
E value
Match length
                  72
% identity
                  93
NCBI Description Z.mays mRNA for plasma membrane H+ ATPase
Seq. No.
                  305360
Seq. ID
                  tfd700574601.h1
Method
                  BLASTX
NCBI GI
                  g2133293
BLAST score
                  339
E value
                  6.0e-32
Match length
                  120
% identity
NCBI Description pectate lyase (EC 4.2.2.2) C - fungus (Fusarium solani)
```

Seq. No. 305361

Seq. ID tfd700574641.h1

Method BLASTX
NCBI GI g1762142
BLAST score 183
E value 1.0e-13
Match length 68
% identity 53



NCBI Description (U48434) putative cytochrome P450 [Solanum chacoense]

305362 Seq. No.

tfd700574659.h1 Seq. ID

Method BLASTN q881484 NCBI GI BLAST score 139 E value 3.0e-72 Match length 296 88 % identity

NCBI Description Mus musculus mSTI1 mRNA, complete cds

305363 Seq. No.

Seq. ID tfd700574720.h1

Method BLASTX g4506841 NCBI GI BLAST score 462 E value 2.0e-46 Match length 99 90 % identity

NCBI Description small inducible cytokine A2 (monocyte chemotactic protein

1, homologous to mouse Sig-je); MCP-1

>gi_126842_sp_P13500_MCP1_HUMAN MONOCYTE CHEMOTACTIC PROTEIN 1 PRECURSOR (MCP-1) (MONOCYTE CHEMOTACTIC AND ACTIVATING FACTOR) (MCAF) (MONOCYTE SECRETORY PROTEIN JE) (MONOCYTE CHEMOATTRACTANT PROTEIN 1) (HC11) (SMALL

INDUCIBLE CYTOKINE A2) >gi 280830 pir A60299 monocyte

chemoattractant protein 1 precursor - human

>gi_34514_emb_CAA32876_ (X14768) monocyte chemoattractant preprotein [Homo sapiens] >gi 240868 bbs 71514 (S71513) monocyte chemoattractant protein-1, MCP-1 [human, Peptide, 99 aa] [Homo sapiens] >gi_307163 (M24545) chemotactic and activating factor precursor [Homo sapiens] >gi_338007 (M28225) monocyte secretory protein [Homo sapiens] >gi 338009 (M28226) monocyte secretory protein [Homo sapiens] >gi 386961 (M31626) monocyte secretory protein [Homo sapiens] >gi_487124 (M37719) monocyte chemotactic

protein [Homo sapiens] >gi_545465_bbs_146618 (S69738) MCP-1=monocyte chemotactic protein [human, aortic endothelial cells, Peptide, 99 aa] [Homo sapiens]

Seq. No. 305364

Seq. ID tfd700574729.h1

Method BLASTX NCBI GI q4510339 BLAST score 297 4.0e-27 E value Match length 107 % identity 52

NCBI Description (AC006921) putative ABC transporter protein [Arabidopsis

thaliana]

Seq. No. 305365

Seq. ID tfd700574772.h1

Method BLASTX NCBI GI g2982318 BLAST score 358



E value 3.0e-34
Match length 100
% identity 70

NCBI Description (AF051244) probable 60S ribosomal protein L15 [Picea

mariana]

Seq. No. 305366

Seq. ID tfd700574820.h1

Méthod BLASTX
NCBI GI g2842493
BLAST score 192
E value 8.0e-15
Match length 88
% identity 48

NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]

Seq. No. 305367

Seq. ID tfd700574824.h1

Method BLASTX
NCBI GI g1362086
BLAST score 503
E value 3.0e-51
Match length 108
% identity 92

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi_2129919_pir__S65957

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase

[Catharanthus roseus]

Seq. No. 305368

Seq. ID tfd700574841.h1

Method BLASTX
NCBI GI g285317
BLAST score 258
E value 1.0e-22
Match length 84
% identity 67

NCBI Description dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea

Seq. No. 305369

Seq. ID tfd700574880.h1

Method BLASTX
NCBI GI g2275210
BLAST score 177
E value 5.0e-13
Match length 86
% identity 41

NCBI Description (AC002337) peptidyl-prolyl cis-trans isomerase isolog

[Arabidopsis thaliana]

Seq. No. 305370

Seq. ID tfd700574884.h1

Method BLASTX NCBI GI g1235569



```
BLAST score
                   207
E value
                  1.0e-16
Match length
                   91
                  51
% identity
NCBI Description (X93301) NAD(P)H oxidase [Oryza sativa]
Seq. No.
                  305371
Seq. ID
                  tfd700575076.h1
Method
                  BLASTX
NCBI GI
                  q431154
BLAST score
                  235
E value
                  8.0e-20
Match length
                  69
% identity
                  65
```

NCBI Description (D21813) ORF [Lilium longiflorum]

 Seq. No.
 305372

 Seq. ID
 tfd700575083.h1

 Method
 BLASTX

 NCBI GI
 g1895084

NCBI GI g1895084
BLAST score 321
E value 7.0e-30
Match length 96
% identity 91

NCBI Description (U89897) golgi associated protein se-wap41 [Zea mays]

Seq. No. 305373

Seq. ID tfd700575088.h1

Method BLASTX
NCBI GI g1657619
BLAST score 224
E value 1.0e-25
Match length 103
% identity 59

NCBI Description (U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236)

putative transmembrane protein G5p [Arabidopsis thaliana]

Seq. No. 305374

Seq. ID tfd700575108.h1

Method BLASTX
NCBI GI g2497953
BLAST score 224
E value 1.0e-18
Match length 90
% identity 52

NCBI Description MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM

COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]

cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No. 305375

Seq. ID tfd700575123.h1

Method BLASTX
NCBI GI g1519253
BLAST score 274
E value 1.0e-24



Match length 91 % identity 66

NCBI Description (U65958) GF14-d protein [Oryza sativa]

Seq. No. 305376

Seq. ID tfd700575137.h1

Method BLASTX
NCBI GI g1296955
BLAST score 175
E value 2.0e-15
Match length 63
% identity 39

NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]

Seq. No. 305377

Seq. ID tfd700575139.h1

Method BLASTN
NCBI GI g633109
BLAST score 38
E value 1.0e-12
Match length 74
% identity 88

NCBI Description Rice mRNA for plasma membrane H+-ATPase, complete cds

Seq. No. 305378

Seq. ID tfd700575162.h1

Method BLASTX
NCBI GI g112994
BLAST score 284
E value 1.0e-25
Match length 78
% identity 74

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077 (X12564)

ABA-inducible gene protein [Zea mays]

>gi_226091_prf__1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 305379

Seq. ID tfd700575163.h1

Method BLASTX
NCBI GI g2282584
BLAST score 444
E value 2.0e-44
Match length 86
% identity 99

NCBI Description (U76259) elongation factor 1-alpha [Zea mays]

Seq. No. 305380

Seq. ID tfd700575259.h1

Method BLASTX
NCBI GI g1619952
BLAST score 263
E value 4.0e-23
Match length 107
% identity 51

43257



```
NCBI Description (U72149) putative RNA helicase [Saccharomyces cerevisiae]
                  305381
Seq. No.
Seq. ID
                  tfd700575293.h1
Method
                  BLASTX
                  q131770
NCBI GI
BLAST score
                  196
                  2.0e-15
E value
Match length
                  57
% identity
                  65
NCBI Description
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
                   (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein
                  [Dictyostelium discoideum]
Seq. No.
                  305382
Seq. ID
                  tfd700575309.h1
Method
                  BLASTN
                  g1370602
NCBI GI
BLAST score
                  84
E value
                  2.0e-39
Match length
                  84
% identity
                  100
NCBI Description Z.mays mRNA for annexin p35
                  305383
Seq. No.
                  tfd700575315.h1
Seq. ID
Method
                  BLASTX
                  g2674203
NCBI GI
BLAST score
                  435
E value
                  3.0e-43
Match length
                  112
                  81
% identity
                   (AF036328) CLP protease regulatory subunit CLPX
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  305384
Seq. ID
                  tfd700575451.hl
Method
                  BLASTN
NCBI GI
                  q1049254
BLAST score
                  51
E value
                  4.0e-20
Match length
                  99
% identity
                  88
NCBI Description Zea mays H+-pyrophosphatase mRNA, partial cds
Seq. No.
                  305385
Seq. ID
                  tfd700575484.h1
Method
                  BLASTN
NCBI GI
                  q3851004
BLAST score
                  49
```

Method BLASTN
NCBI GI g3851004
BLAST score 49
E value 4.0e-19
Match length 84
% identity 93

NCBI Description Zea mays pyruvate dehydrogenase E1 alpha subunit RNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.

Seq. ID

Method

305391

BLASTX

tfd700575827.h1



```
Seq. No.
                  305386
Seq. ID
                  tfd700575547.h1
Method
                  BLASTX
                  g1710841
NCBI GI
BLAST score
                  224
E value
                  6.0e-19
Match length
                   45
                  98
% identity
NCBI Description
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                  HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278 (X79905)
                  S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
Seq. No.
                  305387
Seq. ID
                  tfd700575550.h1
Method
                  BLASTX
NCBI GI
                  q4006900
BLAST score
                  214
                  9.0e-18
E value
Match length
                  59
% identity
                  69
NCBI Description
                  (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  305388
Seq. ID
                  tfd700575558.h1
Method
                  BLASTX
NCBI GI
                  g2959360
BLAST score
                  340
E value
                  1.0e-32
Match length
                  69
% identity
                  100
NCBI Description
                  (AJ222588) poly(ADP-ribose) polymerase [Zea mays]
Seq. No.
                  305389
Seq. ID
                  tfd700575721.h1
Method
                  BLASTN
                  q3687208
NCBI GI
BLAST score
                  35
E value
                  3.0e-10
Match length
                  50
% identity
                  94
NCBI Description
                  Mus musculus chromosome 11, BAC clone 111-181 (LBNL M01),
                  complete sequence [Mus musculus]
Seq. No.
                  305390
Seq. ID
                  tfd700575735.h1
Method
                  BLASTX
NCBI GI
                  q4204849
BLAST score
                  293
E value
                  7.0e-27
Match length
                  74
% identity
                  69
NCBI Description (U55875) protein kinase [Arabidopsis thaliana]
```

43259



```
NCBI GI
                  q3367522
BLAST score
                  193
                  4.0e-15
E value
Match length
                  88
% identity
                  43
NCBI Description
                  (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  305392
Seq. ID
                  tfd700575858.h1
Method
                  BLASTX
NCBI GI
                  q3182916
BLAST score
                  256
E value
                  2.0e-22
Match length
                  86
                  57
% identity
                  ADP-RIBOSYLATION FACTOR >gi_1565278 emb_CAB02498_ (Z80359)
NCBI Description
                  ADP-ribosylation factor [Plasmodium falciparum] >gi 1932731
                  (U57370) ADP-ribosylation factor [Plasmodium falciparum]
Seq. No.
                  305393
Seq. ID
                  tfd700575860.h1
Method
                  BLASTX
NCBI GI
                  g1654034
BLAST score
                  222
E value
                  2.0e-18
Match length
                  83
                  55
% identity
                  (Z81360) hypothetical protein Rv1732c [Mycobacterium
NCBI Description
                  tuberculosis]
Seq. No.
                  305394
Seq. ID
                  tfd700575871.h1
Method
                  BLASTN
NCBI GI
                  g168492
BLAST score
                  89
E value
                  8.0e-43
Match length
                  145
% identity
                  90
NCBI Description Corn histone H3 (H3C3) gene, complete cds
Seq. No.
                  305395
Seq. ID
                  tfd700575874.hl
Method
                  BLASTN
NCBI GI
                  g2795851
BLAST score
                  38
E value
                  1.0e-12
```

Match length 42 98 % identity

NCBI Description Maranta bicolor 18S small subunit nuclear ribosomal RNA

gene

Seq. No. 305396

Seq. ID tfd700575938.h1

Method BLASTX NCBI GI g4557026 BLAST score 177



```
E value
                   6.0e-13
Match length
                  83
% identity
                  11
NCBI Description
                  hect (homologous to the E6-AP (UBE3A) carboxyl terminus)
                  domain and RCC1 (CHC1)-like domain (RLD) 1 >gi 1477565
                   (U50078) p532 [Homo sapiens]
                  305397
Seq. No.
Seq. ID
                  tfd700575992.h1
Method
                  BLASTN
NCBI GI
                  g5468517
BLAST score
                  214
E value
                  1.0e-117
Match length
                  297
% identity
                  93
NCBI Description
                  Homo sapiens serine palmitoyl transferase, subunit II gene,
                  complete cds; and unknown genes
Seq. No.
                  305398
Seq. ID
                  tfd700576034.h1
Method
                  BLASTX
NCBI GI
                  q119355
BLAST score
                  214
E value
                  9.0e-18
Match length
                  54
% identity
                  83
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                  >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
                  4.2.1.11) - maize >gi 22273 emb CAA39454 (X55981) enolase
                   [Zea mays]
Seq. No.
                  305399
Seq. ID
                  tfd700576042.h1
Method
                  BLASTN
NCBI GI
                  g189497
BLAST score
                  220
E value
                  1.0e-120
Match length
                  291
% identity
                  94
NCBI Description Human pyrroline 5-carboxylate reductase mRNA, complete cds
Seq. No.
                  305400
Seq. ID
                  tfd700576090.h1
Method
                  BLASTX
NCBI GI
                  g2462077
BLAST score
                  168
E value
                  2.0e-17
Match length
                  92
% identity
                  53
```

NCBI Description (Y11871) Oxal protein [Arabidopsis thaliana]

Seq. No. 305401

Seq. ID tfd700576093.h1

Method BLASTN NCBI GI g2789655 BLAST score 160

```
E value
                  7.0e-85
Match length
                  285
% identity
                  Homo sapiens histone deacetylase 3 (HDAC3) mRNA, complete
NCBI Description
                  cds
Seq. No.
                  305402
                  tfd700576117.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2505874
BLAST score
                  300
E value
                  2.0e-27
Match length
                  99
% identity
                  61
NCBI Description
                  (Y12776) putative kinase [Arabidopsis thaliana]
```

Seq. No. 305403

Seq. ID tfd700576152.h1 Method BLASTX NCBI GI g2143891 BLAST score 181 2.0e-13 E value

Match length 46 % identity

NCBI Description organic cation transporter - rat >gi_633622_emb_CAA55411_

(X78855) organic cation transporter [Rattus norvegicus] >gi_1092658_prf__2024341A cation transporter [Rattus

norvegicus]

Seq. No. 305404

Seq. ID tfd700576155.h1

Method BLASTX NCBI GI g1362086 BLAST score 202 E value 5.0e-16 Match length 66 % identity

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi 2129919 pir S65957

5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No. 305405

Seq. ID tfd700576190.h1 Method BLASTN

NCBI GI q188585 BLAST score 121 1.0e-61 E value Match length 243 % identity

NCBI Description Human 20-kDa myosin light chain (MLC-2) mRNA, complete cds

Seq. No. 305406

Seq. ID tfd700576262.h1



```
Method BLASTN
NCBI GI g20163
BLAST score 48
E value 2.0e-18
Match length 56
% identity 96
```

NCBI Description O.sativa Rrl5 mRNA for 5S ribosomal RNA

Seq. No. 305407

Seq. ID tfd700576282.h1

Method BLASTN
NCBI GI g432367
BLAST score 89
E value 1.0e-42
Match length 213
% identity 85

NCBI Description Rice mRNA for elongation factor 1 beta, complete cds

Seq. No. 305408

Seq. ID tfd700576307.h1

Method BLASTX
NCBI GI g3033400
BLAST score 380
E value 5.0e-37
Match length 88
% identity 81

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 305409

Seq. ID tfd700576329.h1

Method BLASTX
NCBI GI g99902
BLAST score 294
E value 5.0e-27
Match length 61
% identity 92

NCBI Description translation elongation factor eEF-1 alpha chain (gene

tefS1) - soybean

Seq. No. 305410

Seq. ID tfd700576330.h1

Method BLASTX
NCBI GI g4262186
BLAST score 202
E value 9.0e-21
Match length 84
% identity 67

NCBI Description (AC005508) Highly similar to cullin 3 [Arabidopsis

thaliana]

Seq. No. 305411

Seq. ID tfd700576345.h1

Method BLASTX
NCBI GI g3915826
BLAST score 230
E value 4.0e-25



```
Match length
% identity
                  70
NCBI Description
                  60S RIBOSOMAL PROTEIN L5
                  305412
Seq. No.
                  tfd700576385.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2062176
BLAST score
                  151
E value
                  3.0e-10
Match length
                  78
```

47 % identity NCBI Description (AC001645) Myb-related transcription activator (MybSt1) isolog [Arabidopsis thaliana]

305413

Seq. No. tfd700576388.h1 Seq. ID

Method BLASTX NCBI GI g548900 BLAST score 276 E value 6.0e-25 Match length 80 71 % identity

NCBI Description SUCROSE-BINDING PROTEIN PRECURSOR (SBP)

> >gi_322691_pir__JQ1730 62K sucrose-binding protein precursor - soybean >gi_170064 (L06038) glucose binding

protein [Glycine max]

305414 Seq. No.

Seq. ID tfd700576668.h1

Method BLASTX NCBI GI g3860250 BLAST score 175 E value 1.0e-27 Match length 83 % identity 84

NCBI Description (AC005824) putative chloroplast prephenate dehydratase

[Arabidopsis thaliana]

Seq. No. 305415

Seq. ID tym700023121.f1

Method BLASTX NCBI GI g3341511 BLAST score 320 E value 6.0e-30 Match length 82 % identity 76

NCBI Description (AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]

Seq. No. 305416

Seq. ID tzu700201119.h1

Method BLASTX NCBI GI q2827992 BLAST score 247 E value 1.0e-21 Match length 65 % identity 66



```
NCBI Description (AF034743) UDP-glucuronosyltransferase [Pisum sativum]
Seq. No.
                   305417
Seq. ID
                   tzu700201128.h1
Method
                  BLASTX
NCBI GI
                   g2245004
BLAST score
                   154
E value
                   2.0e-10
Match length
                   47
% identity
                   55
NCBI Description
                  (Z97341) similarity to membrane transport protein
                   [Arabidopsis thaliana]
Seq. No.
                   305418
Seq. ID
                   tzu700201133.h1
Method
                  BLASTN
NCBI GI
                   q550437
BLAST score
                  122
E value
                  1.0e-62
Match length
                  138
% identity
                   97
NCBI Description Z.mays CYP71C2 mRNA for cytochrome P-450
Seq. No.
                  305419
Seq. ID
                  tzu700201151.h1
Method
                  BLASTX
NCBI GI
                  q2446994
BLAST score
                  387
E value
                  1.0e-37
Match length
                  111
% identity
                  69
                  (D63952) fatty acid desaturase [Zea mays]
NCBI Description
Seq. No.
                  305420
Seq. ID
                  tzu700201157.h1
Method
                  BLASTX
NCBI GI
                  g3176667
BLAST score
                  329
E value
                  5.0e-31
Match length
                  88
% identity
                  72
                   (AC004393) Similar to hypothetical 41.9KD protein
NCBI Description
                  gb 1001369 from sequence of Synechocystis sp. gb_D64006.
                   [Arabidopsis thaliana]
Seq. No.
                  305421
Seq. ID
                  tzu700201243.h1
Method
                  BLASTN
NCBI GI
                  g4514636
BLAST score
                  106
```

E value 7.0e-53 Match length 169 % identity 92

NCBI Description Zea mays ZmRCP2 mRNA for root cap protein 2, complete cds

Seq. No. 305422

Seq. ID tzu700201294.h1

```
BLASTX
Method
NCBI GI
                  q3236251
                  242
BLAST score
                  5.0e-21
E value
Match length
                  61
% identity
                  77
                  (AC004684) putative phosphoribosylaminoimidazole
NCBI Description
                  carboxylase [Arabidopsis thaliana]
Seq. No.
                  305423
Seq. ID
                  tzu700201303.h1
Method
                  BLASTX
NCBI GI
                  g2385410
BLAST score
                  145
                  3.0e-09
E value
Match length
                  68
% identity
                  32
                  (AB001372) TFIID subunit taf72p [Schizosaccharomyces pombe]
NCBI Description
                  >gi 3859081 emb CAA21958_ (AL033406) tfiid subunit taf72p.
                   [Schizosaccharomyces pombe]
Seq. No.
                  305424
Seq. ID
                  tzu700201320.h1
Method
                  BLASTN
NCBI GI
                  q3264597
BLAST score
                  81
                  8.0e-38
E value
Match length
                  115
% identity
                  95
NCBI Description Zea mays trypsin inhibitor mRNA, complete cds
                  305425
Seq. No.
Seq. ID
                  tzu700201330.h1
Method
                  BLASTX
NCBI GI
                  q3033384
BLAST score
                  284
                  1.0e-25
E value
Match length
                  95
% identity
                  64
                  (AC004238) putative CTP synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  305426
Seq. ID
                  tzu700201343.h1
Method
                  BLASTX
NCBI GI
                  g626042
BLAST score
                  420
                  2.0e-41
E value
Match length
                  78
```

100 % identity

beta-glucosidase, root meristem (EC 3.2.1.-) precursor -NCBI Description

maize >gi 435313 emb CAA52293 (X74217) beta-glucosidase

[Zea mays]

Seq. No. 305427

Seq. ID tzu700201353.h1

Method BLASTX NCBI GI g3342249



```
BLAST score
                  148
                  5.0e-10
E value
Match length
                  46
                  57
% identity
                   (AF047719) GA3 [Arabidopsis thaliana] >gi 3342251
NCBI Description
                   (AF047720) GA3 [Arabidopsis thaliana]
                  305428
Seq. No.
                  tzu700201362.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076821
BLAST score
                  289
                  1.0e-26
E value
Match length
                  55
% identity
                  95
                  probable 1-acyl-glycerol-3-phosphate acyltransferase -
NCBI Description
                  maize >gi 575960 emb CAA82638 (Z29518)
                  1-acyl-glycerol-3-phosphate acyltransferase (putative) [Zea
                  mays]
                  305429
Seq. No.
                  tzu700201453.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1168261
BLAST score
                  189
                  1.0e-14
E value
Match length
                  53
% identity
                  70
                  ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                   (TRANSAMINASE A) (GLUTAMATE OXALOACETATE TRANSAMINASE-2)
                  >gi 1071843 pir S35960 aspartate transaminase (EC
                   2.6.1.1), mitochondrial - bovine >gi 415324 emb CAA80960
                   (Z25466) aspartate aminotransferase [Bos taurus]
Seq. No.
                  305430
Seq. ID
                  tzu700201508.h1
Method
                  BLASTX
NCBI GI
                   q4262167
BLAST score
                   226
E value
                   5.0e-19
Match length
                  78
% identity
                   62
                   (AC005275) putative LRR receptor-linked protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   305431
                   tzu700201521.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q860676
```

Method BLASTX
NCBI GI g860676
BLAST score 277
E value 5.0e-25
Match length 61
% identity 82

NCBI Description (U24188) calcium/calmodulin-dependent protein kinase

[Lilium longiflorum] >gi 1097385 prf 2113422A

Ca/calmodulin-dependent protein kinase [Lilium longiflorum]

```
305432
Seq. No.
Seq. ID
                   tzu700201552.h1
Method
                   BLASTX
                   g3395440
NCBI GI
BLAST score
                   219
                   6.0e-18
E value
Match length
                   93
% identity
                   45
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   305433
Seq. ID
                   tzu700201553.h1
Method
                   BLASTX
                   g4454452
NCBI GI
BLAST score
                   183
E value
                   4.0e-14
Match length
                   51
% identity
                   61
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                   305434
Seq. No.
Seq. ID
                   tzu700201581.h1
Method
                   BLASTX
                   g2702268
NCBI GI
BLAST score
                   257
E value
                   2.0e-22
Match length
                   102
                   48
% identity
NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]
                   305435
Seq. No.
Seq. ID
                   tzu700201583.h1
Method
                   BLASTX
NCBI GI
                   q3025027
BLAST score
                   162
E value
                   3.0e-11
Match length
                   78
% identity
                   41
NCBI Description
                   HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBIT
                   >gi 1787041 (AE000184) putative ATP-binding component of a
                   transport system [Escherichia coli]
                   >gi_4062387_dbj_BAA35501_ (D90719) Hypothetical protein
HI0658 [Escherichia coli] >gi_4062394_dbj_BAA35508_
                   (D90720) Hypothetical protein HI0658 [Escherichia coli]
                   305436
Seq. No.
Seq. ID
                   tzu700201586.h1
Method
                   BLASTX
NCBI GI
                   g4514635
BLAST score
                   177
                   3.0e-16
E value
                   55
Match length
```

76 % identity

NCBI Description (AB021175) root cap protein 1 [Zea mays]

Seq. No. 305437

tzu700201601.h1 Seq. ID



```
BLASTN
Method
NCBI GI
                  q4218534
BLAST score
                  73
                  4.0e-33
E value
Match length
                  89
                  96
% identity
NCBI Description Triticum sp. mRNA for GRAB1 protein
                  305438
Seq. No.
Seq. ID
                  tzu700201618.h1
Method
                  BLASTN
NCBI GI
                  g4160401
BLAST score
                  48
E value
                  5.0e-18
Match length
                  116
% identity
                  85
NCBI Description Zea mays eIF-5 gene, exons 1-2
                  305439
Seq. No.
                  tzu700201626.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3445397
BLAST score
                  164
                  7.0e-17
E value
Match length
                  79
% identity
                  52
NCBI Description (AJ010166) S-domain receptor-like protein kinase [Zea mays]
Seq. No.
                  305440
                  tzu700201649.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3282393
BLAST score
                  46
E value
                  9.0e-17
Match length
                  122
% identity
NCBI Description Oryza sativa aie2 mRNA, partial cds
Seq. No.
                  305441
Seq. ID
                  tzu700201662.h1
Method
                  BLASTX
NCBI GI
                  g2194128
BLAST score
                  247
E value
                  3.0e-21
Match length
                  80
% identity
                  61
NCBI Description
                   (AC002062) Strong similarity to Arabidopsis receptor-like
                  kinase (gb ATLECGENE) and F20P5.15. [Arabidopsis thaliana]
Seq. No.
                  305442
Seq. ID
                  tzu700201669.h1
Method
                  BLASTX
```

NCBI GI g2911077
BLAST score 361
E value 1.0e-34
Match length 93
% identity 68



NCBI Description (AL021960) gibberellin 20-oxidase-like protein [Arabidopsis thaliana]

Seq. No. 305443

Seq. ID tzu700201679.h1

Method BLASTX
NCBI GI g4510339
BLAST score 359
E value 2.0e-34
Match length 115
% identity 61

NCBI Description (AC006921) putative ABC transporter protein [Arabidopsis

thaliana]

Seq. No. 305444

Seq. ID tzu700201721.h1

Method BLASTX
NCBI GI g3157926
BLAST score 217
E value 7.0e-18
Match length 86
% identity 47

NCBI Description (AC002131) Strong similarity to extensin-like protein

gb Z34465 from Zea mays. [Arabidopsis thaliana]

Seq. No. 305445

Seq. ID tzu700201727.h1

Method BLASTX
NCBI GI g4098250
BLAST score 145
E value 3.0e-09
Match length 34
% identity 74

NCBI Description (U76611) similar to Solanum tuberosum ci21A gene product

encoded by the sequence presented in GenBank Accession

Number U76610 [Solanum tuberosum]

Seq. No. 305446

Seq. ID tzu700201733.h1

Method BLASTX
NCBI GI g2997589
BLAST score 192
E value 6.0e-15
Match length 49
% identity 86

NCBI Description (AF020813) glucose-6-phosphate/phosphate-translocator

precursor [Zea mays]

Seq. No. 305447

Seq. ID tzu700201747.h1

Method BLASTX
NCBI GI g3024871
BLAST score 174
E value 1.0e-12
Match length 90
% identity 47

NCBI Description HYPOTHETICAL 77.3 KD PROTEIN SLL0005





```
>gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis
sp.]
```

Seq. No. 305448

Seq. ID tzu700201785.h1

Method BLASTN
NCBI GI g3282393
BLAST score 43
E value 5.0e-15
Match length 71
% identity 90

NCBI Description Oryza sativa aie2 mRNA, partial cds

Seq. No. 305449

Seq. ID tzu700201790.h1

Method BLASTX
NCBI GI g3386621
BLAST score 240
E value 2.0e-20
Match length 84
% identity 58

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 305450

Seq. ID tzu700201792.h1

Method BLASTX
NCBI GI g548604
BLAST score 372
E value 6.0e-36
Match length 75
% identity 91

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR

(LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi_1076728_pir__S51813 photosystem-I PSI-F chain precursor
- barley >gi_469560 (U08135) photosystem-I PSI-F subunit

precursor [Hordeum vulgare]

Seq. No. 305451

Seq. ID tzu700201828.h1

Method BLASTX
NCBI GI g4467359
BLAST score 319
E value 4.0e-30
Match length 63
% identity 84

NCBI Description (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis

thaliana]

Seq. No. 305452

Seq. ID tzu700201862.h1

Method BLASTX
NCBI GI g2852447
BLAST score 165
E value 5.0e-12
Match length 45
% identity 71

NCBI Description (D88206) protein kinase [Arabidopsis thaliana]

```
305453
Seq. No.
Seq. ID
                  tzu700201864.h1
Method
                  BLASTX
NCBI GI
                  g483410
BLAST score
                  281
                  3.0e-25
E value
Match length
                  65
% identity
                  83
NCBI Description
                  (L01496) calmodulin-binding protein [Zea mays]
Seq. No.
                  305454
                  tzu700201876.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q118106
BLAST score
                  228
E value
                  4.0e-20
Match length
                  94
                  66
% identity
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PRECURSOR (PPIASE)
                  (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  (CPH) >gi_68412_pir__CSNCM peptidylprolyl isomerase (EC
                  5.2.1.8) precursor, mitochondrial - Neurospora crassa
                  >gi_168806 (J03963) cyclophilin precursor [Neurospora
                  crassa] >gi_295926_emb_CAA35681_ (X17692) cyclophilin
                  (mitochondrial precursor) [Neurospora crassa]
Seq. No.
                  305455
Seq. ID
                  tzu700201883.h1
Method
                  BLASTN
NCBI GI
                  g1213276
BLAST score
                  47
E value
                  2.0e-17
Match length
                  115
% identity
                  84
NCBI Description Z.mays ZEMa gene
                  305456
Seq. No.
Seq. ID
                  tzu700201922.hl
                  BLASTN
Method
NCBI GI
                  g398917
BLAST score
                  46
E value
                  4.0e-17
Match length
                  62
                  94
% identity
NCBI Description B.napus cold induced protein (BnC24A) mRNA
                  305457
Seq. No.
Seq. ID
                  tzu700201935.h1
Method
                  BLASTX
                  g2894599
NCBI GI
BLAST score
                  329
```

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(AL021889) putative protein [Arabidopsis thaliana]

7.0e-31

93

66

E value

Match length

NCBI Description

% identity



Seq. No. 305458

Seq. ID tzu700201938.h1

Method BLASTX
NCBI GI g2842717
BLAST score 274
E value 2.0e-24
Match length 111
% identity 50

NCBI Description GLUTATHIONE S-TRANSFERASE 1-5 (CLASS-THETA)

>gi_1632771_emb_CAB03592_ (Z81291) glutathione

S-transferase [Anopheles gambiae]

Seq. No. 305459

Seq. ID tzu700201939.h1

Method BLASTX
NCBI GI g3873976
BLAST score 335
E value 2.0e-31
Match length 93
% identity 65

NCBI Description (Z81461) predicted using Genefinder; similar to

Zinc-binding metalloprotease domain; cDNA EST EMBL:C09095 comes from this gene; cDNA EST EMBL:T00972 comes from this gene; cDNA EST EMBL:T00973 comes from this gene; cDNA EST

EMBL

Seq. No. 305460

Seq. ID tzu700201955.h1

Method BLASTX
NCBI GI g3176686
BLAST score 308
E value 3.0e-28
Match length 117
% identity 57

NCBI Description (AC003671) Similar to high affinity potassium transporter,

HAK1 protein gb_U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 305461

Seq. ID tzu700201996.h1

Method BLASTX
NCBI GI g2146735
BLAST score 377
E value 2.0e-36
Match length 111
% identity 71

NCBI Description glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (clone

E5) - Arabidopsis thaliana (fragment)

>gi_1166405_emb_CAA59011_ (X84229) glucose-6-phosphate

1-dehydrogenase [Arabidopsis thaliana]

Seq. No. 305462

Seq. ID tzu700202053.h1

Method BLASTX
NCBI GI g4164473
BLAST score 155
E value 1.0e-10



```
Match length
                   36
% identity
                   78
NCBI Description
                   (AF061157) negatively light-regulated protein [Vernicia
                   fordii]
Seq. No.
                   305463
Seq. ID
                   tzu700202072.h1
Method
                   BLASTX
NCBI GI
                   q3582344
BLAST score
                   325
E value
                   1.0e-30
Match length
                   71
% identity
                   87
NCBI Description
                   (AC005496) putative cell division protein [Arabidopsis
                  thaliana]
                   305464
Seq. No.
Seq. ID
                   tzu700202084.h1
Method
                   BLASTX
NCBI GI
                   g3242789
BLAST score
                   265
                   9.0e-24
E value
Match length
                   72
% identity
                   74
NCBI Description
                   (AF055357) respiratory burst oxidase protein D [Arabidopsis
                   thaliana]
                   305465
Seq. No.
Seq. ID
                   tzu700202091.h1
Method
                   BLASTX
NCBI GI
                   g1709000
BLAST score
                   327
E value
                   5.0e-31
Match length
                   66
                   91
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine
                   synthetase [Hordeum vulgare]
Seq. No.
                   305466
Seq. ID
                   tzu700202123.h1
Method
                  BLASTX
NCBI GI
                   g2505865
BLAST score
                   188
E value
                   9.0e-15
Match length
                   72
% identity
                   50
NCBI Description
                  (Y12227) putative topoisomerase [Arabidopsis thaliana]
                   305467
Seq. No.
Seq. ID
                  tzu700202149.h1
```

Method BLASTX
NCBI GI g1710780
BLAST score 168
E value 2.0e-12
Match length 38

% identity 40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ NCBI Description (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina] Seq. No. 305468 Seq. ID tzu700202226.h1 Method BLASTX NCBI GI g1899060 BLAST score 297 E value 2.0e-27 Match length 74 % identity 78 NCBI Description (U79669) endosperm C-24 sterol methyltransferase [Zea mays] Seq. No. 305469 Seq. ID tzu700202231.h1 Method BLASTX NCBI GI g3831457 BLAST score 167 E value 3.0e-12 Match length 53 % identity 55 (AC005700) putative ion channel protein [Arabidopsis NCBI Description thaliana] Seq. No. 305470 Seq. ID tzu700202233.h1 Method BLASTX NCBI GI g2462911 BLAST score 197 E value 1.0e-15 Match length 41 % identity 85 NCBI Description (Z83832) UDP-glucose:sterol glucosyltransferase [Avena sativa] Seq. No. 305471 Seq. ID tzu700202269.h1 Method BLASTX NCBI GI g4100433 BLAST score **137** 1.0e-08 E value Match length 42 % identity 64

NCBI Description (AF000378) beta-glucosidase [Glycine max]

Seq. No. 305472

Seq. ID tzu700202311.h1

Method BLASTN
NCBI GI g303856
BLAST score 61
E value 7.0e-26
Match length 69
% identity 97

NCBI Description Rice mRNA for ubiquitin protein fused to a ribosomal

protein, complete cds

```
Seq. No.
                  305473
Seq. ID
                  tzu700202351.h1
                  BLASTX
Method
NCBI GI
                  q131770
BLAST score
                  187
E value
                  1.0e-14
Match length
                  49
% identity
                  69
NCBI Description
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
                   (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein
                   [Dictyostelium discoideum]
Seq. No.
                  305474
Seq. ID
                  tzu700202355.h1
Method
                  BLASTX
NCBI GI
                  g4388731
BLAST score
                  227
E value
                  3.0e-19
Match length
                  46
% identity
                  87
NCBI Description
                  (AC006413) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  305475
Seq. ID
                  tzu700202387.h1
Method
                  BLASTX
NCBI GI
                  a3367522
BLAST score
                  143
E value
                  2.0e-09
Match length
                  68
% identity
NCBI Description
                  (ACO04392) EST gb T04691 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  305476
Seq. ID
                  tzu700202431.h1
Method
                  BLASTX
NCBI GI
                  g4588906
BLAST score
                  341
E value
                  3.0e-32
Match length
                  86
% identity
                  78
NCBI Description
                  (AF118149) ribosomal protein S7 [Secale cereale]
Seq. No.
                  305477
Seq. ID
                  tzu700202437.h1
Method
                  BLASTX
NCBI GI
                  q2960120
BLAST score
                  282
                  2.0e-25
E value
```

Seq. No. 305478

101

55

Match length

% identity

NCBI Description (AL022121) glpK [Mycobacterium tuberculosis]



```
Seq. ID
                   tzu700202486.h1
Method
                  BLASTX
                  q3176715
NCBI GI
BLAST score
                   308
E value
                  1.0e-28
Match length
                   79
% identity
                  73
NCBI Description
                   (AC002392) putative receptor-like protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  305479
Seq. ID
                   tzu700202507.h1
Method
                  BLASTX
NCBI GI
                  q3540193
BLAST score
                  231
                  2.0e-19
E value
Match length
                  48
% identity
                  85
NCBI Description
                  (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  305480
Seq. ID
                  tzu700202513.h1
Method
                  BLASTX
NCBI GI
                  g3549667
BLAST score
                   271
                   5.0e-24
E value
Match length
                  105
% identity
                   57
NCBI Description
                   (AL031394) Arabidopsis dynamin-like protein ADL2
                   [Arabidopsis thaliana]
Seq. No.
                   305481
Seq. ID
                   tzu700202576.h1
Method
                  BLASTX
NCBI GI
                  q4033424
BLAST score
                  274
E value
                   1.0e-24
Match length
                   52
% identity
                   98
NCBI Description
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
                   PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
Seq. No.
                   305482
Seq. ID
                   tzu700202624.h1
Method
                  BLASTX
NCBI GI
                  g3702336
BLAST score
                   150
```

E value 3.0e-10 Match length 45 % identity 67

(AC005397) putative 3-methyl-2-oxobutanoate NCBI Description

hydroxy-methyl-transferase [Arabidopsis thaliana]

Seq. No. 305483

Seq. ID tzu700202864.h1

Method BLASTX



```
NCBI GI
                  q1076678
BLAST score
                  349
E value
                  3.0e-33
Match length
                  82
                  87
% identity
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
                  305484
Seq. No.
                  tzu700202887.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1944575
BLAST score
                  217
E value
                  4.0e-18
Match length
                  50
% identity
                  78
                  (Z94058) pectinesterase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  305485
                  tzu700202891.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076486
BLAST score
                  265
E value
                  2.0e-23
Match length
                  62
                  74
% identity
                  cim1 protein - soybean >gi_555616 (U03860) cytokinin
NCBI Description
                  induced message [Glycine max]
Seq. No.
                  305486
Seq. ID
                  tzu700202892.h1
Method
                  BLASTX
NCBI GI
                  q2182267
BLAST score
                  282
E value
                  2.0e-25
Match length
                  73
% identity
                  75
NCBI Description (L37359) lipoxygenase [Hordeum vulgare]
Seq. No.
                  305487
                  tzu700202947.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3135611
BLAST score
                  265
E value
                  9.0e-24
Match length
                  53
% identity
                  83
NCBI Description
                 (AF062485) cellulose synthase [Arabidopsis thaliana]
                  305488
Seq. No.
Seq. ID
                  tzu700202961.h1
Method
                  BLASTX
                  g118104
NCBI GI
BLAST score
                  174
E value
                  2.0e-13
Match length
                  41
                  95
% identity
```

43278

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) maize >gi 168461 (M55021) cyclophilin [Zea mays] >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 305489

Seq. ID tzu700203006.h1

BLASTX Method NCBI GI g322577 BLAST score 161 4.0e-11 E value Match length 94 % identity 37

NCBI Description Raf protein kinase homolog CTR1 - Arabidopsis thaliana

305490 Seq. No.

tzu700203022.h1 Seq. ID

Method BLASTX NCBI GI g3327196 BLAST score 335 2.0e-31 E value Match length 90

% identity 72

NCBI Description (AB014591) KIAA0691 protein [Homo sapiens]

305491 Seq. No.

Seq. ID tzu700203050.h1

Method BLASTX NCBI GI g3075390 BLAST score 206 9.0e-17 E value Match length 71 % identity 55

NCBI Description (AC004484) protein kinase ARSK1 [Arabidopsis thaliana]

Seq. No. 305492

Seq. ID tzu700203055.h1

Method BLASTN NCBI GI g2865393 BLAST score 200 E value 1.0e-108 Match length 310 97 % identity

NCBI Description Zea mays basic leucine zipper protein (liguleless2) mRNA,

complete cds

Seq. No. 305493

Seq. ID tzu700203085.h1

Method BLASTX NCBI GI g3335359 BLAST score 218 7.0e-18 E value Match length 82 % identity 60

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 305494

E value

Match length

% identity

1.0e-09

51

59



```
tzu700203123.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3885328
BLAST score
                   270
                   6.0e-24
E value
Match length
                   88
% identity
                   51
NCBI Description
                    (AC005623) putative serine/threonine protein kinase
                    [Arabidopsis thaliana]
Seq. No.
                   305495
Seq. ID
                   tzu700203247.h1
Method
                   BLASTX
NCBI GI
                   q3978578
BLAST score
                   198
E value
                   1.0e-15
Match length
                   86
% identity
                   47
                   (AB020528) Polygalacturonase inhibitor [Poncirus
NCBI Description
                   trifoliata]
Seq. No.
                   305496
Seq. ID
                   tzu700203252.h1
Method
                   BLASTX
NCBI GI
                   q462627
BLAST score
                   334
E value
                   1.0e-31
Match length
                   92
% identity
                   68
NCBI Description
                   MSP1 PROTEIN (TAT-BINDING HOMOLOG 4)
                   >gi_1362427_pir__A49506 MSP1 protein - yeast (Saccharomyces cerevisiae) >gi_404217_emb_CAA48191_ (X68055) MSP1 protein
                    [Saccharomyces cerevisiae] >gi 531756 emb CAA56956
                    (X81069) probable regulatory subunit of 26S protease
                    [Saccharomyces cerevisiae] >gi_1323004_emb_CAA97015_
                    (Z72813) ORF YGR028w [Saccharomyces cerevisiae]
Seq. No.
                   305497
Seq. ID
                   tzu700203269.h1
Method
                   BLASTX
NCBI GI
                   g4512659
BLAST score
                   195
E value
                   3.0e-15
Match length
                   46
% identity
                   76
                   (AC006931) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative
                   protein kinase [Arabidopsis thaliana]
Seq. No.
                   305498
Seq. ID
                   tzu700203307.h1
Method
                   BLASTX
NCBI GI
                   g4512711
BLAST score
                   146
```





```
(AC006569) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    305499
Seq. ID
                    tzu700203341.h1
Method
                    BLASTN
NCBI GI
                    g14275
BLAST score
                    254
E value
                    1.0e-141
Match length
                    262
% identity
                    99
NCBI Description Triticum aestivum mitochondrial nadl gene, exons 2 &
Seq. No.
                    305500
Seq. ID
                    tzu700203377.h1
Method
                   BLASTX
NCBI GI
                    a82306
BLAST score
                    303
E value
                    4.0e-28
Match length
                    62
% identity
                   84
NCBI Description myb protein 305 - garden snapdragon
Seq. No.
                   305501
Seq. ID
                   tzu700203384.h1
Method
                   BLASTX
NCBI GI
                   q461990
BLAST score
                    492
E value
                    5.0e-50
Match length
                   96
% identity
                   98
NCBI Description
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                   >gi_422229_pir S35772 translation elongation factor eEF-1
                   alpha chain - fungus (Trichoderma reesei)
                   >gi_312887_emb_CAA80554_ (Z23012) translation elongation
                   factor la [Hypocrea jecorina] >gi 740014 prf 2004295A
                   elongation factor lalpha [Trichoderma reesei]
Seq. No.
                   305502
Seq. ID
                   tzu700203389.h1
Method
                   BLASTX
NCBI GI
                   q1076791
BLAST score
                   194
E value
                   2.0e-15
Match length
                   54
% identity
                   67
                   calcium-binding protein - maize >gi_2119370_pir__$58170 Calreticulin precursor - maize >gi_577612_emb_CAA86728_
NCBI Description
                    (Z46772) calcium-binding protein [\overline{Z}ea may\overline{s}]
                   >gi_927572_emb_CAA61939_ (X89813) Calreticulin precursor
```

[Zea mays] >gi_1587033_prf__2205314A calreticulin [Zea

mays]

Seq. No. 305503

Seq. ID tzu700203417.h1

Method BLASTN NCBI GI g341874 BLAST score 46



```
E value 3.0e-17

Match length 62
% identity 94

NCBI Description Cricetulus sp. histone (H3.2) gene, 5' end and 5' flanking region

Seq. No. 305504
Seq. ID tzu700203439.h1
```

Method BLASTX
NCBI GI g3294469
BLAST score 360
E value 2.0e-34
Match length 66
% identity 100

NCBI Description (U89342) phosphoglucomutase 2 [Zea mays]

Seq. No. 305505

Seq. ID tzu700203508.h1

Method BLASTX
NCBI GI g1709970
BLAST score 392
E value 3.0e-38
Match length 108
% identity 72

NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 305506

Seq. ID tzu700203653.h1

Method BLASTX
NCBI GI g133776
BLAST score 161
E value 1.0e-11
Match length 43
% identity 77

NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi_70944_pir__R4HY14 ribosomal

protein S14 - Chinese hamster >gi_88569_pir_ A25220

ribosomal protein S14 - human >gi_304525 (M11241) ribosomal

protein S14 [Cricetulus griseus] >gi_337499 (M13934) ribosomal protein S14 [Homo sapiens] >gi_387057 (M35008)

ribosomal protein S14 [Cricetulus griseus]

Seq. No. 305507

Seq. ID tzu700203681.h1

Method BLASTX
NCBI GI g3135543
BLAST score 377
E value 3.0e-36
Match length 99
% identity 74

NCBI Description (AF062393) aquaporin [Oryza sativa]

Seq. No. 305508

Seq. ID tzu700203694.h1

Method BLASTN
NCBI GI g2270986
BLAST score 78
E value 2.0e-36

Match length

% identity

67

82



```
Match length
% identity
                   94
NCBI Description
                  Paracoccidioides brasiliensis 28S ribosomal RNA gene,
                   partial sequence
Seq. No.
                   305509
Seq. ID
                   tzu700203707.h1
Method
                  BLASTX
NCBI GI
                   g3643611
BLAST score
                   149
E value
                   4.0e-10
Match length
                   54
% identity
                   50
                  (AC005395) putative casein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  305510
Seq. ID
                  tzu700203717.h1
Method
                  BLASTX
NCBI GI
                  q2662341
BLAST score
                  163
E value
                   9.0e-12
Match length
                   32
% identity
                  97
                  (D63580) EF-1 alpha [Oryza sativa]
NCBI Description
                  >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                  satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                   [Oryza sativa]
Seq. No.
                  305511
Seq. ID
                  tzu700203730.h1
Method
                  BLASTX
NCBI GI
                  g2809246
BLAST score
                  265
E value
                  9.0e-24
Match length
                  69
% identity
                  74
NCBI Description
                  (AC002560) F2401.15 [Arabidopsis thaliana]
Seq. No.
                  305512
Seq. ID
                  tzu700203731.h1
Method
                  BLASTX
NCBI GI
                  g4263722
BLAST score
                  258
E value
                  6.0e-23
Match length
                  58
% identity
                  69
NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]
Seq. No.
                  305513
Seq. ID
                  tzu700203733.h1
Method
                  BLASTX
NCBI GI
                  g2342690
BLAST score
                  286
E value
                  3.0e-26
```

43283

NCBI Description (AC000106) Similar to Homo copine I (gb_U83246).

Seq. No.

305519



[Arabidopsis thaliana]

```
Seq. No.
                   305514
Seq. ID
                   tzu700203846.h1
Method
                   BLASTN
NCBI GI
                   q2431766
BLAST score
                   151
E value
                   8.0e-80
Match length
                   162
                   99
% identity
NCBI Description
                   Zea mays acidic ribosomal protein P3a (rpp3a) mRNA,
                   complete cds
Seq. No.
                   305515
Seq. ID
                   tzu700204010.h1
Method
                   BLASTX
NCBI GI
                   g4426964
BLAST score
                   148
E value
                   5.0e-10
Match length
                   33
% identity
                   70
NCBI Description
                   (AF126255) purple acid phosphatase precursor [Anchusa
                   officinalis]
Seq. No.
                   305516
Seq. ID
                   tzu700204022.h1
Method
                   BLASTX
NCBI GI
                   g4098238
BLAST score
                   203
                   4.0e-16
E value
Match length
                   96
% identity
                   56
NCBI Description
                  (U76384) o-methyltransferase [Triticum aestivum]
Seq. No.
                   305517
Seq. ID
                   tzu700204142.h1
Method
                   BLASTX
NCBI GI
                   g2792210
BLAST score
                   153
E value
                   3.0e-10
Match length
                   94
% identity
                   36
                   (AF032683) NBS-LRR type resistance protein [Hordeum
NCBI Description
                   vulgare]
Seq. No.
                   305518
Seq. ID
                   tzu700204169.h1
Method
                  BLASTX
NCBI GI
                   q4584345
BLAST score
                  154
                   2.0e-10
E value
Match length
                  35
% identity
                   83
NCBI Description
                   (AC007127) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
```

43284



```
Seq. ID
                  tzu700204194.h1
                  BLASTX'
Method
NCBI GI
                  q3834324
BLAST score
                  227
E value
                  6.0e-19
Match length
                  94
% identity
                  52
NCBI Description
                  (AC005679) Similar to gb_X92762 tafazzins protein from Homo
                  sapiens. [Arabidopsis thaliana]
Seq. No.
                  305520
Seq. ID
                  tzu700204196.h1
Method
                  BLASTX
NCBI GI
                  q3142303
```

BLAST score 268 9.0e-24 E value Match length 94 % identity 56

NCBI Description

(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 305521

Seq. ID tzu700204208.h1

Method BLASTX NCBI GI q1946265 BLAST score 285 8.0e-26 E value Match length 74 % identity 69

NCBI Description (Y11414) myb [Oryza sativa]

Seq. No. 305522

Seq. ID tzu700204232.h1

Method BLASTX NCBI GI q3249064 BLAST score 299 E value 2.0e-27 Match length 88 % identity 59

(AC004473) Strong similarity to trehalose-6-phosphate NCBI Description synthase homolog gb 2245136 from A. thaliana chromosome 4

contig gb_Z97344. [Arabidopsis thaliana]

Seq. No. 305523

Seq. ID tzu700204274.h1

Method BLASTX NCBI GI g1076746 BLAST score 224 E value 1.0e-18 Match length 70 % identity 64

NCBI Description heat shock protein 70 - rice (fragment)

>gi_763160_emb_CAA47948_ (X67711) heat shock protein 70

[Oryza sativa]



```
Seq. No.
                   305524
Seq. ID
                   tzu700204305.h1
Method
                   BLASTX
NCBI GI
                   g4006918
BLAST score
                   203
E value
                   6.0e-16
Match length
                   58
% identity
                   69
NCBI Description
                  (Z99708) peroxidase like protein [Arabidopsis thaliana]
Seq. No.
                   305525
Seq. ID
                   tzu700204412.h1
                   BLASTN
```

Method NCBI GI q4239886 BLAST score 187 E value 1.0e-101 Match length 191

% identity 99

Seq. No.

NCBI Description Zea mays mRNA for MAP kinase 4, complete cds

Seq. ID tzu700204451.h1 Method BLASTX NCBI GI q3367519 BLAST score 316 E value 2.0e-29 Match length 100 % identity 61

(AC004392) Contains similarity to gb U51898 NCBI Description

Ca2+-independent phospholipase A2 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 305527

Seq. ID tzu700204456.h1

305526

Method BLASTX NCBI GI g1709563 BLAST score 357 E value 1.0e-34 Match length 72 % identity 97

PHENYLALANINE AMMONIA-LYASE >gi_2130081_pir__\$66313 NCBI Description

phenylalanine ammonia-lyase (EC 4.3.1.5) - rice >gi_871494_emb CAA61198 (X87946) phenylalanine

ammonia-lyase [Oryza sativa]

Seq. No. 305528

Seq. ID tzu700204462.hl

Method BLASTX NCBI GI g3647233 BLAST score 421 E value 1.0e-41 Match length 106 74 % identity

NCBI Description (AF039748) 40S ribosomal protein S4 [Dictyostelium

discoideum]

Seq. No. 305529



```
tzu700204467.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4510339
                   322
BLAST score
E value
                   2.0e-30
Match length
                   78
% identity
                   77
NCBI Description
                   (AC006921) putative ABC transporter protein [Arabidopsis
                   thaliana]
Seq. No.
                   305530
Seq. ID
                   tzu700204479.h1
Method
                  BLASTX
NCBI GI
                   q2191144
BLAST score
                  152
E value
                   4.0e-10
Match length
                   64
% identity
                   48
                  (AF007269) A IG002N01.24 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   305531
Seq. No.
Seq. ID
                   tzu700204491.h1
Method
                  BLASTX
NCBI GI
                  q1737220
BLAST score
                   432
                   6.0e-43
E value
Match length
                  101
% identity
                  70
NCBI Description
                  (U79960) vacuolar sorting receptor homolog [Arabidopsis
                  thaliana]
Seq. No.
                  305532
Seq. ID
                  tzu700204543.h1
Method
                  BLASTX
NCBI GI
                  q542157
BLAST score
                  246
E value
                   3.0e-21
Match length
                  70
% identity
                  71
NCBI Description ribosomal 5S RNA-binding protein - Rice
Seq. No.
                  305533
Seq. ID
                  tzu700204574.h1
Method
                  BLASTX
NCBI GI
                  g2130072
BLAST score
                  177
E value
                   4.0e-13
Match length
                  78
% identity
                  51
NCBI Description
                  ferredoxin--nitrite reductase (EC 1.7.7.1) - rice
                  >gi_809514_dbj_BAA09122_ (D50556) ferredoxin-nitrite
                  reductase [Oryza sativa]
```

Seq. No. 305534

Seq. ID tzu700204588.h1

Method BLASTX



NCBI GI g1362086
BLAST score 394
E value 2.0e-38
Match length 81
% identity 94
NCBI Description 5-methyl

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi_2129919_pir__\$65957

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase

[Catharanthus roseus]

Seq. No. 305535

Seq. ID tzu700204629.h1

Method BLASTX
NCBI GI g2618686
BLAST score 249
E value 2.0e-21
Match length 73
% identity 60

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 305536

Seq. ID tzu700204637.h1

Method BLASTX
NCBI GI g4539671
BLAST score 155
E value 2.0e-10
Match length 47
% identity 62

NCBI Description (AF061282) serine carboxypeptidase [Sorghum bicolor]

Seq. No. 305537

Seq. ID tzu700204638.h1

Method BLASTX
NCBI GI g710626
BLAST score 177
E value 4.0e-13
Match length 39
% identity 72

NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941

(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis

thaliana]

Seq. No. 305538

Seq. ID tzu700204648.h1

Method BLASTX
NCBI GI g4567198
BLAST score 203
E value 4.0e-16
Match length 83
% identity 48

NCBI Description (AC007168) putative GTP-binding protein [Arabidopsis

thaliana]



```
Seq. No.
                   305539
Seq. ID
                  tzu700204652.h1
Method
                  BLASTX
NCBI GI
                  g2244806
BLAST score
                  241
E value
                  1.0e-20
Match length
                   69
% identity
                   62
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  305540
Seq. ID
                  tzu700204693.h1
Method
                  BLASTX
                  g2232017
NCBI GI
BLAST score
                   401
                  3.0e-39
E value
Match length
                  96
                  77
% identity
NCBI Description
                  (U95953) viviparous-14 [Zea mays]
                  305541
Seq. No.
                  tzu700204696.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3063709
                  185
BLAST score
                   4.0e-14
E value
Match length
                  76
                  51
% identity
NCBI Description
                  (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                  305542
                   tzu700204730.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g134976
BLAST score
                   238
E value
                   3.0e-20
Match length
                   53
                  83
% identity
                  GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi 81619 pir S12042
NCBI Description
                   glucose transport protein STP1 - Arabidopsis thaliana
                  >gi_16520_emb_CAA39037_ (X55350) glucose transporter
                   [Arabidopsis thaliana]
Seq. No.
                  305543
Seq. ID
                   tzu700204754.h1
Method
                  BLASTX
NCBI GI
                  g1352469
BLAST score
                   567
E value
                   1.0e-58
Match length
                  101
```

98

% identity NCBI Description

BETA-FRUCTOFURANOSIDASE, CELL WALL ISOZYME PRECURSOR (SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) >qi 736359 (U17695) invertase [Zea mays] >gi_1582380_prf 2118364A

cell wall invertase [Zea mays]

Seq. No.

305544



```
Seq. ID
                  tzu700204755.h1
Method
                  BLASTX
NCBI GI
                  a3024018
BLAST score
                  440
                  7.0e-44
E value
Match length
                  83
% identity
                  99
NCBI Description
                  INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
                  >gi_1546919_emb_CAA69225_ (Y07920) translation initiation
                  factor 5A [Zea mays] >gi_2668738 (AF034943) translation
                  initiation factor 5A [Zea mays]
```

Seq. No. 305545 Seq. ID tzu700204756.h1

305546

305547

Method BLASTX NCBI GI q1743354 BLAST score 295 7.0e-27 E value Match length 98 52 % identity

NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No. tzu700204792.h1 Seq. ID Method BLASTX NCBI GI g2911044 BLAST score 276 E value 1.0e-24 Match length 80 70 % identity

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. ID tzu700204815.h1 Method BLASTX NCBI GI q4056425 BLAST score 144 E value 2.0e-12 Match length 44 % identity 80

Seq. No.

NCBI Description (AC005322) ESTs gb H36249, gb AA59732 and gb AA651219 come

from this gene. [Arabidopsis thaliana]

Seq. No. 305548

Seq. ID tzu700204921.h1

Method BLASTX NCBI GI g3063700 BLAST score 287 6.0e-26 E value Match length 102 % identity

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 305549

Seq. ID tzu700204926.h1

Method BLASTX NCBI GI g4587556



BLAST score E value 7.0e-33 Match length 99 % identity 61

NCBI Description (AC006577) Similar to gi_1653162 (p)ppGpp

3-pyrophosphohydrolase from Synechocystis sp genome gb_D90911. EST gb W43807 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 305550

Seq. ID tzu700204929.h1

Method BLASTX NCBI GI q2144191 BLAST score 147 E value 2.0e-09 Match length 60 48 % identity

NCBI Description glucan 1,4-beta-glucosidase (EC 3.2.1.74) - Microbispora

bispora >gi 149826 (L06134) glucan-glucohydrolase

[Microbispora bispora]

Seq. No. 305551

Seq. ID tzu700204940.h1

Method BLASTX q2435522 NCBI GI BLAST score 151 E value 5.0e-10 Match length 47 % identity 60

(AF024504) contains similarity to other AMP-binding enzymes NCBI Description

[Arabidopsis thaliana]

Seq. No. 305552

Seq. ID tzu700205015.hl

Method BLASTX q1771160 NCBI GI BLAST score 231 E value 8.0e-20 Match length 73 % identity 70

NCBI Description (X98929) SBT1 [Lycopersicon esculentum]

>gi 3687305 emb CAA06999 (AJ006378) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No. 305553

Seq. ID tzu700205019.h1

Method BLASTX NCBI GI q417716 BLAST score 212 E value 1.0e-17 Match length 65 % identity 63

40S RIBOSOMAL PROTEIN S28 >gi_422182_pir__A46703 ribosomal NCBI Description

protein S23.e - yeast (Saccharomyces cerevisiae) >gi 172498 (M96570) ribosomal protein S28 [Saccharomyces cerevisiae] >gi_172500 (M96571) ribosomal protein S28 [Saccharomyces cerevisiae] >gi_1066485 (U40829) 40S ribosomal protein S28



P32827) [Saccharomyce

(Swiss Prot. accession number P32827) [Saccharomyces cerevisiae] >gi_1323191_emb_CAA97128_ (Z72903) ORF YGR118w [Saccharomyces cerevisiae]

Method BLASTX
NCBI GI 94587583
BLAST score 195
E value 2.0e-15
Match length 63
% identity 49

% identity 49
NCBI Description (AC007232) hypothetical protein; 5' partial [Arabidopsis

thaliana]

Seq. No. 305555

Seq. ID tzu700205079.h1

Method BLASTX
NCBI GI g2262166
BLAST score 161
E value 2.0e-18
Match length 63
% identity 84

NCBI Description (AC002329) hypothetical protein [Arabidopsis thaliana]

Seq. No. 305556

Seq. ID tzu700205090.h1

Method BLASTX
NCBI GI g2760844
BLAST score 176
E value 5.0e-13
Match length 50
% identity 64

NCBI Description (AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No. 305557

Seq. ID tzu700205132.h1

Method BLASTX
NCBI GI g3927806
BLAST score 274
E value 2.0e-24
Match length 95
% identity 59

NCBI Description (U96439) aminoalcoholphosphotransferase [Pimpinella

brachycarpa]

Seq. No. 305558

Seq. ID tzu700205143.h1

Method BLASTN
NCBI GI 97271142
BLAST score 112
E value 3.0e-56
Match length 170
% identity 93

NCBI Description F.hygrometrica 25S rRNA gene

Seq. No. 305559



168

81

4.0e-12

E value

Match length

```
Seq. ID
                  tzu700205191.h1
Method
                  BLASTN
NCBI GI
                  g2944039
BLAST score
                  164
                  2.0e-87
E value
Match length
                  200
% identity
                  95
NCBI Description Zea mays indeterminate spikelet 1 (ids1) mRNA, complete cds-
                  305560
Seq. No.
Seq. ID
                  tzu700205411.h1
Method
                  BLASTX
NCBI GI
                  g4538979
                  177
BLAST score
                  4.0e-13
E value
Match length
                  54
% identity
                  48
NCBI Description
                  (AL049487) putative protein [Arabidopsis thaliana]
Seq. No.
                  305561
                  tzu700205455.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213594
BLAST score
                  299
E value
                  2.0e-27
Match length
                  88
% identity
                  62
NCBI Description
                  (AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.
                  305562
Seq. ID
                  tzu700205503.h1
Method
                  BLASTX
NCBI GI
                  g1076777
BLAST score
                  192
E value
                  7.0e-15
Match length
                  61
% identity
                  66
NCBI Description
                  protein H2A - wheat >gi_536890_dbj BAA07277 (D38088)
                  protein H2A [Triticum aestivum]
Seq. No.
                  305563
Seq. ID
                  tzu700205526.h1
Method
                  BLASTX
NCBI GI
                  q4544412
BLAST score
                  284
E value
                  1.0e-25
Match length
                  92
% identity
                  55
NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  305564
Seq. ID
                  tzu700205543.h1
Method
                  BLASTX
NCBI GI
                  g2947063
BLAST score
```



% identity 46
NCBI Description (AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 305565
Seq. ID tzu700205546.h1
Method BLASTX

Method BLASTX
NCBI GI g4008441
BLAST score 173
E value 6.0e-13
Match length 42
% identity 79

NCBI Description (AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST

yk433c6.5 comes from this gene [Caenorhabditis elegans]

Seq. No. 305566

Seq. ID tzu700205554.h1

Method BLASTN
NCBI GI g22292
BLAST score 102
E value 2.0e-50
Match length 158
% identity 91

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 305567

Seq. ID tzu700205626.h1

Method BLASTX
NCBI GI g4321762
BLAST score 213
E value 2.0e-17
Match length 72

% identity 61

NCBI Description (AF061107) transcription factor MYC7E [Zea mays]

Seq. No. 305568

Seq. ID tzu700205786.h1

Method BLASTN
NCBI GI g3420038
BLAST score 88
E value 6.0e-42
Match length 123
% identity 47

NCBI Description Zea mays gypsy/Ty3-type retrotransposon Tekay, complete

sequence

Seq. No. 305569

Seq. ID tzu700205862.h1

Method BLASTX
NCBI GI g2827715
BLAST score 284
E value 1.0e-25
Match length 89
% identity 65

NCBI Description (AL021684) receptor protein kinase - like protein



[Arabidopsis thaliana]

```
305570
Seq. No.
Seq. ID
                   tzu700205984.h1
Method
                  BLASTN
                   q2370460
NCBI GI
BLAST score
                   83
                   6.0e-39
E value
Match length
                   160
% identity
                   94
NCBI Description Sorghum bicolor mRNA for putative glycoprotein
                   305571
Seq. No.
                   tzu700206003.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1220453
BLAST score
                   174
                   5.0e-13
E value
                   35
Match length
                   80
% identity
                  (M79328) alpha-amylase [Solanum tuberosum]
NCBI Description
                   305572
Seq. No.
                   tzu700206042.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2827650
BLAST score
                   223
E value
                   8.0e-19
Match length
                   57
                   72
% identity
NCBI Description
                   (AL021637) potassium transporter-like protein [Arabidopsis
                   thaliana]
                   305573
Seq. No.
                   tzu700206068.h1
Seq. ID
Method
                   BLASTX
                   g3559805
NCBI GI
BLAST score
                   199
                   5.0e-16
E value
Match length
                   52
% identity
                   69
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   305574
Seq. No.
                   tzu700206069.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2642156
BLAST score
                   162
                   2.0e-11
E value
Match length
                   76
% identity
                   45
```

(AC003000) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. Seq. ID

305575

tzu700206106.h1 BLASTX

Method

```
q2342690
NCBI GI
BLAST score
                  441
                  7.0e-44
E value
Match length
                  123
% identity
                  69
NCBI Description
                  (AC000106) Similar to Homo copine I (gb U83246).
                  [Arabidopsis thaliana]
                  305576
Seq. No.
                  tzu700206118.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2444178
BLAST score
                  279
E value
                  2.0e-25
Match length
                  73
                  75
% identity
                  (U94784) unconventional myosin [Helianthus annuus]
NCBI Description
                  305577
Seq. No.
                  tzu700206146.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587578
BLAST score
                  325
E value
                  3.0e-30
Match length
                  122
% identity
                  54
NCBI Description
                  (AC006550) Belongs to PF 00004 ATPases associated with
                  various cellular activities. [Arabidopsis thaliana]
Seq. No.
                  305578
                  tzu700206163.h1
Seq. ID
Method
                  BLASTX
                  g3386611
NCBI GI
BLAST score
                  359
E value
                  2.0e-34
Match length
                  103
                  59
% identity
NCBI Description
                  (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.
                  305579
Seq. ID
                  tzu700206166.h1
Method
                  BLASTX
NCBI GI
                  g3193284
BLAST score
                  235
                  3.0e-20
E value
Match length
                  69
% identity
                  64
NCBI Description
                  (AF069298) No definition line found [Arabidopsis thaliana]
```

Seq. No. 305580

Seq. ID tzu700206188.h1

Method BLASTX NCBI GI q1899188 BLAST score 323 E value 3.0e-30 Match length 88 % identity 59



NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No. 305581

Seq. ID tzu700206192.h1

Method BLASTN
NCBI GI g248338
BLAST score 214
E value 1.0e-117
Match length 218
% identity 85

NCBI Description polyubiquitin [maize, Genomic, 3439 nt]

Seq. No. 305582

Seq. ID tzu700206339.h1

Method BLASTX
NCBI GI g1149569
BLAST score 356
E value 6.0e-34
Match length 118
% identity 60

NCBI Description (Z50851) HD-zip [Arabidopsis thaliana]

Seq. No. 305583

Seq. ID tzu700206422.h1

Method BLASTX
NCBI GI g1173257
BLAST score 250
E value 5.0e-22
Match length 59
% identity 75

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 1076674 pir S47642 ribosomal

protein S4 - potato >gi 457803 emb CAA54095 (X76651)

ribosomal protein S4 [Solanum tuberosum]

Seq. No. 305584

Seq. ID tzu700206454.h1

Method BLASTX
NCBI GI g3953471
BLAST score 420
E value 1.0e-41
Match length 101
% identity 72

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 305585

Seq. ID tzu700206489.h1

Method BLASTX
NCBI GI g1362086
BLAST score 440
E value 7.0e-44
Match length 92
% identity 93

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi_2129919 pir \$65957

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle





>gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

 Seq. No.
 305586

 Seq. ID
 tzu700206505.h1

 Method
 BLASTX

 NCBI GI
 g1076291

 BLAST score
 278

 E value
 2.0e-32

E value 2.00 Match length 109 % identity 64

NCBI Description amino acid transporter AAT1 - Arabidopsis thaliana

>gi_2911069_emb_CAA17531.1_ (AL021960) amino acid transport

protein AAT1 [Arabidopsis thaliana]

Seq. No. 305587

Seq. ID tzu700206514.h1

Method BLASTX
NCBI GI g2347188
BLAST score 168
E value 6.0e-12
Match length 65
% identity 55

NCBI Description (AC002338) laccase isolog [Arabidopsis thaliana]

>gi 3150401 (AC004165) putative laccase [Arabidopsis

thaliana]

Seq. No. 305588

Seq. ID tzu700206527.h1

Method BLASTX
NCBI GI g2804612
BLAST score 521
E value 2.0e-53
Match length 107
% identity 93

NCBI Description (U81165) MOD-E [Podospora anserina]

Seq. No. 305589

Seq. ID tzu700206575.h1

Method BLASTN
NCBI GI g22144
BLAST score 282
E value 1.0e-157
Match length 325
% identity 97

NCBI Description Maize anaerobically regulated gene for fructose

bisphosphate aldolase (EC 4.1.2.13)

Seq. No. 305590

Seq. ID tzu700206603.h1

Method BLASTX
NCBI GI g2462834
BLAST score 150
E value 8.0e-10
Match length 56
% identity 48

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
                  305591
                  tzu700206628.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056506
BLAST score
                  214
E value
                  2.0e-17
Match length
                  78
                  53
% identity
                  (AC005896) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
                  305592
Seq. No.
Seq. ID
                  tzu700206634.h1
Method
                  BLASTX
                  g399854
NCBI GI
BLAST score
                  165
                  1.0e-11
E value
Match length
                  57
                  67
% identity
                  HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize
NCBI Description
                  >gi 22325 emb CAA40565 (X57313) H2B histone [Zea mays]
                  305593
Seq. No.
Seq. ID
                  tzu700206688.h1
Method
                  BLASTX
                  g2827082
NCBI GI
BLAST score
                  185
E value
                  2.0e-14
Match length
                  53
% identity
                  70
NCBI Description (AF020272) malate dehydrogenase [Medicago sativa]
Seq. No.
                  305594
Seq. ID
                  tzu700206727.h1
Method
                  BLASTX
NCBI GI
                  g3212869
BLAST score
                  218
                  3.0e-35
E value
Match length
                  91
% identity
                  82
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  305595
Seq. ID
                  tzu700206728.h1
Method
                  BLASTX
NCBI GI
                  g4521167
BLAST score
                  344
E value
                  1.0e-32
Match length
                  105
% identity
                  57
```

2

NCBI Description (AB011375) 26,29kDa proteinase [Sarcophaga peregrina]

Seq. No. 305596

Seq. ID tzu700206761.h1

Method BLASTX
NCBI GI g2494174
BLAST score 299



E value 2.0e-40 Match length 106 % identity 79

NCBI Description GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi_497979 (U10034)

glutamate decarboxylase [Arabidopsis thaliana]

Seq. No. 305597

Seq. ID tzu700206818.hl

Method BLASTX
NCBI GI g1350783
BLAST score 152
E value 4.0e-10
Match length 99
% identity 41

NCBI Description RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR

>gi_282883_pir__S27756 receptor-like protein kinase
precursor - Arabidopsis thaliana >gi_166850 (M84660)
receptor-like protein kinase [Arabidopsis thaliana]

>gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein

kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No. 305598

Seq. ID tzu700206819.h1

Method BLASTX
NCBI GI g3122071
BLAST score 444
E value 2.0e-44
Match length 86
% identity 99

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_2130148_pir__S66339 translation elongation factor eEF-1
alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408)
alpha subunit of tlanslation elongation factor 1 [Zea mays]

Seq. No. 305599

Seq. ID tzu700206836.h1

Method BLASTX
NCBI GI g2576361
BLAST score 234
E value 9.0e-20
Match length 54
% identity 76

NCBI Description (U39782) lysine and histidine specific transporter

[Arabidopsis thaliana]

Seq. No. 305600

Seq. ID tzu700206861.h1

Method BLASTX
NCBI GI g1684913
BLAST score 255
E value 2.0e-22
Match length 76
% identity 61

NCBI Description (U77888) receptor-like protein kinase [Ipomoea nil]

Seq. No. 305601

Seq. ID tzu700206891.h1

BLAST score

E value

416 5.0e-41



```
Method
                   BLASTX
NCBI GI
                   g246248
BLAST score
                   240
                   8.0e-21
E value
Match length
                   68
                   71
% identity
                   GmPK2=protein kinase [Glycine max L.=soybeans, Peptide, 119
NCBI Description
                   305602
Seq. No.
                   tzu700206894.h1
Seq. ID
                   BLASTX
Method
                   q1632822
NCBI GI
                   153
BLAST score
E value
                   1.0e-10
Match length
                   50
                   64
% identity
                   (Y08962) transmembrane protein [Oryza sativa] >gi_1667594
NCBI Description
                   (U77297) transmembrane protein [Oryza sativa]
Seq. No.
                   305603
                   tzu700206931.h1
Seq. ID
                   BLASTX
Method
                   g101772
NCBI GI
BLAST score
                   441
E value
                   6.0e-44
                   108
Match length
% identity
                   74
                   anthranilate synthase multifunctional protein - Aspergillus
NCBI Description
                   awamori
                   305604
Seq. No.
                   tzu700206973.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4105772
                   277
BLAST score
                   8.0e-25
E value
Match length
                   77
% identity
                   65
NCBI Description
                   (AF049917) PGP9B [Petunia x hybrida]
Seq. No.
                   305605
                   tzu700206979.h1
Seq. ID
Method
                   BLASTX
                   g2677830
NCBI GI
BLAST score
                   216
                   5.0e-18
E value
Match length
                   56
% identity
                   80
NCBI Description
                   (U93168) ribosomal protein L12 [Prunus armeniaca]
Seq. No.
                   305606
                   tzu700207017.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2511715
```



Match length 74 % identity

(AF019380) putative phosphatidylinositol-4-phosphate NCBI Description 5-kinase [Arabidopsis thaliana]

Seq. No.

305607

Seq. ID

tzu700207035.h1

Method BLASTX g2244940 NCBI GI 182 BLAST score 1.0e-22 E value

67 Match length 85 % identity

(Z97339) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

305608

Seq. ID

tzu700207045.h1

BLASTX Method q312179 NCBI GI BLAST score 353 1.0e-33 E value 74 Match length 93 % identity

(X73151) glyceraldehyde 3-phosphate dehydrogenase NCBI Description

(phosphorylating) [Zea mays] >gi 1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi 1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Seq. No.

305609

Seq. ID

tzu700207068.h1

BLASTX Method g1699220 NCBI GI BLAST score 153 E value 3.0e-10 102 Match length % identity 39

NCBI Description

D-ERp60=protein disulphide isomerase

isoform/multifunctional endoplasmic reticulum luminal polypeptide [Drosophila melanogaster, Peptide, 489 aa]

Seq. No.

305610

Seq. ID

uC-zmflB73002a04b1

Method BLASTX NCBI GI g3510255 BLAST score 191 2.0e-14 E value 57 Match length % identity 67

NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No.

305611

Seq. ID

uC-zmflB73002b10b1

Method BLASTX NCBI GI g2460298 BLAST score 234 E value 1.0e-19



Match length 119 % identity 38

NCBI Description (AF022152) AP-3 complex beta3B subunit [Homo sapiens]

Seq. No. 305612

Seq. ID uC-zmflB73002c03b1

Method BLASTX
NCBI GI g129939
BLAST score 343
E value 2.0e-32
Match length 113
% identity 51

NCBI Description POLYGALACTURONASE 2A PRECURSOR (PG-2A) (PECTINASE)

>gi_82101_pir__A25534 polygalacturonase (EC 3.2.1.15)
precursor - tomato >gi_19292 emb_CAA28254_ (X04583)
precursor polypeptide (AA -71 to 386) [Lycopersicon

esculentum] >gi_19298_emb_CAA29148_ (X05656)

polygalacturonase (AA 1-457) [Lycopersicon esculentum] >gi_170473 (M37304) polygalacturonase [Lycopersicon

esculentum] >gi_295813_emb_CAA32235_ (X14074) polygalacturonase [Lycopersicon esculentum]

Seq. No. 305613

Seq. ID uC-zmflB73002e12b1

Method BLASTX
NCBI GI g123593
BLAST score 201
E value 3.0e-16
Match length 59
% identity 75

NCBI Description HEAT SHOCK 70 KD PROTEIN >gi 82697 pir A25089 heat shock

protein 70 - maize

Seq. No. 305614

Seq. ID uC-zmflB73002f11b1

Method BLASTX
NCBI GI g3386613
BLAST score 329
E value 1.0e-30
Match length 82
% identity 79

NCBI Description (AC004665) putative ATP-dependent RNA helicase [Arabidopsis

thaliana]

Seq. No. 305615

Seq. ID uC-zmflB73003d12b1

Method BLASTX
NCBI GI g2384758
BLAST score 167
E value 4.0e-12
Match length 50
% identity 76

NCBI Description (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza

sativa]

Seq. No. 305616

Seq. ID uC-zmflB73003f02b1



```
Method
                  BLASTN
NCBI GI
                  g3688588
BLAST score
                  49
                  7.0e-19
E value
Match length
                  81
                  90
% identity
NCBI Description Triticum aestivum TaMADS#11 mRNA for MADS box transcription
                  factor, complete cds
                  305617
Seq. No.
                  uC-zmflB73003g01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263721
BLAST score
                  200
                  6.0e-16
E value
                  91
Match length
                  46
% identity
                  (AC006223) putative DNA repair protein RAD50 [Arabidopsis
NCBI Description
                  thaliana]
                  305618
Seq. No.
                  uC-zmflB73004a04b1
Seq. ID
Method
                  BLASTX
                  g4204265
NCBI GI
BLAST score
                  254
E value
                  7.0e-22
                  104
Match length
% identity
                  46
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
                  305619
Seq. No.
                  uC-zmflB73004b02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263787
BLAST score
                  164
                  2.0e-11
E value
Match length
                  43
                  74
% identity
NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]
                  305620
Seq. No.
Seq. ID
                  uC-zmflB73004b11b1
Method
                  BLASTX
NCBI GI
                  q1708107
BLAST score
                  346
E value
                  1.0e-32
Match length
                  91
                  80
% identity
NCBI Description HISTONE H2B >gi 473605 (U08226) histone H2B [Zea mays]
Seq. No.
                  305621
                  uC-zmflB73004c04b1
Seq. ID
```

Method BLASTX NCBI GI g2160166 BLAST score 167 1.0e-11 E value 74 Match length

```
% identity
NCBI Description
                  (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                  305622
                  uC-zmflB73004d01b1
Seq. ID
                  BLASTN
Method
                  q22332
NCBI GI
BLAST score
                  72
                  1.0e-32
E value
Match length
                  80
                  97
% identity
NCBI Description
                  Z.mays HRGP gene
                  305623
Seq. No.
Seq. ID
                  uC-zmflB73004e02b1
Method
                  BLASTX
NCBI GI
                  q114420
BLAST score
                  310
                  2.0e-28
E value
Match length
                  80
% identity
                  80
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi 100882 pir S11491 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - maize
                  >gi 22173 emb CAA38140 (X54233) ATPase F1 subunit protein
                  [Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea
                  mays]
Seq. No.
                  305624
                  uC-zmflB73004f04b1
Seq. ID
Method
                  BLASTX
                  g2274859
NCBI GI
BLAST score
                  394
                  3.0e-38
E value
                  73
Match length
% identity
                  96
                  (AJ000016) Cks1 protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4510420_gb_AAD21506.1_ (AC006929) putative
                  cyclin-dependent kinase regulatory subunit [Arabidopsis
                  thaliana]
Seq. No.
                  305625
                  uC-zmflB73004f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406807
BLAST score
                  175
E value
                  3.0e-22
Match length
                  73
% identity
NCBI Description
                  (AC006201) putative elongation factor beta-1 [Arabidopsis
                  thaliana]
```

Seq. No. 305626

Seq. ID uC-zmflB73004h12b1

Method BLASTX NCBI GI g4467137 BLAST score 228

```
E value
                  6.0e-19
Match length
                  67
% identity
                  67
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                  305627
Seq. No.
                  uC-zmflB73005b03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g137460
BLAST score
                  339
                  4.0e-33
E value
                  99
Match length
                  78
% identity
NCBI Description
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
```

SUBUNIT) >gi 67952 pir PXPZV9 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 69K chain - carrot >gi_167560 (J03769)

vacular H+-ATPase [Daucus carota]

305628 Seq. No. uC-zmflB73005d01b1 Seq. ID Method BLASTX g123558 NCBI GI BLAST score 185 6.0e-14 E value

Match length 87 43 % identity

NCBI Description CHLOROPLAST SMALL HEAT SHOCK PROTEIN PRECURSOR

>gi 71500 pir HHPM21 heat shock protein 21 precursor garden pea >gi 20764 emb CAA30167 (X07187) pre-hsp21 (AA 1

- 232) [Pisum sativum]

305629 Seq. No.

Seq. ID uC-zmflB73005g07b1

Method BLASTN NCBI GI g22174 BLAST score 38 2.0e-12 E value Match length 66 89 % identity

NCBI Description Maize Aux311 gene for auxin-binding protein

305630 Seq. No.

uC-zmflB73005g10b1 Seq. ID

Method BLASTX NCBI GI g2104534 BLAST score 178 1.0e-13 E value Match length 47 % identity 74

(AF001308) hypothetical protein [Arabidopsis thaliana] NCBI Description

305631 Seq. No.

uC-zmflB73006a07b1 Seq. ID

Method BLASTN NCBI GI q2198852 BLAST score 60 E value 6.0e-25



Match length 112 % identity 88

NCBI Description Zea mays cystathionine gamma-synthase (CGS1) gene, complete

cds

Seq. No. 305632

Seq. ID uC-zmflB73006b12b1

Method BLASTN
NCBI GI g4140643
BLAST score 61
E value 1.0e-25
Match length 225

% identity 88
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 305633

Seq. ID uC-zmflB73006d03b1

Method BLASTX
NCBI GI g122022
BLAST score 431
E value 1.0e-42
Match length 127
% identity 72

NCBI Description HISTONE H2B >gi 283025 pir S22323 histone H2B - wheat

>gi_21801_emb_CAA42530 (X59873) histone H2B [Triticum

aestivum]

Seq. No. 305634

Seq. ID uC-zmflB73006g01b1

Method BLASTX
NCBI GI g2117634
BLAST score 214
E value 4.0e-17
Match length 141
% identity 38

NCBI Description lipoxygenase (EC 1.13.11.12) - common tobacco

>gi_899344_emb_CAA58859_ (X84040) lipoxygenase [Nicotiana

tabacum]

Seq. No. 305635

Seq. ID uC-zmflB73006g07b1

Method BLASTX
NCBI GI g2342679
BLAST score 221
E value 7.0e-18
Match length 128
% identity 37

NCBI Description (AC000106) Similar to Vicia sativa ENBP1 (gb_X95995).

[Arabidopsis thaliana]

Seq. No. 305636

Seq. ID uC-zmflB73006g11b1

Method BLASTX
NCBI GI g283037
BLAST score 153
E value 2.0e-10



120

```
Match length
                  56
% identity
                  54
NCBI Description chitinase (EC 3.2.1.14) A - maize
                  305637
Seq. No.
                  uC-zmflB73007a09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2104679
BLAST score
                  276
E value
                  2.0e-24
```

% identity 49 NCBI Description (X97906) transcription factor [Vicia faba]

Seq. No. 305638 Seq. ID uC-zmflB73007b08b1 Method BLASTX

NCBI GI g1168547 BLAST score 247 E value 6.0e-21 Match length 63

% identity 71

Match length

HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-6 (HD-ZIP PROTEIN NCBI Description ATHB-6) >gi_629505_pir__S47136 homeotic protein Athb-6 -

Arabidopsis thaliana >gi 499162 emb CAA47427 (X67034)

7-

Athb-6 [Arabidopsis thaliana]

Seq. No. 305639

Seq. ID uC-zmflB73007c04b1

Method BLASTN NCBI GI g2668741 BLAST score 128 E value 9.0e-66 Match length 172 % identity 94

NCBI Description Zea mays glycine-rich RNA binding protein (GRP) mRNA,

complete cds

Seq. No. 305640

Seq. ID uC-zmflB73007c07b1

Method BLASTX NCBI GI g1871187 BLAST score 253 9.0e-22 E value Match length 92 % identity 53

NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

305641 Seq. No.

Seq. ID uC-zmflB73007c10b1

Method BLASTX g1001935 NCBI GI BLAST score 539 E value 3.0e-55 Match length 110 96 % identity

NCBI Description (X81199) ZMM1 [Zea mays] >gi 1167914 (U31522) MADS box



protein [Zea mays]

```
Seq. No.
                  305642
Seq. ID
                  uC-zmf1B73007c12b1
Method
                  BLASTX
NCBI GI
                  q2984709
BLAST score
                  347
E value
                  7.0e-33
Match length
                  74
% identity
                  91
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  305643
Seq. No.
Seq. ID
                  uC-zmflB73007d02b1
Method
                  BLASTX
NCBI GI
                  q286122
BLAST score
                  375
E value
                  4.0e-49
Match length
                  98
% identity
                  100
NCBI Description
                  (D14576) glutamine synthetase [Zea mays]
Seq. No.
                  305644
Seq. ID
                  uC-zmflB73007d08b1
Method
                  BLASTX
NCBI GI
                  q4096099
BLAST score
                  642
E value
                  3.0e-67
Match length
                  124
% identity
                  100
                  (U23161) NADPH-dependent reductase [Zea mays]
NCBI Description
                  305645
Seq. No.
                  uC-zmflB73007e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2668744
BLAST score
                  284
E value
                  1.0e-25
Match length
                  73
% identity
                  74
                  (AF034946) ubiquitin conjugating enzyme [Zea mays]
NCBI Description
Seq. No.
                  305646
                  uC-zmflB73007q03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2921303
BLAST score
                  45
E value
                  1.0e-16
Match length
                  69
                  91
% identity
                  Zea mays herbicide safener binding protein (SBP1) mRNA,
NCBI Description
                  complete cds
```

Seq. No. 305647

Seq. ID uC-zmflB73007g07b1

Method BLASTX NCBI GI g2244971



```
BLAST score
                   9.0e-36
E value
                   97
Match length
% identity
                   71
NCBI Description
                   (Z97340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   305648
                   uC-zmflB73007q08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4581207
BLAST score
                   441
                   9.0e-44
E value
Match length
                   131
% identity
                   63
NCBI Description
                   (Y17914) cyclic nucleotide and calmodulin-regulated ion
                   channel [Arabidopsis thaliana]
                   305649
Seq. No.
                   uC-zmflB73007q11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2984709
BLAST score
                   287
                   6.0e-26
E value
Match length
                   66
% identity
                   82
NCBI Description
                   (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                   305650
                   uC-zmflB73008a07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2564237
BLAST score
                   317
                   1.0e-37
E value
Match length
                   106
% identity
                   72
NCBI Description
                   (Y10112) omega-6 desaturase [Gossypium hirsutum]
                   305651
Seq. No.
                   uC-zmflB73008b02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3880625
                   270
BLAST score
                   1.0e-23
E value
```

Match length 89 % identity 56

NCBI Description (Z93785) predicted using Genefinder; similar to RNA

recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this

ge

305652 Seq. No.

uC-zmflB73008b10b1 Seq. ID

Method BLASTX g3789940 NCBI GI BLAST score 250 2.0e-21 E value



```
Match length
% identity
                  (AF093504) tetra-ubiquitin [Saccharum hybrid cultivar
NCBI Description
                  H32-8560]
Seq. No.
                  305653
                  uC-zmflB73008c07b1
Seq. ID
                  BLASTX
Method
                  q1871182
NCBI GI
BLAST score
                  226
E value
                  1.0e-18
                  132
Match length
% identity
NCBI Description (U90439) phospholipase D isolog [Arabidopsis thaliana]
                  305654
Seq. No.
Seq. ID
                  uC-zmf1B73008c11b1
Method
                  BLASTN
                  q22149
NCBI GI
                  47
BLAST score
                  2.0e-17
E value
Match length
                  191
% identity
                  78
NCBI Description Z.mays mRNA for alpha-tubulin
                  305655
Seq. No.
Seq. ID
                  uC-zmflB73008d11b1
                  BLASTX
Method
                  q4467128
NCBI GI
BLAST score
                   250
                   2.0e-21
E value
                   99
Match length
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   305656
Seq. No.
Seq. ID
                   uC-zmflB73008e05b1
Method
                   BLASTX
                   g2464901
NCBI GI
BLAST score
                   235
E value
                   1.0e-19
Match length
                   60
% identity
                   77
                   (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   305657
Seq. No.
                   uC-zmflB73008f02b1
Seq. ID
                   BLASTX
Method
                   g4582787
NCBI GI
                   348
BLAST score
                   6.0e-33
E value
Match length
                   104
% identity
                   70
                   (AJ012281) adenosine kinase [Zea mays]
NCBI Description
```

Seq. No. 305658

Seq. ID uC-zmflB73008f08b1



```
BLASTX
Method
                  q135411
NCBI GI
                  359
BLAST score
                   3.0e-34
E value
                  90
Match length
                  76
% identity
                  TUBULIN ALPHA-2 CHAIN >gi_82732_pir__S15772 tubulin alpha-2
NCBI Description
                   chain - maize >gi_22148_emb CAA33733 (X15704)
                  alpha2-tubulin [Zea mays]
                   305659
Seq. No.
                  uC-zmflB73008g02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1345587
BLAST score
                   550
                   1.0e-56
E value
Match length
                   112
                   100
% identity
                  14-3-3-LIKE PROTEIN GF14-6 >gi 998430 bbs 164522 (S77133)
NCBI Description
                   GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261
                   aa] [Zea mays]
                   305660
Seq. No.
                   uC-zmf1B73008g09b1
Seq. ID
                   BLASTN
Method
                   g21856
NCBI GI
BLAST score
                   86
                   9.0e-41
E value
                   223
Match length
                   86
% identity
NCBI Description Wheat rDNA 25S-18S intergenic region EcoRI-BamHI fragment
                   305661
Seq. No.
                   uC-zmflB73009a06b1
Seq. ID
                   BLASTX
Method
                   g137460
NCBI GI
BLAST score
                   295
E value
                   7.0e-27
                   73
Match length
% identity
                   VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                   SUBUNIT) >gi_67952_pir__PXPZV9 H+-transporting ATPase (EC
                   3.6.1.35), vacuolar, 69K chain - carrot >gi_167560 (J03769)
                   vacular H+-ATPase [Daucus carota]
Seq. No.
                   305662
                   uC-zmflB73009b12b1
 Seq. ID
Method
                   BLASTX
                   g3096935
NCBI GI
                   353
BLAST score
                   2.0e-33
```

E value 97 Match length % identity 76

(AL023094) putative protein [Arabidopsis thaliana] NCBI Description

305663 Seq. No.

uC-zmflB73009e03b1 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  q3075394
BLAST score
                  403
                  2.0e-39
E value
Match length
                  100
% identity
                  78
                  (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead
                  protein [Arabidopsis thaliana]
```

 Seq. No.
 305664

 Seq. ID
 uC-zmf1B73009g01b1

Method BLASTX
NCBI GI g2984709
BLAST score 343
E value 2.0e-32
Match length 72
% identity 90

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

 Seq. No.
 305665

 Seq. ID
 uC-zmf1B73009h01b1

 Method
 BLASTX

 NCBI GI
 g2642448

 BLAST score
 146

 A 00 00

BLAST score 146
E value 4.0e-09
Match length 106
% identity 34

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana] >gi 3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 305666

Seq. ID uC-zmflB73010a08b1

Method BLASTN
NCBI GI g22275
BLAST score 134
E value 3.0e-69
Match length 368
% identity 84

NCBI Description Maize mRNA for ferritin (clone FM1)

Seq. No. 305667

Seq. ID uC-zmflB73010a09b1

Method BLASTX
NCBI GI g4249385
BLAST score 295
E value 1.0e-26
Match length 74
% identity 74

NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No. 305668

Seq. ID uC-zmflB73010a10b1

Method BLASTX
NCBI GI g2341061
BLAST score 149



```
E value
                  9.0e-10
Match length
                  63
% identity
                  (U73459) translational initiation factor eIF-4A [Zea mays]
NCBI Description
Seq. No.
                  305669
                  uC-zmflB73010d02b1
Seq. ID
Method
                  BLASTX
                  g2984709
NCBI GI
                  502
BLAST score
E value
                  7.0e-51
                  99
Match length
% identity
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                  305670
Seq. No.
Seq. ID
                  uC-zmflB73010d09b1
Method
                  BLASTX
NCBI GI
                  g2245044
BLAST score
                  156
                  2.0e-10
E value
Match length
                  96
% identity
                  38
                   (Z97342) similarity to reverse transcriptase - Arabidopsis
NCBI Description
                  thaliana retrotransposon 2 (fragment) [Arabidopsis
                  thaliana]
                   305671
Seq. No.
                   uC-zmflB73010f02b1
Seq. ID
Method
                  BLASTX
                   g134597
NCBI GI
BLAST score
                   162
E value
                   5.0e-12
Match length
                   69
                   55
% identity
                   SUPEROXIDE DISMUTASE-4A (CU-ZN) >gi_100926_pir__S07007
NCBI Description
                   superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 4, cytosolic -
                   maize
                   305672
Seq. No.
Seq. ID
                   uC-zmflB73010g04b1
Method
                   BLASTX
NCBI GI
                   g3776581
BLAST score
                   489
E value
                   3.0e-49
Match length
                   168
% identity
                   55
                   (AC005388) Similar to Beta integral membrane protein
NCBI Description
                   homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]
                   305673
Seq. No.
                   uC-zmflB73010g11b1
Seq. ID
```

Method BLASTN

NCBI GI g1800216 BLAST score 40 E value 5.0e-13 Match length 127



36

% identity

NCBI Description

```
% identity
NCBI Description
                  Sorghum bicolor phytochrome B (PHYB) gene, partial cds
                  305674
Seq. No.
Seq. ID
                  uC-zmflB73021a01b1
Method
                  BLASTX
                  g3776005
NCBI GI
                  398
BLAST score
E value
                  1.0e-38
Match length
                  90
% identity
                  87
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
                  305675
Seq. No.
                  uC-zmflB73021a09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g232033
BLAST score
                  165
E value
                  1.0e-11
Match length
                  70
% identity
                  56
NCBI Description
                  ELONGATION FACTOR 1 BETA' >gi 479830 pir S35501
                  translation elongation factor eEF-1 beta chain - wheat
                  >gi 218341 dbj BAA02436 (D13147) elongation factor 1 beta'
                  [Triticum aestivum]
                  305676
Seq. No.
Seq. ID
                  uC-zmflB73021b08b1
Method
                  BLASTX
NCBI GI
                  g4204315
BLAST score
                  384
                  5.0e-37
E value
Match length
                  146
                  53
% identity
NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]
                  305677
Seq. No.
Seq. ID
                  uC-zmflB73021c10b1
Method
                  BLASTN
NCBI GI
                  g22237
BLAST score
                  43
E value
                  4.0e-15
Match length
                  178
% identity
                  80
NCBI Description Maize mRNA for cytosolic GAPDH (GapC)
                  glyceraldehyde-3-phosphate dehydrogenase
Seq. No.
                  305678
Seq. ID
                  uC-zmflB73021d11b1
Method
                  BLASTX
NCBI GI
                  g2586082
BLAST score
                  156
E value
                  2.0e-10
Match length
                  116
```

(U72725) retrofit [Oryza longistaminata]



```
305679
Seq. No.
                  uC-zmf1B73021e05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3452497
BLAST score
                  262
                  7.0e-23
E value
Match length
                  131
% identity
                  47
NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum]
                  305680
Seq. No.
Seq. ID
                  uC-zmflB73021e06b1
                  BLASTX
Method
NCBI GI
                  q136063
BLAST score
                  215
                  2.0e-17
E value
Match length
                  111
                   50
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi 68426 pir ISZMT triose-phosphate isomerase (EC
                   5.3.1.1) - maize >gi 168647 (L00371) triosephosphate
                   isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)
                   triosephosphate isomerase [Zea mays]
                   305681
Seq. No.
                  uC-zmflB73021e07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1762144
                   371
BLAST score
                   2.0e-35
E value
Match length
                   119
% identity
                   59
NCBI Description (U48435) putative cytochrome P450 [Solanum chacoense]
                   305682
Seq. No.
                   uC-zmflB73021f05b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2668739
BLAST score
                   140
E value
                   6.0e-73
Match length
                   169
% identity
                   95
NCBI Description
                   Zea mays translation initiation factor GOS2 (TIF) mRNA,
                   complete cds
                   305683
Seq. No.
Seq. ID
                   uC-zmflB73021h04b1
Method
                   BLASTN
NCBI GI
                   g2995383
```

BLAST score 72 E value 2.0e-32 Match length 119 % identity 89

NCBI Description Zea mays mays mRNA for cytochrome P450 monooxygenase,

partial

305684 Seq. No.



```
uC-zmflB73021h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g974782
BLAST score
                  228
E value
                   2.0e-19
Match length
                  89
% identity
                   (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
Seq. No.
                   305685
Seq. ID
                   uC-zmf1B73022b07b1
                   BLASTX
Method
                   q1778093
NCBI GI
BLAST score
                   372
E value
                   1.0e-35
Match length
                   150
% identity
                   49
                   (U64902) putative sugar transporter; member of major
NCBI Description
                   facilitative superfamily; integral membrane protein [Beta
                   vulgaris]
                   305686
Seq. No.
                   uC-zmflB73022c04b1
Seq. ID
                   BLASTX
Method
                   g4455340
NCBI GI
BLAST score
                   161
                   7.0e-11
E value
                   112
Match length
% identity
                   38
                   (AL035522) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   305687
                   uC-zmflB73022c07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1574938
BLAST score
                   368
E value
                   3.0e-35
Match length
                   107
                   70
% identity
                   (U34726) superoxide dismutase 4 [Zea mays]
NCBI Description
Seq. No.
                   305688
                   uC-zmflB73022e07b1
Seq. ID
                   BLASTX
Method
                   g2944389
NCBI GI
BLAST score
                   193
                   5.0e-15
E value
                   85
Match length
% identity
                   51
                   (AF049106) actin 4 [Glycine max]
NCBI Description
                   305689
Seq. No.
                   uC-zmflB73022g10b1
Seq. ID
                   BLASTX
Method
```

43317

g3913517

450

NCBI GI BLAST score



E value 1.0e-44 Match length 172 % identity 3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE NCBI Description (3'(2'), 5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >qi 1109672 (U33283) 3'(2'),5-diphosphonucleoside 3'(2') phosphohydrolase [Oryza sativa] >gi 1586671 prf 2204308A diphosphonucleoside phosphohydrolase [Oryza sativa] Seq. No. 305690 Seq. ID uC-zmf1B73022h11b1

Method BLASTX

NCBI GI g4586021

BLAST score 216

E value 8.0e-18

Match length 73

% identity 60

NCBI Description (AC007170) putative cytoplasmic aconitate hydratase

[Arabidopsis thaliana]

Seq. No. 305691

Seq. ID uC-zmflB73025a09b2

Method BLASTX
NCBI GI g3420299
BLAST score 186
E value 2.0e-14
Match length 55
% identity 67

% identity 67

NCBI Description (AF072849) jab1 protein [Oryza sativa subsp. indica]

Seq. No. 305692

Seq. ID uC-zmflB73025b03b2

Method BLASTX
NCBI GI g2129648
BLAST score 438
E value 2.0e-43
Match length 104
% identity 75

NCBI Description MYB-related protein 33,3K - Arabidopsis thaliana

>qi 1263095 emb CAA90809 (Z54136) MYB-related protein

[Arabidopsis thaliana]

Seq. No. 305693

Seq. ID uC-zmflB73025c03b2

Method BLASTX
NCBI GI g1076385
BLAST score 621
E value 9.0e-65
Match length 161
% identity 73

NCBI Description protein kinase (EC 2.7.1.37) tousled - Arabidopsis thaliana

>gi_433052 (L23985) protein kinase [Arabidopsis thaliana]

Seq. No. 305694

Seq. ID uC-zmflB73025c04b2

Method BLASTX

```
q4510345
NCBI GI
BLAST score
                  161
E value
                  6.0e-11
Match length
                  53
% identity
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
                  305695
Seq. No.
Seq. ID
                  uC-zmf1B73025d10b2
Method
                  BLASTX
NCBI GI
                  q2511531
                  712
BLAST score
                  1.0e-75
E value
                  138
Match length
% identity
NCBI Description
                  (AF008120) alpha tubulin 1 [Eleusine indica]
                  >gi 3163944 emb CAA06618_ (AJ005598) alpha-tubulin 1
                  [Eleusine indica]
                  305696
Seq. No.
                  uC-zmflB73025g12b2
Seq. ID
Method
                  BLASTX
                  q283037
NCBI GI
BLAST score
                  225
                  2.0e-18
E value
                  61
Match length
% identity
NCBI Description chitinase (EC 3.2.1.14) A - maize
Seq. No.
                  305697
Seq. ID
                  uC-zmf1B73042b01b1
Method
                  BLASTX
NCBI GI
                  q2832625
BLAST score
                  163
E value
                  2.0e-11
Match length
                  71
% identity
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
                  305698
Seq. No.
Seq. ID
                  uC-zmflB73042c12b1
```

Method BLASTN
NCBI GI g440868
BLAST score 47
E value 2.0e-17
Match length 107
% identity 86

NCBI Description Rice mRNA for major intrinsic protein, complete cds

Seq. No. 305699

Seq. ID uC-zmflB73042g02b1

Method BLASTX
NCBI GI g1101025
BLAST score 208
E value 4.0e-17
Match length 57
% identity 70



```
NCBI Description (U37794) alpha-tubulin [Eucalyptus globulus]

Seq. No. 305700
Seq. ID uC-zmflB73042h11b1
Method BLASTX
NCBI GI 93123286
```

NCBI GI g3123286
BLAST score 423
E value 1.0e-41
Match length 161
% identity 55

NCBI Description LEUCYL-TRNA SYNTHETASE (LEUCINE--TRNA LIGASE) (LEURS) >gi_2293181 (AF008220) leucine tRNA synthetase [Bacillus subtilis] >gi_2635516 emb CAB15010 (Z99119) leucyl-tRNA

synthetase [Bacillus subtilis]

Seq. No. 305701

Seq. ID uC-zmflB73043b07b1

Method BLASTX
NCBI GI g135411
BLAST score 207
E value 2.0e-16
Match length 78
% identity 59

NCBI Description TUBULIN ALPHA-2 CHAIN >gi 82732 pir S15772 tubulin alpha-2

chain - maize >gi 22148 emb CAA33733 (X15704)

alpha2-tubulin [Zea mays]

Seq. No. 305702

Seq. ID uC-zmflB73043c03b1

Method BLASTX
NCBI GI g115771
BLAST score 548
E value 6.0e-66
Match length 125
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >qi 82682 pir S04453 chlorophyll

a/b-binding protein precursor - maize

>gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 305703

Seq. ID uC-zmflB73043e03b1

Method BLASTX
NCBI GI g135411
BLAST score 150
E value 8.0e-21
Match length 125
% identity 52

NCBI Description TUBULIN ALPHA-2 CHAIN >gi 82732 pir S15772 tubulin alpha-2

chain - maize >gi 22148 emb CAA33733 (X15704)

alpha2-tubulin [Zea mays]

Seq. No. 305704

Seq. ID uC-zmflB73043f07b1

Method BLASTX NCBI GI g2655098



```
BLAST score
                   313
E value
                   6.0e-29
Match length
                  112
% identity
                   57
NCBI Description
                  (AF023472) peptide transporter [Hordeum vulgare]
Seq. No.
                   305705
Seq. ID
                  uC-zmflB73043g11b1
Method
                  BLASTX
NCBI GI
                   g2773154
BLAST score
                  200
E value
                   2.0e-15
Match length
                  92
% identity
                   42
NCBI Description
                   (AF039573) abscisic acid- and stress-inducible protein
                   [Oryza sativa]
                   305706
Seq. No.
Seq. ID
                   uC-zmflB73043h01b1
Method
                  BLASTN
NCBI GI
                   g22332
BLAST score
                   55
E value
                   2.0e-22
Match length
                   121
% identity
                   87
NCBI Description Z.mays HRGP gene
                   305707
Seq. No.
Seq. ID
                   uC-zmflB73043h03b1
Method
                  BLASTX
NCBI GI
                   g2773154
BLAST score
                   177
E value
                   6.0e-13
Match length
                   95
% identity
                   42
NCBI Description
                   (AF039573) abscisic acid- and stress-inducible protein
                   [Oryza sativa]
                   305708
Seq. No.
Seq. ID
                   uC-zmf1B73044a04b1
Method
                  BLASTX
NCBI GI
                   g1335966
BLAST score
                   145
E value
                   1.0e-14
Match length
                  58
% identity
NCBI Description (U58598) acetyl CoA carboxylase [Zea mays]
                   305709
Seq. No.
Seq. ID
                  uC-zmflB73044a05b1
Method
                  BLASTN
NCBI GI
                   g303852
                   37
BLAST score
```

BLAST score 37 E value 2.0e-11 Match length 53

% identity 92

NCBI Description Rice mRNA for ribosomal protein L3, complete cds

NCBI Description

```
305710
Seq. No.
                  uC-zmflB73044a10b1
Seq. ID
                  BLASTX
Method
                  g548770
NCBI GI
                  468
BLAST score
                  5.0e-47
E value
Match length
                  122
                  74
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                  305711
                  uC-zmflB73044b03b1
Seq. ID
                  BLASTX
Method
                  g168558
NCBI GI
BLAST score
                   181
E value
                   1.0e-13
Match length
                   64
% identity
                   (M95071) putative. similar to GTP-binding proteins [Zea
NCBI Description
                   mays]
Seq. No.
                   305712
                   uC-zmflB73044b06b1
Seq. ID
                   BLASTX
Method
                   g3024703
NCBI GI
                   192
BLAST score
E value
                   9.0e-15
                   64
Match length
                   61
% identity
                   PROBABLE T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA)
NCBI Description
                   (CCT-ETA) >gi_2104461_emb_CAB08778_ (Z95397) Cct7p
                   [Schizosaccharomyces pombe]
                   305713
Seq. No.
Seq. ID
                   uC-zmflB73044c02b1
                   BLASTX
Method
NCBI GI
                   g3859548
BLAST score
                   492
                   3.0e-51
E value
                   110
Match length
                   94
% identity
                   (AF097182) protein phosphatase 2A catalytic subunit [Oryza
NCBI Description
                   sativa]
                   305714
Seq. No.
Seq. ID
                   uC-zmflB73044c07b1
                   BLASTX
Method
                   q4455351
NCBI GI
                   159
BLAST score
                   1.0e-10
E value
Match length
                   56
% identity
```

(AL035524) putative protein [Arabidopsis thaliana]



Seq. No. 305715

Seq. ID uC-zmflB73044e03b1

Method BLASTX
NCBI GI 94503521
BLAST score 202
E value 1.0e-15
Match length 67

% identity 58

NCBI Description murine mammary tumor integration site 6 (oncogene homolog)

>gi 2498490 sp 064252 INT6 MOUSE VIRAL INTEGRATION SITE PROTEIN INT-6 >gi 1854579 (L35556) Int-6 [Mus musculus] >gi 2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi 2351382 (U54562) eIF3-p48 [Homo sapiens] >gi 2688818 (U85947) Int-6 [Homo sapiens] >gi 2695701 (U94175) mammary

tumor-associated protein INT6 [Homo sapiens]

Seq. No. 305716

Seq. ID uC-zmflB73044h07b1

Method BLASTX
NCBI GI g4006900
BLAST score 234
E value 2.0e-19
Match length 162
% identity 39

NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 305717

Seq. ID uC-zmflB73045c09b1

Method BLASTX
NCBI GI g132171
BLAST score 158
E value 1.0e-10
Match length 101
% identity 41

NCBI Description REGULATOR OF CHROMOSOME CONDENSATION >gi_109453_pir__A34726

DNA-binding protein RCC1 - golden hamster >gi_506396

(M33579) RCC1 [Cricetus cricetus]

Seq. No. 305718

Seq. ID uC-zmflB73045d03b1

Method BLASTX
NCBI GI g417154
BLAST score 238
E value 1.0e-20
Match length 71
% identity 76

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi 20256 emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 305719

Seq. ID uC-zmflB73045d12b1

Method BLASTN
NCBI GI g4160401
BLAST score 55
E value 6.0e-22

```
Match length
% identity
                  86
NCBI Description Zea mays eIF-5 gene, exons 1-2
                  305720
Seq. No.
```

Seq. ID uC-zmflB73045f03b1 Method BLASTX NCBI GI g3738331 BLAST score 145 6.0e-09 E value 45 Match length 56 % identity

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

305721 Seq. No. Seq. ID uC-zmflB73045f09b1 Method BLASTX NCBI GI g2702270 BLAST score 347 E value 1.0e-32 Match length 149

NCBI Description (AC003033) unknown protein [Arabidopsis thaliana]

305722 Seq. No. Seq. ID uC-zmflB73045q11b1 Method BLASTX NCBI GI g2662310 BLAST score 510 7.0e-52 E value 109

44

Match length 87 % identity

% identity

NCBI Description (AB009307) bpw1 [Hordeum vulgare]

305723 Seq. No.

Seq. ID uC-zmflB73045h03b1

Method BLASTX NCBI GI g3986691 220 BLAST score E value 5.0e-18 Match length 67 % identity 66

NCBI Description (AF101421) heat shock protein [Cichorium intybus]

305724 Seq. No.

uC-zmflB73045h06b1 Seq. ID

Method BLASTX NCBI GI g3264598 BLAST score 167 5.0e-12 E value Match length 62 % identity

(AF057184) trypsin inhibitor [Zea mays] NCBI Description

Seq. No. 305725

Seq. ID uC-zmflB73045h10b1

Method BLASTX

```
q4220529
NCBI GI
BLAST score
                  227
                  9.0e-19
E value
Match length
                  135
% identity
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                  305726
Seq. No.
Seq. ID
                  uC-zmflB73045h11b1
Method
                  BLASTX
NCBI GI
                  g3378650
BLAST score
                  181
                  3.0e-13
E value
Match length
                  91
% identity
                  (X97606) abscisic acid activated [Medicago sativa]
NCBI Description
Seq. No.
                  uC-zmflB73045h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1632822
BLAST score
                   286
E value
                   1.0e-25
Match length
                   121
                   37
% identity
                   (Y08962) transmembrane protein [Oryza sativa] >gi_1667594
NCBI Description
                   (U77297) transmembrane protein [Oryza sativa]
                   305728
Seq. No.
Seq. ID
                   uC-zmflB73046a06b1
Method
                   BLASTN
NCBI GI
                   g3264597
BLAST score
                   61
                   1.0e-25
E value
Match length
                   145
% identity
                   86
                   Zea mays trypsin inhibitor mRNA, complete cds
NCBI Description
                   305729
Seq. No.
                   uC-zmflB73046a08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2911068
                   216
BLAST score
                   2.0e-17
E value
                   44
Match length
% identity
                   86
                   (AL021960) G10-like protein [Arabidopsis thaliana]
NCBI Description
                   305730
Seq. No.
                   uC-zmflB73046a11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3080416
                   247
BLAST score
                   4.0e-21
E value
                   62
Match length
% identity
                   81
                   (AL022604) UDP-galactose transporter-like protein
NCBI Description
```



[Arabidopsis thaliana]

```
305731
Seq. No.
                  uC-zmf1B73046b08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4512674
                  295
BLAST score
E value
                  1.0e-26
                  104
Match length
                  20
% identity
NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]
                  305732
Seq. No.
                  uC-zmflB73047a12b1
Seq. ID
                  BLASTX
Method
                  g542175
NCBI GI
                  324
BLAST score
                   4.0e-30
E value
Match length
                  89
                  70
% identity
                  endoxyloglucan transferase - wheat >gi_469511_dbj_BAA03924_
NCBI Description
                   (D16457) endo-xyloglucan transferase [Triticum aestivum]
Seq. No.
                   305733
                  uC-zmflB73047f09b1
Seq. ID
                  BLASTX
Method
                   g134597
NCBI GI
                   232
BLAST score
                   1.0e-19
E value
Match length
                   54
                   85
% identity
                   SUPEROXIDE DISMUTASE-4A (CU-ZN) >gi 100926_pir S07007
NCBI Description
                   superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 4, cytosolic -
                   maize
                   305734
Seq. No.
                   uC-zmflB73106a05b1
Seq. ID
                   BLASTN
Method
                   g998429
NCBI GI
                   42
BLAST score
                   3.0e-14
E value
                   86
Match length
                   87
% identity
                   GRF1=general regulatory factor [Zea mays, XL80, Genomic,
NCBI Description
                   5348 nt]
                   305735
Seq. No.
                   uC-zmflB73106a09b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2062705
BLAST score
                   36
                   1.0e-10
E value
                   36
Match length
% identity
                   Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
```

305736

Seq. No.

Seq. ID Method



```
uC-zmflB73106b09b1
Seq. ID
                  BLASTX
Method
                  q4249419
NCBI GI
BLAST score
                  168
                  1.0e-11
E value
                  137
Match length
                  35
% identity
                  (AC006072) hypothetical protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
                  305737
Seq. No.
                  uC-zmflB73106c06b1
Seq. ID
                  BLASTX
Method
                   q3021344
NCBI GI
                   177
BLAST score
                   8.0e-13
E value
                   50
Match length
                   56
% identity
NCBI Description (AJ004959) hypothetical protein [Cicer arietinum]
Seq. No.
                   305738
                   uC-zmflB73106d01b1
Seq. ID
                   BLASTX
Method
                   g1174718
NCBI GI
                   180
BLAST score
                   5.0e-13
E value
Match length
                   106
                   36
% identity
                   PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR
NCBI Description
                   >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC
                   2.7.1.-) precursor - Arabidopsis thaliana >gi_166888
                   (L00670) protein kinase [Arabidopsis thaliana]
                   305739
Seq. No.
                   uC-zmflB73106d06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1808684
                   207
BLAST score
                   2.0e-16
E value
                   117
Match length
% identity
                   43
                   (Y10782) hypothetical protein [Sporobolus stapfianus]
NCBI Description
                   305740
Seq. No.
                   uC-zmflB73106d07b1
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   g4510373
 BLAST score
                   287
 E value
                    1.0e-25
Match length
                   114
                    47
 % identity
                    (AC007017) putative harpin-induced protein [Arabidopsis
 NCBI Description
                    thaliana]
                    305741
 Seq. No.
```

uC-zmflB73106d12b1

BLASTX

Seq. ID

Method

NCBI GI



```
g4468984
NCBI GI
                  355
BLAST score
                                                  **
E value
                   1.0e-33
Match length
                  155
% identity
                   46
                   (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                   uC-zmflB73106e06b1
Method
                  BLASTX
NCBI GI
                   q312179
BLAST score
                   511
                   7.0e-52
E value
Match length
                   119
% identity
                   85
                   (X73151) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                   (phosphorylating) [Zea mays] >gi 1184772 (U45855) cytosolic
                   glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                   >gi 1185554 (U45858) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays]
                   305743
Seq. No.
                   uC-zmflB73106f05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2984709
BLAST score
                   485
                   8.0e-49
E value
Match length
                   94
                   98
% identity
NCBI Description
                   (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                   305744
                   uC-zmflB73106f10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3643603
BLAST score
                   271
                   8.0e-24
E value
                   143
Match length
                   42
% identity
                   (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
                   305745
Seq. No.
                   uC-zmflB73106g01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2137619
                   376
BLAST score
                   4.0e-36
E value
                   151
Match length
                   54
% identity
                   p62 ras-GAP associated phosphoprotein - mouse >gi_608528
NCBI Description
                   (U17046) p62 ras-GAP associated phosphoprotein [Mus
                   musculus]
                   305746
Seq. No.
```

43328

uC-zmflB73108a01b2

BLASTX

g113621



162 BLAST score 1.0e-11 E value Match length 47 70 % identity FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME NCBI Description >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850 emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A cytoplasmic aldolase [Zea mays] 305747 Seq. No. uC-zmflB73108a08b2 Seq. ID BLASTX Method g2792214 NCBI GI 177 BLAST score 5.0e-13 E value 79 Match length 51 % identity (AF032685) NBS-LRR type resistance protein [Hordeum NCBI Description vulgare] 305748 Seq. No. uC-zmflB73108c04b2 Seq. ID Method BLASTN NCBI GI g20280 BLAST score 41 E value 6.0e-14 85 Match length 87 % identity NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5) 305749 Seq. No. uC-zmflB73108c07b2 Seq. ID Method BLASTX NCBI GI q553898 BLAST score 189 8.0e-15 E value Match length 35 % identity NCBI Description (J00375) alpha-A-ins crystallin [Mus musculus] 305750 Seq. No. uC-zmflB73108c12b2 Seq. ID Method BLASTX NCBI GI g1729927 BLAST score 185 E value 4.0e-14 52 Match length % identity 63

NCBI Description QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE

TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi_940182 (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]

Seq. No. 305751

Seq. ID uC-zmflB73108g04b2

Method BLASTX

BLAST score

Match length

NCBI Description

% identity

E value

36

47

66

9.0e-11



```
q2129550
NCBI GI
                  156
BLAST score
                  6.0e-11
E value
                  44
Match length
% identity
                  64
                  calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -
NCBI Description
                  Arabidopsis thaliana >gi_2129554_pir__S71901
                  calcium-dependent protein kinase 6 - Arabidopsis thaliana
                  >gi 836940 (U20623) calcium-dependent protein kinase
                   [Arabidopsis thaliana] >gi_836944 (U20625)
                   calcium-dependent protein \overline{k}inase [Arabidopsis thaliana]
                   >gi 4454034 emb CAA23031.1_ (AL035394) calcium-dependent
                  protein kinase (CDPK6) [Arabidopsis thaliana]
                   305752
Seq. No.
                   uC-zmf1B73111b04b2
Seq. ID
                  BLASTX
Method
                   g3540206
NCBI GI
                   215
BLAST score
                   6.0e-18
E value
                   70
Match length
                   61
% identity
                   (AC004260) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   305753
Seq. No.
                   uC-zmflB73111e01b2
Seq. ID
Method
                   BLASTX
                   g3367517
NCBI GI
                   176
BLAST score
                   6.0e-13
E value
                   87
Match length
                   39
% identity
                   (AC004392) Similar to F4I1.26 putative beta-glucosidase
NCBI Description
                   gi 3128187 from A. thaliana BAC gb_AC004521. ESTs
                   gb_N97083, gb_F19868 and gb_F15482 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   305754
                   uC-zmflB73111q09b2
Seq. ID
                   BLASTX
Method
                   g2996096
NCBI GI
BLAST score
                   368
                   1.0e-46
E value
                   102
Match length
% identity
                   (AF030517) translation elongation factor-1 alpha; EF-1
NCBI Description
                   alpha [Oryza sativa]
Seq. No.
                   305755
                   uC-zmflB73112d09b2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3821780
```

43330

Xenopus laevis cDNA clone 27A6-1



```
305756
Seq. No.
                  uC-zmflB73112d12b2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3821780
                  35
BLAST score
                  2.0e-10
E value
Match length
                  35
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   305757
Seq. No.
                   uC-zmflB73112f11b2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4582435
BLAST score
                   238
E value
                   1.0e-20
                   70
Match length
% identity
                   (AC007196) putative selenium-binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   305758
Seq. ID
                   uC-zmflB73112h02b2
Method
                   BLASTN
NCBI GI
                   q473602
                   7.4
BLAST score
                   2.0e-33
E value
Match length
                   130
% identity
                   89
                   Zea mays W-22 histone H2A mRNA, complete cds
NCBI Description
                   305759
Seq. No.
                   uC-zmflB73112h12b2
Seq. ID
Method
                   BLASTX
                   g2130149
NCBI GI
                   149
BLAST score
                   4.0e-10
E value
                   33
Match length
                   91
% identity
                   translation elongation factor eEF-1 alpha chain - maize
NCBI Description
                   (fragment)
                   305760
Seq. No.
Seq. ID
                   uC-zmflB73113f03b1
Method
                   BLASTX
                   g1498597
NCBI GI
                   244
BLAST score
                   9.0e-21
E value
Match length
                   87
% identity
                  (U66105) phospholipid transfer protein [Zea mays]
NCBI Description
```

Seq. No. 305761

Seq. ID uC-zmflB73113f09b1

Method BLASTN NCBI GI g927571



```
BLAST score
                  46
E value
                  8.0e-17
Match length
                  130
                  85
% identity
NCBI Description Z.mays mRNA for calreticulin precursor
                  305762
Seq. No.
                  uC-zmflB73113h05b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22272
BLAST score
                  37
                  1.0e-11
E value
                  77
Match length
% identity
                  87
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
Seq. No.
                  305763
Seq. ID
                  uC-zmflB73113h11b1
Method
                  BLASTX
NCBI GI
                  g1899060
BLAST score
                  159
E value
                  5.0e-11
Match length
                  66
                  53
% identity
NCBI Description (U79669) endosperm C-24 sterol methyltransferase [Zea mays]
                  305764
Seq. No.
                  uC-zmflMo17002a08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g553073
BLAST score
                  185
                  7.0e-14
E value
Match length
                  71
% identity
                  55
NCBI Description (M94481) reverse transcriptase [Zea mays]
Seq. No.
                  305765
                  uC-zmflMo17002c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3201627
BLAST score
                  483
                  1.0e-48
E value
Match length
                  127
% identity
                  72
NCBI Description
                  (AC004669) putative SWH1 protein [Arabidopsis thaliana]
Seq. No.
                  305766
                  uC-zmflMo17002e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170409
BLAST score
                  198
E value
                  5.0e-20
Match length
                  85
                  65
% identity
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22)
NCBI Description
                  >gi 549887 (U09336) homeobox protein [Arabidopsis thaliana]
```

>gi 549888 (U09337) homeobox protein [Arabidopsis thaliana]



>gi_4490724_emb_CAB38927.1_ (AL035709) homeobox protein HAT22 [Arabidopsis thaliana]

Seq. No. 305767

Seq. ID uC-zmflMo17002e07b1

Method BLASTX
NCBI GI g2641619
BLAST score 232
E value 2.0e-19

Match length 71 % identity 70

NCBI Description (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea

mays]

Seq. No. 305768

Seq. ID uC-zmflMo17002f11b1

Method BLASTX
NCBI GI g2088652
BLAST score 224
E value 1.0e-18
Match length 98
% identity 48

NCBI Description (AF002109) 26S proteasome regulatory subunit S12 isolog

[Arabidopsis thaliana] >gi_2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis

thaliana]

Seq. No. 305769

Seq. ID uC-zmflMo17002h09b1

Method BLASTX
NCBI GI 94455220
BLAST score 234
E value 9.0e-20
Match length 77

Match length 77 % identity 57

NCBI Description (AL035440) putative aconitase [Arabidopsis thaliana]

Seq. No. 305770

Seq. ID uC-zmflMo17003a02b1

Method BLASTN
NCBI GI g257040
BLAST score 143
E value 1.0e-74
Match length 179
% identity 95

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 305771

Seq. ID uC-zmflMo17003a04b1

78

Method BLASTX
NCBI GI g3024657
BLAST score 329
E value 1.0e-30
Match length 82

% identity

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi_2668740 (AF034944) translation initiation factor; GOS2



[Zea mays]

```
305772
Seq. No.
                   uC-zmflMo17003b01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3880432
                   152
BLAST score
                   8.0e-10
E value
Match length
                   35
                   71
% identity
NCBI Description
```

NCBI Description (Z66521) similar to kinensin-like protein; cDNA EST yk198e10.3 comes from this gene; cDNA EST yk198e10.5 comes

from this gene [Caenorhabditis elegans]

```
      Seq. No.
      305773

      Seq. ID
      uC-zmflMo17003b03b1

      Method
      BLASTX

      NCBI GI
      g4544445

      BLAST score
      416

      E value
      9.0e-41

      Match length
      162

      % identity
      51
```

NCBI Description (AC006592) putative pyrophosphate--fructose 6-phosphate

1-phosphotransferase [Arabidopsis thaliana]

```
Seq. No. 305774
Seq. ID uC-zmflMo17003d07b1
Method BLASTX
NCBI GI g2739168
BLAST score 184
```

E value 1.0e-13
Match length 62
% identity 56

NCBI Description (AF032386) aldose-1-epimerase-like protein [Nicotiana

tabacum]

Seq. No. 305775 Seq. ID uC-zmflMo17003f07b1 Method BLASTX

Method BLASTX
NCBI GI 94105798
BLAST score 244
E value 3.0e-23
Match length 115
% identity 48

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 305776 Seq. ID uC-zmflMo17003g04b1 Method BLASTN

NCBI GI g22332
BLAST score 48
E value 6.0e-18
Match length 247
% identity 81

NCBI Description Z.mays HRGP gene

Seq. No. 305777

Seq. ID Method



```
uC-zmflMo17003h04b1
Seq. ID
                  BLASTX
Method
                  a115786
NCBI GI
                  332
BLAST score
                  5.0e-31
E value
                  98
Match length
                  70
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding
                  protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
                  mays]
                  305778
Seq. No.
                  uC-zmflMo17003h12b1
Seq. ID
                  BLASTX
Method
                  g4587513
NCBI GI
                  369
BLAST score
                  2.0e-35
E value
                  132
Match length
                  54
% identity
                  (AC007060) Contains eukaryotic protein kinase domain
NCBI Description
                  PF 00069. [Arabidopsis thaliana]
                   305779
Seq. No.
                   uC-zmflMo17004a08b1
Seq. ID
                  BLASTX
Method
                   g4204263
NCBI GI
                                                         " .¥
                   271
BLAST score
                   7.0e-24
E value
                   81
Match length
                   54
% identity
NCBI Description (AC005223) 40409 [Arabidopsis thaliana]
                   305780
Seq. No.
                   uC-zmflMo17004a10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3063455
                   356
BLAST score
                   9.0e-34
E value
                   88
Match length
 % identity
                   (AC003981) F22013.17 [Arabidopsis thaliana]
NCBI Description
                   305781
 Seq. No.
                   uC-zmflMo17004d11b1
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   q2062691
 BLAST score
                   34
                   1.0e-09
 E value
 Match length
                   42
                   95
 % identity
                   Human sodium phosphate transporter (NPT4) mRNA, complete
 NCBI Description
                   305782
 Seq. No.
```

uC-zmflMo17004e03b1

BLASTX

```
q136125
NCBI GI
                   172
BLAST score
E value
                   3.0e-12
                   114
Match length
% identity
                   38
                   PUTATIVE AC TRANSPOSASE (ORFA) >gi_22113_emb_CAA29005_
NCBI Description
                   (X05424) ORFa [Zea mays]
Seq. No.
                   305783
                   uC-zmflMo17004e10b1
```

Seq. ID uC-zmflM Method BLASTN NCBI GI g312180 BLAST score 54 E value 2.0e-21 Match length 8 identity 83

NCBI Description Z.mays GapC4 gene

 Seq. No.
 305784

 Seq. ID
 uC-zmflMo17004f05b1

 Method
 BLASTX

 NCBI GI
 g4586308

 BLAST score
 309

 E value
 4.0e-32

 Match length
 134

% identity 55
NCBI Description (AB025102) protoporphyrinogen IX oxidase [Glycine max]

Seq. No. 305785
Seq. ID uC-zmflMo17004h05b1
Method BLASTN
NCBI GI g22332
BLAST score 233
E value 1.0e-128

Match length 380 % identity 91

NCBI Description Z.mays HRGP gene

Seq. No. 305786

Seg. ID uC-zmflMo17005a03b1

Method BLASTX
NCBI GI g2244749
BLAST score 272
E value 6.0e-24
Match length 82
% identity 63

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 305787

Seq. ID uC-zmflMo17005c01b1

Method BLASTX
NCBI GI 94587513
BLAST score 186
E value 5.0e-14
Match length 108
% identity 38

NCBI Description (AC007060) Contains eukaryotic protein kinase domain



PF 00069. [Arabidopsis thaliana]

```
Seq. No.
                  305788
                  uC-zmflMo17005e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421876
BLAST score
                  144
                  4.0e-09
E value
Match length
                  43
% identity
                  probable ATP synthase chain - soybean
NCBI Description
                  >gi_396230_emb_CAA52349_ (X74296) putative ATP synthase
                  subunit [Glycine max]
Seq. No.
                  305789
                  uC-zmflMo17005e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1931642
BLAST score
                  167
E value
                  1.0e-11
                  127
Match length
% identity
                  (U95973) Ser/Thr protein kinase isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  305790
                  uC-zmflMo17005e06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827143
BLAST score
                  263
E value
                   2.0e-32
Match length
                   111
% identity
                   68
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   305791
Seq. No.
                   uC-zmflMo17005e12b1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g22332
                   152
BLAST score
                   5.0e-80
E value
                   291
Match length
                   89
% identity
NCBI Description Z.mays HRGP gene
                   305792
Seq. No.
                   uC-zmflMo17005f06b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4455240
                   282
BLAST score
                                                                      50
                   4.0e-28
E value
                   99
Match length
% identity
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
```

43337

305793

Seq. No.

```
uC-zmflMo17005g02b1
Seq. ID
                  BLASTN
Method
                  q257040
NCBI GI
BLAST score
                  203
                  1.0e-110
E value
                  247
Match length
                  96
% identity
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
Seq. No.
                  uC-zmflMo17005h02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2129533
BLAST score
                  169
                   2.0e-12
E value
Match length
                   67
                   57
% identity
                   adenine nucleotide translocase - Arabidopsis thaliana
NCBI Description
                   >gi_1051109_emb_CAA89201_ (Z49227) adenine nucleotide
                   translocase [Arabidopsis thaliana]
                   305795
Seq. No.
                   uC-zmflMo17006b12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2494144
                   169
BLAST score
E value
                   7.0e-12
                   51
Match length
                   69
% identity
                   (AC002329) predicted leucine-rich protein [Arabidopsis
NCBI Description
                   thaliana]
                   305796
Seq. No.
                   uC-zmflMo17006d01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1711469
BLAST score
                   181
                   2.0e-13
E value
Match length
                   110
% identity
                   DIBENZOTHIOPHENE DESULFURIZATION ENZYME C (DBT SULFUR
NCBI Description
                   DIOXYGENASE) >gi 595293 (U08850) dibenzothiophene
                   desulfurization enzyme [Rhodococcus sp.]
                   >gi 1582652_prf 2119215C dibenzothiophene desulfurization
                   enzyme [Rhodococcus sp.]
Seq. No.
                   305797
                   uC-zmflMo17006d06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q417154
                   434
BLAST score
E value
                   3.0e-49
                   101
Match length
                   94
% identity
                   HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
```

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82



(HSP82) [Oryza sativa]

305798 Seq. No. Seq. ID uC-zmflMo17006d11b1 Method BLASTX q417154 NCBI GI 353 BLAST score 4.0e-34 E value Match length 66 -100 % identity

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 305799

Seq. ID uC-zmflMo17006d12b1

Method BLASTN
NCBI GI g557695
BLAST score 43
E value 3.0e-15
Match length 111
% identity 85

NCBI Description Zea mays GTP binding protein beta subunit (ZGB1) mRNA,

complete cds

Seq. No. 305800

Seq. ID uC-zmflMo17007b09b1

Method BLASTX
NCBI GI g4539452
BLAST score 252
E value 1.0e-21
Match length 125
% identity 50

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No. 305801

Seq. ID uC-zmflMo17007c01b1

Method BLASTX
NCBI GI g2288887
BLAST score 278
E value 9.0e-25
Match length 64
% identity 81

NCBI Description (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis

thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate

diphosphate decarboxylase [Arabidopsis thaliana]

>gi 3786002 (AC005499) mevalonate diphosphate decarboxylase

[Arabidopsis thaliana]

Seq. No. 305802

Seq. ID uC-zmflMo17007c04b1

Method BLASTX
NCBI GI g2959324
BLAST score 490
E value 2.0e-49

```
126
Match length
                   79
 % identity
                   (Y15224) Importin alpha-like protein [Arabidopsis thaliana]
NCBI Description
                   305803
 Seq. No.
                   uC-zmflMo17007d04b1
 Seq. ID
Method
                   BLASTN
 NCBI GI
                   g4007864
 BLAST score
                   33
                   3.0e-09
 E value
 Match length
                   69
                   87
 % identity
 NCBI Description Zea mays HRGP gene, AC1503 line
                    305804
 Seq. No.
                    uC-zmflMo17007e01b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1946364
 BLAST score
                    262
                    1.0e-22
 E value
                    73
 Match length
                    62
 % identity
 NCBI Description (U93215) lipase isolog [Arabidopsis thaliana]
                    305805
 Seq. No.
                    uC-zmflMo17007e11b1
 Seq. ID
. Method
                    BLASTX
                    g2760834
 NCBI GI
                    230
 BLAST score
 E value
                    5.0e-19
                    130
 Match length
 % identity
                    (AC003105) putative nitrate transporter [Arabidopsis
 NCBI Description
                    thaliana]
                    305806
 Seq. No.
                    uC-zmflMo17007g03b1
 Seq. ID
                    BLASTX
 Method
                    g82696
 NCBI GI
                    394
 BLAST score
                    2.0e-38
 E value
                    84
 Match length
                    92
  % identity
                    glycine-rich protein - maize >gi_22293_emb_CAA43431_
 NCBI Description
                    (X61121) glycine-rich protein [Zea mays]
                    305807
  Seq. No.
                    uC-zmflMo17007q10b1
  Seq. ID
                    BLASTX
  Method
                    g1170507
  NCBI GI
                    176
  BLAST score
                    5.0e-13
  E value
                    69
  Match length
  % identity
                    EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)
  NCBI Description
                     >gi 100276 pir_ S22579 translation initiation factor eIF-4A
```

- curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206)



305808

nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]

Seq. ID uC-zmflMo17008a11b1
Method BLASTN
NCBI GI g717080
BLAST score 79
E value 2.0e-36
Match length 145
% identity 89

Seq. No.

NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (GapC4)

gene, promoter region

Seq. No. 305809

Seq. ID uC-zmflMo17008b06b1

Method BLASTN
NCBI GI g22149
BLAST score 40
E value 3.0e-13
Match length 96
% identity 85

NCBI Description Z.mays mRNA for alpha-tubulin

Seq. No. 305810

Seq. ID uC-zmflMo17008c02b1

Method BLASTX
NCBI GI g1168537
BLAST score 160
E value 2.0e-11
Match length 77
% identity 48

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732

aspartic proteinase (EC 3.4.23.-) - rice

>gi 218143 dbj BAA02242 (D12777) aspartic proteinase

- 3

[Oryza sativa]

Seq. No. 305811

Seq. ID uC-zmflMo17008f01b1

Method BLASTX
NCBI GI g2996096
BLAST score 255
E value 1.0e-29
Match length 90
% identity 80

NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1

alpha [Oryza sativa]

Seq. No. 305812

Seq. ID uC-zmflMo17008f02b1

Method BLASTX
NCBI GI g1170937
BLAST score 275
E value 2.0e-24
Match length 76
% identity 70

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE



ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No. 305813

Seq. ID uC-zmflMo17008g03b1

Method BLASTX
NCBI GI g1168536
BLAST score 344
E value 9.0e-33
Match length 86
% identity 71

NCBI Description PHYTEPSIN PRECURSOR (ASPARTIC PROTEINASE)

>gi 100567_pir S19697 aspartic proteinase (EC 3.4.23.-)

precursor - barley >gi_18904_emb_CAA39602_ (X56136)

aspartic proteinase [Hordeum vulgare]

Seq. No. 305814

Seq. ID uC-zmflMo17009a11b1

Method BLASTX
NCBI GI g1181615
BLAST score 240
E value 1.0e-20
Match length 68
% identity 66

NCBI Description (D83078) nitrilase [Nicotiana tabacum]

Seq. No. 305815

Seq. ID uC-zmflMo17009c01b1

Method BLASTX
NCBI GI g3142301
BLAST score 241
E value 3.0e-20
Match length 164
% identity 40

NCBI Description

(AC002411) Contains similarity to neural cell adhesion molecule 2, large isoform precursor gb_M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb_Q05946. ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101,

gb_H3630

Seq. No.

305816

Seq. ID uC-zmflMo17009e12b1

Method BLASTX
NCBI GI g2244868
BLAST score 219
E value 1.0e-17
Match length 98
% identity 46

NCBI Description (Z97337) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 305817

Seq. ID uC-zmflMo17009h03b1

Method BLASTX
NCBI GI g3915826
BLAST score 202
E value 6.0e-16



Match length % identity 48

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No.

305818

Seq. ID

uC-zmflMo17010a06b1

Method NCBI GI BLASTX g1352468

BLAST score E value

444

Match length % identity

3.0e-44 118 77

NCBI Description

BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE

HYDROLASE 1) (INVERTASE 1) >gi 1122439 (U16123) invertase

[Zea mays]

Seq. No.

305819

Seq. ID Method

uC-zmflMo17010f08b1

NCBI GI

BLASTX g112994

BLAST score

361

E value

1.0e-34

Match length % identity

84 88

NCBI Description

GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]

>gi_226091_prf 1410284A abscisic acid inducible gene [Zea

mays]

Seq. No.

305820

Seq. ID

uC-zmflMo17010g12b1

Method NCBI GI BLASTX g1841464

BLAST score

159

E value Match length 9.0e-11 79

% identity

NCBI Description

(Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No.

305821

Seq. ID

uC-zmflMo17013f05b1

Method

BLASTN

NCBI GI

g2984708

BLAST score

50

E value

2.0e-19

Match length % identity

73 92

NCBI Description

Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete

Seq. No.

305822

Seq. ID

uC-zmflMo17013g07b1

Method

BLASTX

NCBI GI

q4455274

BLAST score



E value 2.0e-41 Match length 155 % identity 81

NCBI Description (AL035527) spliceosome associated protein-like [Arabidopsis

thaliana]

Seq. No. 305823

Seq. ID uC-zmflMo17013h02b1

Method BLASTX
NCBI GI g2252844
BLAST score 228
E value 9.0e-19
Match length 125
% identity 46

NCBI Description (AF013293) belongs to the cytochrome p450 family

[Arabidopsis thaliana]

Seq. No. 305824

Seq. ID uC-zmflMo17013h06b1

Method BLASTX
NCBI GI g123593
BLAST score 493
E value 5.0e-50
Match length 119
% identity 84

NCBI Description HEAT SHOCK 70 KD PROTEIN >qi 82697 pir A25089 heat shock

protein 70 - maize

Seq. No. 305825

Seq. ID uC-zmflMo17014a05b1

Method BLASTX
NCBI GI g4567279
BLAST score 168
E value 8.0e-12
Match length 101
% identity 39

NCBI Description (AC006841) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 305826

Seq. ID uC-zmflMo17014a11b1

Method BLASTX
NCBI GI g134101
BLAST score 213
E value 4.0e-17
Match length 101
% identity 49

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD

CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi 72958 pir HHCSBA ribulose-bisphosphate carboxylase

subunit-binding protein alpha chain - castor bean

(fragment)

Seq. No. 305827

Seq. ID uC-zmflMo17014a12b1

Method BLASTX NCBI GI g2827139

NCBI GI

E value

BLAST score

Match length

g22332

9.0e-94

175

294



```
BLAST score
                  173
                  2.0e-21
E value
Match length
                  105
% identity
                  55
NCBI Description
                   (AF027172) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana] >gi 4049343 emb CAA22568 (AL034567)
                  cellulose synthase catalytic subunit (RSW1) [Arabidopsis
                  thaliana]
Seq. No.
                  305828
Seq. ID
                  uC-zmflMo17014b01b1
Method
                  BLASTN
                  q4007864
NCBI GI
BLAST score
                  275
E value
                  1.0e-153
Match length
                  419
% identity
                  60
NCBI Description
                  Zea mays HRGP gene, AC1503 line
Seq. No.
                  305829
Seq. ID
                  uC-zmflMo17014b07b1
Method
                  BLASTN
NCBI GI
                  q22332
BLAST score
                  248
E value
                  1.0e-137
Match length
                  355
% identity
                  93
NCBI Description Z.mays HRGP gene
                  305830
Seq. No.
Seq. ID
                  uC-zmflMo17014d12b1
Method
                  BLASTN
NCBI GI
                  q3309177
BLAST score
                  38
E value
                  8.0e-12
Match length
                  62
% identity
                  90
NCBI Description
                  Zea mays starch branching enzyme I (sbel) gene, complete
Seq. No.
                  305831
Seq. ID
                  uC-zmflMo17016d02b1
Method
                  BLASTX
NCBI GI
                  g3269282
BLAST score
                  148
E value
                  3.0e-09
Match length
                  54
% identity
NCBI Description
                  (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                  305832
Seq. ID
                  uC-zmflMo17018a06b1
Method
                  BLASTN
```



% identity

NCBI Description Z.mays HRGP gene

Seq. No.

305833

Seq. ID

uC-zmflMo17018a12b1

Method NCBI GI BLASTN g1498596

BLAST score E value

122 4.0e-62 243

Match length % identity

87

NCBI Description Zea mays phospholipid transfer protein mRNA, complete cds

Seq. No.

305834

Seq. ID

uC-zmflMo17018d02b1

BLASTX Method NCBI GI g3123130 BLAST score 145 5.0e-09 E value Match length 49 61

% identity

NCBI Description

HYPOTHETICAL 61.8 KD TRP-ASP REPEATS CONTAINING PROTEIN

T32G6.2 IN CHROMOSOME II >gi 2618685 (AC002510) putative

small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana] >gi 3241948 (AC004625) putative small nuclear

ribonucleoprotein Prp4p [Arabidopsis thaliana]

Seq. No.

305835

Seq. ID

uC-zmflMo17018h07b1

BLASTX Method NCBI GI g4559358 278 BLAST score E value 8.0e-25 99 Match length % identity 53

(AC006585) putative steroid binding protein [Arabidopsis NCBI Description

thaliana]

Seq. No.

305836

uC-zmflMo17018h12b1 Seq. ID

Method BLASTX NCBI GI g3805962 BLAST score 494 E value 6.0e-50 Match length 152 % identity 63

NCBI Description (Y13772) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No.

305837

Seq. ID

uC-zmflMo17019a08b1

Method BLASTX NCBI GI q4581116 BLAST score 198 E value 3.0e-15 Match length 91 % identity

NCBI Description (AC005825) putative beta-galactosidase [Arabidopsis



thaliana]

```
305838
Seq. No.
                  uC-zmflMo17019c01b1
Seq. ID
                  BLASTX
Method
                  g4454480
NCBI GI
                  181
BLAST score
E value
                  3.0e-13
Match length
                  48
% identity
                   (AC006234) putative (1-4)-beta-mannan endohydrolase
NCBI Description
                   [Arabidopsis thaliana]
                   305839
Seq. No.
                   uC-zmflMo17019c07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1430907
BLAST score
                   186
E value
                   7.0e-14
                   69
Match length
                   57
% identity
                   (Z49144) multidrug resistance-associated protein 2
NCBI Description
                   [Oryctolagus cuniculus]
                   305840
Seq. No.
                   uC-zmflMo17019c09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q82696
                   303
BLAST score
E value
                   1.0e-27
                   91
Match length
                   66
% identity
                   glycine-rich protein - maize >gi 22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                   305841
                   uC-zmflMo17019f10b1
Seq. ID
                   BLASTN
Method
                   g2062705
NCBI GI
BLAST score
                   34
                   2.0e-09
E value
                   34
Match length
                   100
% identity
                   Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
Seq. No.
                   305842
                   uC-zmflMo17019h02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g82040
BLAST score
                   500
                   6.0e-51
E value
                   102
Match length
                   25
% identity
                   ubiquitin precursor - flax (fragment) >gi_168304 (M57895)
NCBI Description
                   ubiquitin [Linum usitatissimum]
```

305843

Seq. No.



```
uC-zmflMo17019h04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2624417
BLAST score
                   545
E value
                   8.0e-56
Match length
                   108
% identity
                   92
NCBI Description
                   (AJ002959) Ubiquitin carrier protein [Zea mays]
Seq. No.
                   305844
                   uC-zmflMo17062a04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2501499
BLAST score
                   154
E value
                   2.0e-10
Match length
                   55
% identity
NCBI Description
                   INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE (IAA-GLU
                   SYNTHETASE) ((URIDINE
                   5'-DIPHOSPHATE-GLUCOSE: INDOL-3-YLACETYL) -BETA-D-GLUCOSYL
                   TRANSFERASE) >gi_626043_pir__A54739 indole-3-acetate beta-glucosyltransferase (EC 2.4.1.121) - maize >gi_548195
                   (L34847) IAA-glu synthetase [Zea mays]
Seq. No.
                   305845
Seq. ID
                   uC-zmflMo17062b06b1
Method
                   BLASTX
NCBI GI
                   q2911057
BLAST score
                   259
E value
                   2.0e-22
                   79
Match length
% identity
                   65
                   (AL021961) caffeoyl-CoA O-methyltransferase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   305846
                   uC-zmflMo17062c04b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4185305
BLAST score
                   59
E value
                   2.0e-24
Match length
                   131
                   87
% identity
                   Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                   protein, polyprotein, and copia protein genes, complete
                   cds; and unknown genes
                   305847
Seq. No.
Seq. ID
                   uC-zmflMo17062d10b1
Method
                   BLASTX
NCBI GI
                   g2262105
BLAST score
                   276
```

E value 2.0e-24 Match length 138 % identity 41

(AC002343) unknown protein [Arabidopsis thaliana] NCBI Description

E value

2.0e-12

```
Seq. No.
                    305848
 Seq. ID
                    uC-zmflMo17063a04b1
 Method
                    BLASTX
 NCBI GI
                    q1800147
 BLAST score
                    415
                    1.0e-40
 E value
                    145
 Match length
 % identity
                    61
                    (U83655) membrane associated protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    305849
                    uC-zmflMo17063a12b1
 Seq. ID
                    BLASTN
 Method
                    q902200
 NCBI GI
 BLAST score
                    51
 E value
                    1.0e-19
 Match length
                    352
                    39
 % identity
                   Z.mays complete chloroplast genome
 NCBI Description
                    305850
 Seq. No.
 Seq. ID
                    uC-zmflMo17063c06b1
 Method
                    BLASTX
 NCBI GI
                    g1181673
 BLAST score
                    548
                    3.0e-56
🏋 value
 Match length
                    115
                    91
 % identity
 NCBI Description
                   (U41652) heat shock protein cognate 70 [Sorghum bicolor]
                    305851
 Seq. No.
 Seq. ID
                    uC-zmflMo17063f02b1
 Method
                    BLASTX
 NCBI GI
                    q4582436
 BLAST score
                    427
 E value
                    4.0e-42
 Match length
                    100
 % identity
                    82
                    (AC007196) unknown protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    305852
                    uC-zmflMo17063g08b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g553073
 BLAST score
                    351
 E value
                    4.0e-33
 Match length
                    96
                    75
 % identity
 NCBI Description
                   (M94481) reverse transcriptase [Zea mays]
                    305853
 Seq. No.
                    uC-zmflMo17064a05b1
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g417154
 BLAST score
                    169
```



```
Match length
                  50
% identity
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
                  305854
Seq. No.
Seq. ID
                  uC-zmflMo17064c03b1
Method
                  BLASTX
NCBI GI
                  q1890575
BLAST score
                  610
E value
                  1.0e-63
Match length
                  140
                  77
```

% identity (X93174) xyloglucan endotransglycosylase (XET) [Hordeum NCBI Description vulgare]

305855 Seq. No. Seq. ID uC-zmflMo17064d06b1 Method BLASTX NCBI GI g3402758 BLAST score 412 E value 2.0e-40 Match length 114 % identity 71

(AL031187) serine/threonine kinase - like protein NCBI Description

[Arabidopsis thaliana]

305856 Seq. No. Seq. ID uC-zmflMo17064d12b1 Method BLASTX NCBI GI g1170937 BLAST score 262 E value 6.0e-23

Match length 103 % identity 55

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

305857 Seq. No.

Seq. ID uC-zmflMo17064e01b1

Method BLASTX NCBI GI g135417 BLAST score 275 2.0e-24 E value Match length 60 85 % identity

TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin NCBI Description

alpha-3 chain - maize >gi 22150 emb CAA44861 (X63176) Alpha-tubulin #3 [Zea mays] >gi 485377 (M60171) alpha-3

tubulin [Zea mays]

Seq. No. 305858

Seq. ID uC-zmflMo17064e07b1

Match length

% identity

122



```
BLASTN
Method
                  g22371
NCBI GI
BLAST score
                  70
                  5.0e-31
E value
                  158
Match length
                  55
% identity
NCBI Description Maize Mu4 transposable element DNA
                  305859
Seq. No.
                  uC-zmflMo17064e11b1
Seq. ID
                  BLASTX
Method
                  q4581156
NCBI GI
                  195
BLAST score
                  6.0e-15
E value
                  50
Match length
                   78
% identity
NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
                   305860
Seq. No.
                  uC-zmflMo17064f01b1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g312180
BLAST score
                   63
                   5.0e-27
E value
                   94
Match length
                   93
% identity
NCBI Description Z.mays GapC4 gene
Seq. No.
                   305861
                   uC-zmflMo17064f12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3461846
BLAST score
                   210
E value
                   1.0e-16
                   134
Match length
                   18
% identity
                   (AC005315) putative zinc-finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   305862
Seq. No.
Seq. ID
                   uC-zmflMo17065a06b1
                   BLASTX
Method
NCBI GI
                   g4582436
BLAST score
                   192
                   4.0e-15
E value
                   59
Match length
% identity
NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]
                   305863
Seq. No.
Seq. ID
                   uC-zmflMo17065a11b1
                   BLASTX
Method
                   q4582436
NCBI GI
BLAST score
                   376
E value
                   4.0e-36
```

Seq. ID

Method





```
(AC007196) unknown protein [Arabidopsis thaliana]
NCBI Description
                  305864
Seq. No.
                  uC-zmflMo17065b08b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g22091
BLAST score
                  158
E value
                  1.0e-83
Match length
                  203
                  95
% identity
                  Z.diploperennis gene for hydroxyproline-rich glycoprotein
NCBI Description
                  305865
Seq. No.
Seq. ID
                  uC-zmflMo17065e07b1
Method
                  BLASTX
NCBI GI
                  g4588012
BLAST score
                  272
E value
                  5.0e-24
Match length
                  100
% identity
                  57
                   (AF085717) putative callose synthase catalytic subunit
NCBI Description
                   [Gossypium hirsutum]
                  305866
Seq. No.
Seq. ID
                  uC-zmflMo17065g07b1
Method
                  BLASTX
NCBI GI
                   g1360090
BLAST score
                  276
E value
                   2.0e-24
Match length
                   67
                  79
% identity
NCBI Description (X95576) C1C-Nt1 [Nicotiana tabacum]
                   305867
Seq. No.
Seq. ID
                  uC-zmflMo17065h07b1
Method
                  BLASTN
NCBI GI
                   g666088
BLAST score
                   57
                   2.0e-23
E value
                   96
Match length
                   90
% identity
NCBI Description S.bicolor mRNA for p-(S)-hydroxymandelonitrile lyase
                   305868
Seq. No.
Seq. ID
                   uC-zmflMo17067a10b1
Method
                   BLASTN
                   g2984708
NCBI GI
BLAST score
                   40
                   2.0e-13
E value
Match length
                   104
                   85
% identity
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
NCBI Description
Seq. No.
                   305869
```

43352

uC-zmflMo17067b12b1

BLASTN

```
g871985
NCBI GI
                  49
BLAST score
                  1.0e-18
E value
                  193
Match length
                  81
% identity
                  A.sativa Aspkl1 mRNA
NCBI Description
Seq. No.
                  305870
                  uC-zmflMo17067c08b1
Seq. ID
Method
                  BLASTX
                  q2668742
NCBI GI
                  242
BLAST score
                   3.0e-24
E value
Match length
                   91
                   67
% identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   305871
Seq. No.
                   uC-zmflMo17067e05b1
Seq. ID
                   BLASTX
Method
                   q82696
NCBI GI
BLAST score
                   376
                   4.0e-36
E value
                   76
Match length
% identity
                   96
                   glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   305872
Seq. No.
                   uC-zmflMo17067e12b1
Seq. ID
                   BLASTX
Method
                   g3859536
NCBI GI
                   414
BLAST score
                   1.0e-40
E value
                   133
Match length
                   64
% identity
                  (AF095453) asparagine synthetase [Arabidopsis thaliana]
NCBI Description
                   305873
Seq. No.
Seq. ID
                   uC-zmflMo17067f12b1
                   BLASTX
Method
                   g2827002
NCBI GI
BLAST score
                   188
                   3.0e-16
E value
Match length
                   73
% identity
                   68
                  (AF005993) HSP70 [Triticum aestivum]
NCBI Description
                   305874
Seq. No.
Seq. ID
                   uC-zmflMo17068a10b1
                   BLASTX
Method
NCBI GI
                   g2286111
BLAST score
                   145
                   2.0e-09
E value
Match length
                   34
% identity
                  (U78891) MADS box protein [Oryza sativa]
NCBI Description
```

```
305875
Seq. No.
Seq. ID
                   uC-zmf1Mo17068b07b1
Method
                   BLASTX
NCBI GI
                   g20559
BLAST score
                   370
E value
                   1.0e-35
Match length
                   99
% identity
                   78
NCBI Description
                   (X13301) hsp70 (AA 6 - 651) [Petunia x hybrida]
Seq. No.
Seq. ID
                   uC-zmflMo17068c05b1
Method
                   BLASTX
NCBI GI
                   q1076315
BLAST score
                   191
E value
                   6.0e-15
Match length
                   65
                   57
% identity
NCBI Description
                   cytochrome P450 - Arabidopsis thaliana
                   >gi_853719_emb_CAA60793_ (X87367) CYP90 protein
                   [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368)
                   CYP90 protein [Arabidopsis thaliana]
                   305877
Seq. No.
Seq. ID
                   uC-zmflMo17068e08b1
Method
                   BLASTX
NCBI GI
                   q118104
BLAST score
                   394
E value
                   2.0e-38
Match length
                   98
% identity
                   78
NCBI Description
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
                   >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
                   305878
Seq. No.
Seq. ID
                   uC-zmflMo17068e09b1
Method
                   BLASTX
NCBI GI
                   g1743277
BLAST score
                   290
E value
                   4.0e-26
                   122
Match length
% identity
                   52
NCBI Description
                   (Y09741) beta-tubulin 1 [Hordeum vulgare]
Seq. No.
                   305879
Seq. ID
                   uC-zmflMo17082a02b1
Method
                   BLASTX
NCBI GI
                   g1076809
BLAST score
                   181
E value
                   2.0e-13
Match length
                   47
% identity
                   77
NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize
```



>gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
[Zea mays]

Seq. No. 305880

Seq. ID uC-zmflMo17082b08b1

Method BLASTX
NCBI GI g3024657
BLAST score 228
E value 6.0e-19
Match length 79

Match length 79 % identity 61

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi_2668740 (AF034944) translation initiation factor; GOS2

[Zea mays]

Seq. No. 305881

Seq. ID uC-zmflMo17082e11b1

Method BLASTX
NCBI GI 94378875
BLAST score 164
E value 8.0e-12
Match length 73

% identity 44

NCBI Description (AF124360) delta-12 desaturase [Brassica carinata]

Seq. No. 305882

Seq. ID uC-zmflMo17082e12b1

Method BLASTX
NCBI GI g115679
BLAST score 212
E value 4.0e-17
Match length 85
% identity 58

NCBI Description CATALASE ISOZYME

Seq. No. 305883

Seq. ID uC-zmflMo17082f03b1

Method BLASTN
NCBI GI g257040
BLAST score 206
E value 1.0e-112
Match length 307

% identity 95

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 305884

Seq. ID uC-zmflMo17082g01b1

Method BLASTX
NCBI GI g3135543
BLAST score 172
E value 7.0e-18
Match length 65
% identity 78

NCBI Description (AF062393) aquaporin [Oryza sativa]

Seq. No. 305885

Seq. ID uC-zmflMo17083c12b1

E value

Match length

5.0e-37 99



```
BLASTX
Method
                  g4415925
NCBI GI
                  170
BLAST score
                  5.0e-12
E value
Match length
                  122
                  37
% identity
                   (AC006282) putative glucosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                   305886
Seq. No.
                  uC-zmflMo17083d10b1
Seq. ID
                  BLASTN
Method
                   q1060934
NCBI GI
BLAST score
                   117
E value
                   3.0e-59
Match length
                   129
                   98
% identity
NCBI Description Maize mRNA for mLIP15 (DNA-binding factor), complete cds
Seq. No.
                   uC-zmflMo17083e12b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4140643
BLAST score
                   52
                   2.0e-20
E value
Match length
                   104
% identity
                   88
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   305888
Seq. No.
                   uC-zmflMo17083h11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1332579
BLAST score
                   509
E value
                   3.0e-58
                   135
Match length
% identity
                   (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                   305889
Seq. No.
                   uC-zmflMo17084a11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3126967
BLAST score
                   647
                   7.0e-68
E value
                   145
Match length
                   16
% identity
                   (AF061807) polyubiquitin [Elaeagnus umbellata]
NCBI Description
                   305890
Seq. No.
                   uC-zmflMo17084h03b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2984709
BLAST score
                   381
```

Seq. No.



```
% identity
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  305891
Seq. ID
                  uC-zmflMo17085c10b1
Method
                  BLASTN
NCBI GI
                  g257040
BLAST score
                  239
E value
                  1.0e-132
Match length
                  304
% identity
                  97
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
```

Seq. No. 305892 Seq. ID uC-zmflMo17085d10b1

Method BLASTX NCBI GI q4581203 BLAST score 262 E value 8.0e-23 Match length 84 % identity 57

NCBI Description (Y17912) cyclic nucleotide and calmodulin-regulated ion

channel [Arabidopsis thaliana]

Seq. ID uC-zmflMo17085e02b1 Method BLASTX NCBI GI q3033401 BLAST score 544 E value 6.0e-56 Match length 129 % identity 79

NCBI Description (AC004238) putative potassium transporter [Arabidopsis

thaliana]

305893

Seq. No. 305894

Seq. ID uC-zmflMo17085e03b1

Method BLASTX NCBI GI q132147 BLAST score 413 E value 2.0e-40 Match length 74 97 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_68089_pir__RKZMS

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - maize >gi_22474_emb_CAA29784_ (X06535)

ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi 359512 prf 1312317A ribulosebisphosphate carboxylase

[Zea mays]

Seq. No. 305895

Seq. ID uC-zmflMo17085e07b1

Method BLASTX NCBI GI g3342823

```
BLAST score
                   261
E value
                   1.0e-22
                   50
Match length
                   92
% identity
NCBI Description
                   (AF076955) eukaryotic translation initiation factor p28
                   subunit [Zea mays]
Seq. No.
                   305896
Seq. ID
                   uC-zmflMo17085f01b1
Method
                   BLASTX
NCBI GI
                   g3135543
BLAST score
                   373
E value
                   5.0e-36
Match length
                   87
% identity
                   84
NCBI Description
                  (AF062393) aquaporin [Oryza sativa]
Seq. No.
                   305897
Seq. ID
                   uC-zmflMo17085h03b1
Method
                  BLASTX
NCBI GI
                   g4490752
BLAST score
                   244
E value
                   3.0e-21
                   70
Match length
% identity
                   69
NCBI Description
                   (AL035708) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   305898
Seq. ID
                   uC-zmflMo17085h12b1
Method
                   BLASTN
NCBI GI
                   g257040
BLAST score
                   204
E value
                   1.0e-111
Match length
                   248
                   96
% identity
NCBI Description
                  hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
Seq. No.
                   305899
Seq. ID
                   uC-zmflMo17086a11b1
Method
                   BLASTN
NCBI GI
                   g4007864
BLAST score
                   287
E value
                   1.0e-160
Match length
                   362
% identity
                   61
NCBI Description
                  Zea mays HRGP gene, AC1503 line
Seq. No.
                   305900
```

Seq. ID uC-zmflMo17086c03b1

Method BLASTX NCBI GI g135398 BLAST score 635 E value 2.0e-66 Match length 125 % identity

TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1 NCBI Description



chain - maize >gi_22147_emb_CAA33734_ (X15704)
alphal-tubulin [Zea mays]

Seq. No. 305901

Seq. ID uC-zmflMo17086c07b1

Method BLASTX
NCBI GI g498643
BLAST score 657
E value 5.0e-69
Match length 148
% identity 91

NCBI Description (U10270) G-box binding factor 1 [Zea mays]

Seq. No. 305902

Seg. ID uC-zmflMo17086c11b1

Method BLASTX
NCBI GI g2828296
BLAST score 477
E value 6.0e-48
Match length 96
% identity 91

NCBI Description (AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No. 305903

Seq. ID uC-zmflMo17086d01b1

Method BLASTX
NCBI GI g3126967
BLAST score 559
E value 1.0e-57
Match length 117
% identity 17

NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]

Seq. No. 305904

Seq. ID uC-zmflMo17086d07b1

Method BLASTX
NCBI GI g3126967
BLAST score 390
E value 7.0e-38
Match length 112
% identity 13

NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]

Seq. No. 305905

Seq. ID uC-zmflMo17086g01b1

Method BLASTX
NCBI GI g2921304
BLAST score 411
E value 5.0e-43
Match length 126
% identity 77

NCBI Description (AF033496) herbicide safener binding protein [Zea mays]

Seq. No. 305906

Seq. ID uC-zmflMo17086h08b1

Method BLASTX NCBI GI g2392895

Match length

```
BLAST score
                  343
                  1.0e-32
E value
Match length
                  97
% identity
                  67
NCBI Description
                  (AF017056) brassinosteroid insensitive 1 [Arabidopsis
                  thaliana]
Seq. No.
                  305907
Seq. ID
                  uC-zmflMo17086h11b1
Method
                  BLASTX
NCBI GI
                  q3126967
BLAST score
                  300
E value
                  2.0e-27
Match length
                  96
% identity
                  12
NCBI Description
                  (AF061807) polyubiquitin [Elaeagnus umbellata]
                  305908
Seq. No.
                  uC-zmflMo17087b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135398
BLAST score
                  252
E value
                  2.0e-32
Match length
                  91
                  70
% identity
NCBI Description
                  TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1
                  chain - maize >gi_22147_emb_CAA33734_ (X15704)
                  alphal-tubulin [Zea mays]
Seq. No.
                  305909
                  uC-zmflMo17087d11b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22312
BLAST score
                  80
E value
                  3.0e-37
Match length
                  124
% identity
                  91
NCBI Description
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
                  abscisic acid)
Seq. No.
                  305910
Seq. ID
                  uC-zmflMo17087e04b1
Method
                  BLASTN
NCBI GI
                  g22292
BLAST score
                  119
E value
                  2.0e-60
Match length
                  258
                  89
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
Seq. No.
                  305911
Seq. ID
                  uC-zmflMo17087f11b1
Method
                  BLASTX
NCBI GI
                  g100490
BLAST score
                  162
E value
                  3.0e-11
```



```
% identity
NCBI Description
                   polyubiquitin - garden snapdragon (fragment)
                   >gi 16071 emb CAA48140 (X67957) ubiquitin [Antirrhinum
                   majus]
Seq. No.
                   305912
Seq. ID
                   uC-zmflMo17087g07b1
Method
                   BLASTX
NCBI GI
                   q3451074
BLAST score
                   200
E value
                   7.0e-16
Match length
                   64
% identity
                   58
NCBI Description
                   (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                   305913
Seq. ID
                   uC-zmflMo17087q10b1
Method
                   BLASTX
NCBI GI
                   g2129946
BLAST score
                   194
E value
                   6.0e-15
Match length
                   64
% identity
                   67
NCBI Description
                   ADP-ribosylation factor homolog GTP-binding protein NTGB1 -
                   common tobacco (fragment) >gi 1184987 (U46927) NTGB1
                   [Nicotiana tabacum]
Seq. No.
                   305914
Seq. ID
                   uC-zmflMo17089a09b1
Method
                   BLASTX
NCBI GI
                   g3264596
BLAST score
                   269
E value
                   9.0e-24
Match length
                   90
% identity
                   63
NCBI Description
                   (AF057183) putative tonoplast aquaporin [Zea mays]
Seq. No.
                   305915
Seq. ID
                   uC-zmflMo17089d01b1
Method
                   BLASTX
NCBI GI
                   g283045
BLAST score
                   157
E value
                   1.0e-10
Match length
                   83
% identity
                   46
NCBI Description
                   hydroxyproline-rich glycoprotein - maize
                   >gi_22333_emb_CAA44844 (X63134) hydroxyproline-rich
glycoprotein [Zea mays] >gi_228936_prf__1814452A Hyp-rich
                   glycoprotein [Zea mays]
Seq. No.
                   305916
Seq. ID
                   uC-zmflMo17089f02b1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g4205079
BLAST score 407
E value 1.0e-39
Match length 145



% identity 55

NCBI Description (U70425) ankyrin repeat-containing protein 2 [Arabidopsis

thaliana]

Seq. No. 305917

Seq. ID uC-zmflMo17089f06b1

Method BLASTX
NCBI GI g2801433
BLAST score 321
E value 1.0e-29
Match length 90
% identity 69

NCBI Description (AF017991) salt stress inducible small GTP binding protein

Ran1 homolog [Arabidopsis thaliana] >gi 3559764 (U75601)

unknown [Arabidopsis thaliana]

Seq. No. 305918

Seq. ID uC-zmflMo17089g06b1

Method BLASTX
NCBI GI g2058280
BLAST score 168
E value 6.0e-12
Match length 44
% identity 77

NCBI Description (X97381) atran3 [Arabidopsis thaliana]

Seq. No. 305919

Seq. ID uC-zmflMo17089g07b1

Method BLASTN
NCBI GI g2345085
BLAST score 95
E value 4.0e-46
Match length 138
% identity 92

NCBI Description Zea mays ribosomal RNA intergenic spacer, partial sequence

Seq. No. 305920

Seq. ID uC-zmflMo17089h06b1

Method BLASTX
NCBI GI g135060
BLAST score 298
E value 4.0e-27
Match length 112
% identity 58

NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)

(SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose

synthase [Zea mays] $> \overline{gi}_224\overline{8}8 = \overline{mb}_CAA262\overline{2}9$ (X02382)

sucrose synthase [Zea mays]

Seq. No. 305921

Seq. ID uC-zmflMo17091a08b1

Method BLASTN
NCBI GI g1906603
BLAST score 115
E value 7.0e-58
Match length 338



```
% identity
NCBI Description
                   Zea mays ACCase gene, intron containing colonist1 and
                   colonist2 retrotransposons and reverse transcriptase
                   pseudogene, complete sequence
                   305922
Seq. No.
Seq. ID
                   uC-zmflMo17091b08b1
Method
                   BLASTX
NCBI GI
                   q112994
BLAST score
                   350
E value
                   3.0e-33
Match length
                   82
% identity
                   87
NCBI Description
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                   >gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >gi_226091 prf 1410284A abscisic acid inducible gene [Zea
                   mays]
Seq. No.
                   305923
Seq. ID
                   uC-zmflMo17091c09b1
Method
                   BLASTX
NCBI GI
                   q2668742
BLAST score
                   417
E value
                   4.0e-41
Match length
                   84
% identity
                   95
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
                   305924
Seq. ID
                   uC-zmflMo17091g04b1
Method
                   BLASTX
NCBI GI
                   g3184082
BLAST score
                   291
E value
                   3.0e-26
Match length
                   102
% identity
                   51
                   (AL023781) N-terminal acetyltransferase 1
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                   305925
Seq. ID
                   uC-zmflMo17092b05b1
Method
                   BLASTX
NCBI GI
                   g115771
BLAST score
                   400
E value
                   5.0e-39
Match length
                   93
% identity
                   82
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
```

(CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll

a/b-binding protein precursor - maize

>gi_22224 emb CAA32900 (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 305926

Seq. ID uC-zmflMo17092b06b1



Method BLASTX NCBI GI g1076591 BLAST score 205 E value 4.0e-16 Match length 111 42 % identity NCBI Description

polygalacturonase inhibitor protein - tomato >gi_469457 (L26529) polygalacturonase inhibitor protein [Lycopersicon

esculentum]

Seq. No. 305927

Seq. ID uC-zmflMo17093b05b1

Method BLASTN NCBI GI q2921303 BLAST score 46 E value 5.0e-17 Match length 78

% identity Zea mays herbicide safener binding protein (SBP1) mRNA, NCBI Description

complete cds

305928 Seq. No.

Seq. ID uC-zmflMo17093d09b1

90

Method BLASTN NCBI GI q4007864 BLAST score 144 E value 2.0e-75 Match length 236 90 % identity

NCBI Description Zea mays HRGP gene, AC1503 line

305929 Seq. No.

uC-zmflb73001a01b1 Seq. ID

Method BLASTX NCBI GI g3776567 BLAST score 189 7.0e-23 E value Match length 150 49 % identity

(AC005388) Strong similarity to F21B7.33 gi 2809264 from A. NCBI Description

thaliana BAC gb AC002560. EST gb N65119 comes from this

gene. [Arabidopsis thaliana]

305930 Seq. No.

uC-zmf1b73001a04b1Seq. ID

Method BLASTX NCBI GI q115815 BLAST score 268 E value 2.0e-23 Match length 90 56 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll

a/b-binding protein precursor - maize

>gi 22355 emb CAA39376 (X55892) light-harvesting

chlorophyll a/b binding protein [Zea mays]

Seq. ID Method

305936

BLASTX

uC-zmflb73001f07b1



```
305931
Seq. No.
                  uC-zmflb73001a06b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g639721
                  37
BLAST score
                  2.0e-11
E value
                  69
Match length
% identity
                  88
                  Zea mays calcium-dependent protein kinase (CDPK) gene,
NCBI Description
                  exons 1-7 and partial cds
                  305932
Seq. No.
                  uC-zmflb73001c12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454483
                  240
BLAST score
                   5.0e-20
E value
                  73
Match length
% identity
                   66
                   (AC006234) putative kinase, 5' partial [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   305933
                   uC-zmflb73001d02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4529972
BLAST score
                   336
E value
                   2.0e-31
                   120
Match length
% identity
                   54
                  (AC002330) putative chloroplast outer envelope 86-like
NCBI Description
                   protein [Arabidopsis thaliana]
                   305934
Seq. No.
                   uC-zmflb73001d07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4062934
                   169
BLAST score
                   1.0e-13
E value
                   75
Match length
                   59
% identity
                  (D88272) formate dehydrogenase [Hordeum vulgare]
NCBI Description
                   305935
Seq. No.
                   uC-zmflb73001e01b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22379
BLAST score
                   84
                   2.0e-39
E value
Match length
                   200
                   85
% identity
                   Z.mays mRNA for CAAT-box DNA binding protein subunit B
NCBI Description
                   (NF-YB)
```

% identity

NCBI Description

39

```
q2262105
NCBI GI
BLAST score
                   368
E value
                   4.0e-35
Match length
                   132
% identity
                   53
                   (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   305937
Seq. ID
                   uC-zmflb73001f11b1
Method
                   BLASTX
NCBI GI
                   q3779024
BLAST score
                   149
E value
                   2.0e-09
Match length
                   57
% identity
                   53
NCBI Description
                  (AC005171) unknown protein [Arabidopsis thaliana]
Seq. No.
                   305938
Seq. ID
                   uC-zmflb73001g12b1
Method
                   BLASTX
NCBI GI
                   q2222798
BLAST score
                   500
E value
                   1.0e-50
Match length
                   125
                   80
% identity
NCBI Description
                  (Y14008) gibberellin 20-oxidase [Triticum aestivum]
Seq. No.
                   305939
                   uC-zmflb73003c01b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22091
BLAST score
                   129
                   2.0e-66
E value
Match length
                   225
% identity
                   89
NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein
                   305940
Seq. No.
Seq. ID
                   uC-zmflb73003f03b1
                   BLASTN
Method
NCBI GI
                   g22159
BLAST score
                   71
E value
                   8.0e-32
Match length
                   75
                   99
% identity
                   Zea mays mRNA for adenine nucleotide translocator (ATP/ADP
NCBI Description
                   translocator)
                   305941
Seq. No.
Seq. ID
                   uC-zmflb73003g01b1
Method
                   BLASTX
NCBI GI
                   g4263721
BLAST score
                   168
E value
                   5.0e-12
Match length
                   101
```

(AC006223) putative DNA repair protein RAD50 [Arabidopsis

% identity

NCBI Description

84

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thaliana]

```
Seq. No.
                   305942
Seq. ID
                  uC-zmflb73003q04b1
Method
                  BLASTX
NCBI GI
                  q2708745
BLAST score
                  257
E value
                   1.0e-23
Match length
                  65
                  89
% identity
NCBI Description
                   (AC003952) putative calcium-dependent ser/thr protein
                  kinase [Arabidopsis thaliana]
                   305943
Seq. No.
Seq. ID
                  uC-zmflb73003q06b1
Method
                  BLASTN
NCBI GI
                  q3219148
BLAST score
                  46
E value
                  1.0e-16
Match length
                  70
% identity
                   91
NCBI Description
                  Mesembryanthemum crystallinum cdc2 related mRNA, partial
Seq. No.
                  305944
Seq. ID
                  uC-zmflb73003h02b1
Method
                  BLASTX
NCBI GI
                  q1518540
BLAST score
                  226
E value
                   3.0e-19
Match length
                  57
% identity
                  70
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                  305945
Seq. ID
                  uC-zmflb73003h03b1
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                  308
E value
                  2.0e-28
Match length
                  80
                  72
% identity
NCBI Description
                  glycine-rich protein - maize >gi 22293 emb CAA43431
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                  305946
Seq. ID
                  uC-zmflb73003h08b1
Method
                  BLASTX
NCBI GI
                  g135460
BLAST score
                  247
E value
                  2.0e-21
Match length
                  57
```

tubulin (AA 1-444) [Zea mays]

TUBULIN BETA-2 CHAIN >gi_100933_pir__ S14702 tubulin beta-2 chain - maize >gi_22184_emb_CAA37061_ (X52879) beta 2



```
305947
Seq. No.
                  uC-zmflb73004a07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455259
BLAST score
                  418
                  5.0e-41
E value
                  134
Match length
% identity
                  (AL035523) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  305948
Seq. No.
                  uC-zmflb73005f09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1706103
                  148
BLAST score
                  2.0e-09
E value
                  72
Match length
                  43
% identity
                  CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD
NCBI Description
                  SUBUNIT (CPSF 100 KD SUBUNIT) >gi_1363022 pir__A56351
                  cleavage and polyadenylation specificity factor 100K chain
                   - bovine >gi_599683_emb_CAA53535_ (X75931) Cleavage and
                  Polyadenylation specificity factor (CPSF) 100kD subunit
                   [Bos taurus]
                   305949
Seq. No.
                  uC-zmflb73006b03a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3036803
BLAST score
                   348
                   8.0e-33
E value
Match length
                   104
                   63
% identity
NCBI Description (AL022373) hypothetical protein [Arabidopsis thaliana]
                   305950
Seq. No.
                   uC-zmflb73006d11a1
Seq. ID
Method
                   BLASTX
                   g4079798
NCBI GI
BLAST score
                   141
                   6.0e-09
E value
Match length
                   35
                   77
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   305951
Seq. No.
                   uC-zmf1b73006f07a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q435174
```

NCBI GI g435174
BLAST score 38
E value 5.0e-12
Match length 102
% identity 84

NCBI Description A.sativa (Pewi) ASTCP-K36 mRNA for t complex polypeptide



```
305952
Seq. No.
                  uC-zmflb73008b09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g862310
                  271
BLAST score
                  8.0e-24
E value
Match length
                  54
                   100
% identity
NCBI Description (L28001) G protein alpha-subunit [Oryza sativa]
Seq. No.
                   305953
                   uC-zmflb73008c05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1574938
BLAST score
                   380
E value
                   1.0e-36
Match length
                   76
                   93
% identity
                  (U34726) superoxide dismutase 4 [Zea mays]
NCBI Description
                   305954
Seq. No.
Seq. ID
                   uC-zmflb73008e10a1
Method
                   BLASTX
NCBI GI
                   q2464901
BLAST score
                   234
E value
                   3.0e-24
Match length
                   80
% identity
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   305955
Seq. No.
                   uC-zmflb73008f06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3033375
BLAST score
                   358
E value
                   6.0e - 34
                   148
Match length
                   49
% identity
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
                   thaliana]
                   305956
Seq. No.
                   uC-zmf1b73008g02b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g998429
BLAST score
                   118
                   4.0e-60
E value
                   171
Match length
                   99
% identity
                   GRF1=general regulatory factor [Zea mays, XL80, Genomic,
NCBI Description
```

Seq. ID uC-zmflb73008g04b1

5348 nt]

Method BLASTX NCBI GI g1930081 BLAST score 457

```
9.0e-51
E value
Match length
                  140
                  72
% identity
                  (U92878) acyl-ACP thioesterase [Garcinia mangostana]
NCBI Description
Seq. No.
                  uC-zmflb73008h12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4249377
                  206
BLAST score
E value
                  4.0e-16
Match length
                  54
                  70
% identity
                   (AC005966) Similar to gi 2829865 F3I6.4 from Arabidopsis
NCBI Description
                  thaliana BAC gb AC002396. [Arabidopsis thaliana]
                  305959
Seq. No.
                  uC-zmflb73011b10b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3341647
                  88
BLAST score
                  1.0e-41
E value
Match length
                  247
% identity
                   85
NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase
                   305960
Seq. No.
                  uC-zmflb73011c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q401238
BLAST score
                   706
E value
                   1.0e-74
Match length
                   163
% identity
NCBI Description
                  UBIQUITIN-ACTIVATING ENZYME E1 3 >gi 170686 (M90664)
                   ubiquitin activating enzyme [Triticum aestivum]
                   305961
Seq. No.
                   uC-zmflb73011c04b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2623247
BLAST score
                   122
E value
                   6.0e-62
Match length
                   438
                   91
% identity
NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds
                   305962
Seq. No.
                   uC-zmflb73011c12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2459426
BLAST score
                   308
                   5.0e-28
E value
                   120
Match length
                   53
% identity
                   (AC002332) putative splicing factor U2AF large chain
NCBI Description
```

43370

[Arabidopsis thaliana]



```
305963
Seq. No.
                  uC-zmflb73011d08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1706956
                  208
BLAST score
                  1.0e-24
E value
Match length
                  119
% identity
                  54
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]
Seq. No.
                   305964
Seq. ID
                  uC-zmflb73011e11b1
Method
                  BLASTX
                   g2984709
NCBI GI
BLAST score
                   409
                   4.0e-49
E value
Match length
                   135
                   78
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                   305965
Seq. No.
                   uC-zmflb73011f11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3063457
BLAST score
                   178
E value
                   8.0e-13
Match length
                   118
                   35
% identity
NCBI Description (AC003981) F22013.19 [Arabidopsis thaliana]
                   305966
Seq. No.
                   uC-zmflb73011h10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3426037
                   603
BLAST score
                   1.0e-62
E value
                   148
Match length
                   75
% identity
                   (AC005168) putative ABC transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   305967
Seq. No.
                   uC-zmflb73012a07b1
Seq. ID
                   BLASTX
Method
                   g2244913
NCBI GI
                   192
BLAST score
                   1.0e-14
E value
                   97
Match length
                   51
 % identity
                   (Z97339) similar to SEN1 protein - yeast [Arabidopsis
NCBI Description
                   thaliana]
                   305968
 Seq. No.
 Seq. ID
                   uC-zmflb73012b06b1
```

43371

BLASTX

q1351904

Method

NCBI GI

% identity

```
BLAST score
                  596
E value
                  8.0e-62
Match length
                  184
                  52
% identity
                  ASPARTOKINASE 1 / HOMOSERINE DEHYDROGENASE 1 CHLOROPLAST
NCBI Description
                  PRECURSOR (AK-HSDH 1) (AKHSDH1) >gi 500851 (L33912)
                  aspartate kinase-homoserine dehydrogenase [Zea mays]
Seq. No.
                  305969
                  uC-zmflb73012c01a2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585972
BLAST score
                  366
E value
                  5.0e-35
Match length
                  102
% identity
                   65
NCBI Description (AC005287) Putative ATPase [Arabidopsis thaliana]
                  305970
Seq. No.
Seq. ID
                  uC-zmflb73012d08b1
Method
                  BLASTN
                  g169818
NCBI GI
BLAST score
                  213
E value
                  1.0e-116
Match length
                  456
                  87
% identity
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                   305971
                  uC-zmflb73012f06b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q483411
BLAST score
                   143
E value
                   2.0e-74
Match length
                   303
% identity
                   98
NCBI Description
                  Zea Mays calmodulin-binding protein mRNA, 3'end
Seq. No.
                   305972
Seq. ID
                   uC-zmflb73012g05b1
Method
                  BLASTX
NCBI GI
                   g3413704
BLAST score
                   526
E value
                   1.0e-53
Match length
                  139
% identity
NCBI Description
                  (AC004747) hypothetical protein [Arabidopsis thaliana]
                   305973
Seq. No.
Seq. ID
                   uC-zmflb73012g11b1
Method
                   BLASTX
NCBI GI
                   g3096922
BLAST score
                   265
E value
                   4.0e-23
                  82
Match length
```

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

305979

```
Seq. No.
                   305974
Seq. ID
                   uC-zmflb73012h02b1
Method
                   BLASTN
NCBI GI
                   g4185305
BLAST score
                   60
E value
                   6.0e-25
Match length
                   305
% identity
                   84
NCBI Description
                   Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                   protein, polyprotein, and copia protein genes, complete
                   cds; and unknown genes
Seq. No.
                   305975
                   uC-zmflb73013a04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4585876
BLAST score
                   356
E value
                   5.0e-34
Match length
                   103
% identity
                   60
NCBI Description
                   (AC005850) Putative serine/threonine kinase [Arabidopsis
                   thaliana]
Seq. No.
                   305976
                   uC-zmflb73013b05a2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3176660
BLAST score
                   181
E value
                   2.0e-13
Match length
                   100
% identity
                   45
NCBI Description
                   (AC004393) Similar to ERECTA receptor protein kinase
                   gb U47029 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                   305977
Seq. ID
                   uC-zmflb73013e07a2
Method
                   BLASTX
NCBI GI
                   q3242715
BLAST score
                   209
E value
                   5.0e-17
                   75
Match length
% identity
NCBI Description
                   (AC003040) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   305978
Seq. ID
                   uC-zmflb73013f04b1
Method
                   BLASTX
NCBI GI
                   q4063747
BLAST score
                   392
E value
                   4.0e-38
                   94
Match length
% identity
                   (AC005851) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

43373



```
uC-zmflb73013f05b1
Seq. ID -
                  BLASTN
Method
NCBI GI
                  g22091
                  240
BLAST score
                  1.0e-132
E value
                  313
Match length
                  94
% identity
NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein
Seq. No.
                  uC-zmflb73013f07a2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3355486
BLAST score
                   228
E value
                   6.0e-19
Match length
                   63
% identity
                  (AC004218) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   305981
                   uC-zmflb73013h09a2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q577818
BLAST score
                   38
                   2.0e-12
E value
Match length
                   90
                   86
% identity
                  Z.mays gene for H2B histone (gH2B4)
NCBI Description
                   305982
Seq. No.
                   uC-zmflb73014a09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3435306
BLAST score
                   173
E value
                   1.0e-12
Match length
                   54
                   59
% identity
NCBI Description (AF082874) glycolate oxidase [Medicago sativa]
                   305983
Seq. No.
                   uC-zmflb73014e10b1
Seq. ID
                   BLASTX
Method
                   g3337356
NCBI GI
                   437
BLAST score
                   1.0e-56
E value
Match length
                   130
% identity
                   86
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   305984
Seq. No.
                   uC-zmflb73014e12b1
Seq. ID
                   BLASTX
Method
                   g2961437
NCBI GI
BLAST score
                   328
E value
                   2.0e-30
```

134

Match length



```
% identity
                   (L37527) MADS box protein [Oryza sativa]
NCBI Description
                   305985
Seq. No.
                  uC-zmflb73014f11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1935021
BLAST score
                  178
E value
                   7.0e-13
Match length
                   81
                   47
% identity
                  (Z93775) monosaccharid transport protein [Vicia faba]
NCBI Description
Seq. No.
                   305986
Seq. ID
                   uC-zmflb73014g11b1
Method
                   BLASTN
NCBI GI
                   g4539654
BLAST score
                   118
E value
                   1.0e-59
Match length
                   214
% identity
                   89
NCBI Description Sorghum bicolor 22 kDa kafirin cluster
Seq. No.
                   305987
Seq. ID
                   uC-zmflb73015c07b1
Method
                   BLASTX
NCBI GI
                   g3599491
BLAST score
                   235
E value
                   2.0e-19
Match length
                   55
                   78
% identity
                  (AF085149) putative aminotransferase [Capsicum chinense]
NCBI Description
                   305988
Seq. No.
Seq. ID
                   uC-zmflb73015d06b1
Method
                   BLASTX
NCBI GI
                   g3913427
BLAST score
                   362
E value
                   2.0e-49
Match length
                   144
                   77
% identity
                   S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767)
                   S-adenosylmethionine decarboxylase [Zea mays]
Seq. No.
                   305989
Seq. ID
                   uC-zmflb73015f02b1
```

Method BLASTX NCBI GI g3176661 BLAST score 454 4.0e-45 E value Match length 195 % identity 46

NCBI Description (ACO04393) Similar to putative DNA polymerase gb_M29683

from S. cerevisiae. [Arabidopsis thaliana]

305990 Seq. No.

```
Seq. ID
                   uC-zmflb73015h07a2
Method
                   BLASTX
NCBI GI
                   g4586034
BLAST score
                   163
E value
                   2.0e-11
Match length
                   87
% identity
                   49
NCBI Description
                   (AC007109) unknown protein [Arabidopsis thaliana]
Seq. No.
                   305991
Seq. ID
                   uC-zmflb73016b03b1
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
E value
                   9.0e-11
Match length
                   48
                   67
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   305992
Seq. ID
                   uC-zmflb73016c08a1
Method
                  BLASTX
NCBI GI
                   g209603
BLAST score
                   227
E value
                   7.0e-19
                   49
Match length
% identity
                   90
NCBI Description
                   (M31426) ubiquitin/relaxin fusion protein [Artificial gene]
Seq. No.
                   305993
Seq. ID
                  uC-zmflb73016e01a1
Method
                  BLASTN
NCBI GI
                  g22204
BLAST score
                  132
E value
                   4.0e-68
Match length
                  188
% identity
                   93
NCBI Description
                  Maize Bz-McC gene for UDPqlucose flavonoid
                  glycosyl-transferase
Seq. No.
                  305994
Seq. ID
                  uC-zmflb73016e09b1
Method
                  BLASTX
NCBI GI
                  g4056503
BLAST score
                  158
E value
                  1.0e-10
Match length
                  36
% identity
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
                  305995
Seq. No.
Seq. ID
                  uC-zmflb73016h04b1
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  318
E value
                  2.0e-29
```

43376

to Aug.

Match length

67

Match length

% identity

248

84



```
% identity
NCBI Description
                  photosystem II oxygen-evolving complex protein 1 - rice
                   (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                   305996
Seq. ID
                  uC-zmflb73016h09b1
Method
                  BLASTX
NCBI GI
                  g2662375
BLAST score
                  148
E value
                  1.0e-09
Match length
                  70
% identity
                   43
NCBI Description (D89060) oligosaccharyltransferase [Homo sapiens]
                  305997
Seq. No.
Seq. ID
                  uC-zmflb73017a03b1
Method
                  BLASTX
NCBI GI
                  g3482929
BLAST score
                  335
E value
                  2.0e-31
Match length
                  68
% identity
                  82
NCBI Description
                  (AC003970) Putative transcription factor [Arabidopsis
                  thaliana]
Seq. No.
                  305998
Seq. ID
                  uC-zmflb73017c11a2
Method
                  BLASTX
NCBI GI
                  g3335376
BLAST score
                  178
                  7.0e-13
E value
                  60
Match length
% identity
                  55
                  (AC003028) putative ammonium transporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  305999
Seq. ID
                  uC-zmflb73017d01b1
Method
                  BLASTX
NCBI GI
                  g3702335
BLAST score
                  290
E value
                  5.0e-26
Match length
                  76
% identity
                  67
NCBI Description
                  (AC005397) putative DNA binding protein [Arabidopsis
                  thalianal
Seq. No.
                  306000
Seq. ID
                  uC-zmflb73017d07a2
Method
                  BLASTN
NCBI GI
                  g498772
BLAST score
                  89
E value
                  1.0e-42
```

NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein



```
Seq. No.
                  306001
Seq. ID
                  uC-zmflb73017d11b1
Method
                  BLASTX
NCBI GI
                  g312179
BLAST score
                  477
E value
                  5.0e-48
Match length
                  109
% identity
                  89
NCBI Description
                   (X73151) glyceraldehyde 3-phosphate dehydrogenase
                   (phosphorylating) [Zea mays] >gi 1184772 (U45855) cytosolic
                  glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                  >gi 1185554 (U45858) glyceraldehyde-3-phosphate
                  dehydrogenase [Zea mays]
                  306002
Seq. No.
Seq. ID
                  uC-zmflb73017e03b1
Method
                  BLASTX
NCBI GI
                  g1168536
BLAST score
                  629
E value
                  1.0e-65
Match length
                  154
                  79
% identity
NCBI Description
                  PHYTEPSIN PRECURSOR (ASPARTIC PROTEINASE)
                  >gi_100567_pir__S19697 aspartic proteinase (EC 3.4.23.-)
                  precursor - barley >gi_18904_emb_CAA39602_ (X56136)
                  aspartic proteinase [Hordeum vulgare]
Seq. No.
                  306003
Seq. ID
                  uC-zmflb73017e04a2
Method
                  BLASTN
NCBI GI
                  q13918
BLAST score
                  109
E value
                  2.0e-54
Match length
                  259
% identity
                  94
NCBI Description Maize mitochondrial DNA for 5kB alpha-R1 repeat
                  306004
Seq. No.
Seq. ID
                  uC-zmflb73017e04b1
Method
                  BLASTN
NCBI GI
                  g13919
BLAST score
                  336
E value
                  0.0e+00
Match length
                  348
% identity
                  99
NCBI Description Maize mitochondrial DNA for 5kB beta-R2 repeat
                  306005
```

Seq. ID uC-zmflb73017f10b1

Method BLASTX NCBI GI g2914700 BLAST score 630 E value 6.0e-66 Match length 135 % identity

NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis

Method

BLASTX



thaliana]

```
306006
Seq. No.
Seq. ID
                  uC-zmflb73017g11b1
Method
                  BLASTX
NCBI GI
                  g2465923
BLAST score
                   403
                   3.0e-39
E value
                  175
Match length
                   24
% identity
                  (AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   306007
Seq. No.
Seq. ID
                  uC-zmflb73017h05b1
Method
                  BLASTX
NCBI GI
                   g3176726
BLAST score
                   263
                   2.0e-27
E value
Match length
                   96
                   72
% identity
                  (AC002392) putative serine proteinase [Arabidopsis
NCBI Description
                   thaliana]
                   306008
Seq. No.
Seq. ID
                   uC-zmflb73018b01b1
Method
                   BLASTX
NCBI GI
                   g3046815
BLAST score
                   426
E value
                   6.0e-42
Match length
                   98
                   79
% identity
NCBI Description
                  (AL021687) cytochrome P450 [Arabidopsis thaliana]
                   306009
Seq. No.
Seq. ID
                   uC-zmflb73018c11a1
Method
                   BLASTX
NCBI GI
                   g3688602
BLAST score
                   221
E value
                   5.0e-18
Match length
                   65
                   65
% identity
NCBI Description
                  (AB009031) Oxidosqualene Cyclase [Panax ginseng]
                   306010
Seq. No.
Seq. ID
                   uC-zmflb73018f05a1
Method
                   BLASTX
NCBI GI
                   q4582450
BLAST score
                   316
E value
                   4.0e-29
Match length
                   105
% identity
NCBI Description
                  (AC007071) putative APG protein [Arabidopsis thaliana]
Seq. No.
                   306011
Seq. ID
                   uC-zmflb73018f06b1
```



```
NCBI GI
                   q1881662
BLAST score
                   299
E value
                   5.0e-27
Match length
                   168
% identity
                   38
NCBI Description
                   (U89264) kinesin like protein 67a [Drosophila melanogaster]
Seq. No.
                   306012
Seq. ID
                   uC-zmflb73018f08a1
Method
                   BLASTN
                   g4530610
NCBI GI
BLAST score
                   67
E value
                   3.0e-29
Match length
                   79
% identity
                   96
NCBI Description
                   Oryza sativa subsp. indica serine/threonine protein
                   phosphatase PP2A-2 catalytic subunit (Pp2A) gene, complete
Seq. No.
                   306013
Seq. ID
                   uC-zmflb73018f12b1
Method
                   BLASTX
NCBI GI
                   g2335108
BLAST score
                   495
E value
                   6.0e-50
Match length
                   142
% identity
                   68
NCBI Description
                   (AC002339) putative isulinase [Arabidopsis thaliana]
Seq. No.
                   306014
Seq. ID
                   uC-zmflb73018g09b1
Method
                   BLASTX
NCBI GI
                   g2129559
BLAST score
                   170
E value
                   3.0e-12
Match length
                   96
% identity
                   41
NCBI Description
                   cellulase homolog OR16pep - Arabidopsis thaliana
                   >gi 1022807 (U37702) cellulase [Arabidopsis thaliana]
                        3493633 (AF074092) cellulase [Arabidopsis thaliana]
                   >gi_
                   >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana]
>gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
                   [Arabidopsis thaliana]
Seq. No.
                   306015
Seq. ID
                   uC-zmflb73019b03a1
Method
                   BLASTX
NCBI GI
                   g2760323
BLAST score
                   235
E value
                   1.0e-19
```

Match length 76 % identity

NCBI Description (AC002130) F1N21.8 [Arabidopsis thaliana]

Seq. No. 306016

Seq. ID uC-zmflb73019c06b1

BLASTX Method

```
g2996096
NCBI GI
BLAST score
                   176
E value
                   1.0e-12
Match length
                   81
% identity
                   52
                   (AF030517) translation elongation factor-1 alpha; EF-1
NCBI Description
                   alpha [Oryza sativa]
Seq. No.
                   306017
Seq. ID
                   uC-zmflb73019f03b1
Method
                   BLASTX
NCBI GI
                   g1170937
BLAST score
                   704
E value
                   2.0e-74
Match length
                   142
% identity
                   94
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
Seq. No.
                   306018
Seq. ID
                   uC-zmflb73019f08b1
Method
                   BLASTX
NCBI GI
                   q2984709
BLAST score
                   492
E value
                   1.0e-49
Match length
                   101
% identity
                   91
NCBI Description
                   (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                   306019
Seq. No.
Seq. ID
                   uC-zmflb73019g11b1
Method
                   BLASTX
NCBI GI
                   g2655008
BLAST score
                   305
E value
                   8.0e-28
Match length
                   132
                   43
% identity
                   (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
NCBI Description
                   esculentum]
Seq. No.
                   306020
Seq. ID
                   uC-zmflb73020b06b1
Method
                   BLASTX
NCBI GI
                   g4522008
BLAST score
                   468
                   7.0e-47
E value
                   139
Match length
% identity
                   64
NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   306021
Seq. ID
                   uC-zmflb73020c05b1
Method
                   BLASTX
```

43381

g939785

331

NCBI GI BLAST score

```
E value
                  7.0e-31
Match length
                  110
% identity
                  64
                  (L46400) MADS box protein [Zea mays]
NCBI Description
Seq. No.
                  306022
                  uC-zmflb73020d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432863
BLAST score
                  223
E value
                  4.0e-18
Match length
                  68
% identity
NCBI Description
                  (AC006300) putative phosphate/phosphoenolpyruvate
                  translocator protein [Arabidopsis thaliana]
Seq. No.
                  306023
Seq. ID
                  uC-zmflb73020e12b1
Method
                  BLASTX
NCBI GI
                  g1172977
BLAST score
                  175
E value
                  9.0e-19
Match length
                  115
% identity
                  53
NCBI Description
                  60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
                  ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                  306024
Seq. ID
                  uC-zmflb73020f12b1
Method
                  BLASTX
NCBI GI
                  g2654868
BLAST score
                  167
E value
                  3.0e-19
Match length
                  72
% identity
                  71
NCBI Description
                  (AF015301) RbohAp108 [Arabidopsis thaliana]
                  306025
Seq. No.
Seq. ID
                  uC-zmflb73020g03b1
Method
                  BLASTN
NCBI GI
                  g168436
BLAST score
                  88
E value
                  9.0e-42
                  236
Match length
% identity
                  84
NCBI Description Zea mays catalase (Cat3) gene, complete cds
Seq. No.
                  306026
Seq. ID
                  uC-zmflb73020h08a1
Method
                  BLASTX
NCBI GI
                  g2494132
BLAST score
                  143
E value
                  5.0e-09
Match length
                  71
% identity
                  41
NCBI Description
                  (AC002376) Contains similarity to human dimethylaniline
                  monooxygenase (gb M64082). [Arabidopsis thaliana]
```

NCBI Description



```
306027
Seq. No.
                   uC-zmflb73020h08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3142293
                   288
BLAST score
                   9.0e-26
E value
Match length
                   129
% identity
                   47
                   (AC002411) Contains similarity to myosin IB heavy chain
NCBI Description
                   gb_X70400 from Gallus gallus. [Arabidopsis thaliana]
                   306028
Seq. No.
                   uC-zmflb73020h11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3169178
BLAST score
                   153
                   6.0e-10
E value
Match length
                   44
% identity
NCBI Description (AC004401) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   306029
                   uC-zmflb73021h06a2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3461815
BLAST score
                   169
                   2.0e-12
E value
Match length
                   43
% identity
NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]
                   306030
Seq. No.
                   uC-zmflb73022a04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3023512
                   171
BLAST score
                   4.0e-12
E value
                   61
Match length
                   51
% identity
                   PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT
NCBI Description
                   PRECURSOR (ENDOPEPTIDASE CLP) >gi_2134793_pir__S68421
                   ATP-dependent Clp proteinase (EC \overline{3}.4.21.9\overline{2}) chain P homolog
                   - human >gi 963048_emb_CAA90705_ (Z50853) CLPP [Homo
                   sapiens]
                   306031
Seq. No.
                   uC-zmflb73022f01a1
Seq. ID
                   BLASTN
Method
                   g309569
NCBI GI
BLAST score
                   66
                   4.0e-29
E value
                   134
Match length
                   89
% identity
```

synthesis gene, complete cds

Zea mays transcriptional activator for anthocyanin



Seq. ID uC-zmflb73022g01a1

Method BLASTX NCBI GI g731415 191 BLAST score 1.0e-14 E value Match length 82

49 % identity

NCBI Description PROBABLE CALCIUM-TRANSPORTING ATPASE 6

>gi_1077608_pir__S50428 hypothetical protein YEL031w yeast (Saccharomyces cerevisiae) >gi_602398 (U18530) P-type

ATPase; YEL031W [Saccharomyces cerevisiae]

306033 Seq. No.

uC-zmflb73023b01a1 Seq. ID

BLASTN Method g168617 NCBI GI 190 BLAST score 1.0e-102 E value Match length 226 96 % identity

NCBI Description Maize putative protein kinase mRNA, 3' end

306034

Seq. No.

uC-zmflb73023g02a1 Seq. ID

Method BLASTX NCBI GI q2554835 155 BLAST score 1.0e-10 E value Match length 42 % identity

NCBI Description

Chain I, Acetohydroxy Acid Isomeroreductase Complexed With

Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate) >gi_2554836_pdb_1YVE_J Chain J,

Acetohydroxy Acid Isomeroreductase Complexed With Nadph,

Magnesium And Inhibitor Ipoha (N-Hydroxy-N-

Isopropyloxamate) >gi 2554837 pdb 1YVE_K Chain K,

Acetohydroxy Acid Isomeroreductase Complexed With Nadph,

Magnesium And Inhibitor Ipoha (N-Hydroxy-N-

Isopropyloxamate) >gi_2554838_pdb_1YVE_L Chain L,

Acetohydroxy Acid Isomeroreductase Complexed With Nadph,

Magnesium And Inhibitor Ipoha (N-Hydroxy-N-

Isopropyloxamate)

306035 Seq. No.

uC-zmflb73025d02a1 Seq. ID

Method BLASTX q3298474 NCBI GI 273 BLAST score 2.0e-24 E value 88 Match length % identity 68

(AB012765) ovpl [Oryza sativa] NCBI Description

306036 Seq. No.

uC-zmflb73026a04b1 Seq. ID

BLASTX Method

```
NCBI GI
                   q4539662
BLAST score
                   227
E value
                   1.0e-18
                   135
Match length
% identity
                   40
                   (AF061282) polyprotein [Sorghum bicolor]
NCBI Description
Seq. No.
                   306037
Seq. ID
                   uC-zmflb73026b08b1
Method
                   BLASTX
NCBI GI
                   g3063465
BLAST score
                   147
E value
                   4.0e-09
Match length
                   113
% identity
                   35
NCBI Description
                   (AC003981) F22013.27 [Arabidopsis thaliana]
Seq. No.
                   306038
Seq. ID
                   uC-zmflb73026c01b1
Method
                   BLASTX
NCBI GI
                   g2773154
BLAST score
                   154
E value
                   4.0e-10
Match length
                   91
% identity
                   40
NCBI Description
                   (AF039573) abscisic acid- and stress-inducible protein
                   [Oryza sativa]
                   306039
Seq. No.
Seq. ID
                   uC-zmf1b73026d01b1
Method
                   BLASTN
NCBI GI
                   g1042268
BLAST score
                   130
                   9.0e-67
E value
Match length
                   134
% identity
                   99
NCBI Description
                   {Mul element insertion site, clone 20} [maize, Transposon,
                   134 nt]
Seq. No.
                   306040
Seq. ID
                   uC-zmflb73026d04b1
Method
                   BLASTX
NCBI GI
                   g3075394
BLAST score
                   331
E value
                   7.0e-31
                   78
Match length
```

82 % identity

NCBI Description (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311 (AJ010713) fiddlehead

protein [Arabidopsis thaliana]

Seq. No. 306041

Seq. ID uC-zmflb73026g02b1

Method BLASTN NCBI GI g902200 BLAST score 358 E value 0.0e + 00

% identity

NCBI Description

45

plumbaginifolia]



```
Match length
                  100
% identity
                  Z.mays complete chloroplast genome
NCBI Description
                  306042
Seq. No.
Seq. ID
                  uC-zmflb73026h10b1
Method
                  BLASTX
NCBI GI
                  g629775
BLAST score
                  343
E value
                  3.0e - 32
Match length
                  69
                  91
% identity
NCBI Description beta-ketoacyl-ACP synthase - barley (fragment)
                  306043
Seq. No.
Seq. ID
                  uC-zmflb73027a04b1
Method
                  BLASTX
NCBI GI
                  g3805842
BLAST score
                  185
E value
                  1.0e-13
Match length
                  89
% identity
                  52
NCBI Description (AL031986) putative protein [Arabidopsis thaliana]
                  306044
Seq. No.
Seq. ID
                  uC-zmflb73027b03a1
Method
                  BLASTX
NCBI GI
                  g3522942
BLAST score
                  209
E value
                  1.0e-16
Match length
                  82
                  54
% identity
NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  306045
Seq. ID
                  uC-zmflb73027b11b1
Method
                  BLASTX
NCBI GI
                  g2498883
BLAST score
                  382
E value
                  7.0e-50
Match length
                  145
% identity
                   69
NCBI Description
                  SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150)
                  >gi 1173905 (U41371) spliceosome associated protein [Homo
                  sapiens]
                  306046
Seq. No.
Seq. ID
                  uC-zmflb73027d12b1
Method
                  BLASTX
NCBI GI
                  g4376203
BLAST score
                  200
E value
                  1.0e-21
Match length
                  120
```

43386

(U35226) putative cytochrome P-450 [Nicotiana



```
306047
Seq. No.
Seq. ID
                    uC-zmflb73027e06b1
Method
                    BLASTX
NCBI GI
                    g114643
BLAST score
                    256
E value
                    3.0e-22
Match length
                    93
% identity
                    62
NCBI Description
                    ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
                    >gi_67879_pir__PWSPG H+-transporting ATP synthase (EC
                    3.6.1.34) gamma chain precursor, chloroplast - spinach >gi_21238_emb_CAA35158_ (X17257) gamma-subunit of
                    chloroplast ATP synthase [Spinacia oleracea]
                    >gi_531111_emb_CAA53734_ (X76131) gamma subunit of the
                    chloroplast ATP synthase [Spinacia oleracea]
Seq. No.
                    306048
Seq. ID
                    uC-zmflb73027f01b1
Method
                    BLASTN
NCBI GI
                    g22091
BLAST score
                    97
E value
                    3.0e-47
Match length
                    161
% identity
                    90
NCBI Description
                    Z.diploperennis gene for hydroxyproline-rich glycoprotein
Seq. No.
                    306049
Seq. ID
                    uC-zmflb73027f11b1
Method
                    BLASTX
NCBI GI
                    g4049346
BLAST score
                    240
E value
                    4.0e-20
Match length
                    87
% identity
NCBI Description
                    (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                    306050
Seq. ID
                    uC-zmflb73027h10a1
Method
                    BLASTX
NCBI GI
                    g1351974
BLAST score
                    154
E value
                    2.0e-10
Match length
                    35
% identity
                    83
NCBI Description
                    ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325
                    ADP-ribosylation factor - maize >gi_1076789_pir_ S53486
ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_
                    (X80042) ADP-ribosylation factor [Zea mays]
```

Seq. ID uC-zmflb73028b07b1

Method BLASTX
NCBI GI g1168536
BLAST score 587
E value 7.0e-61
Match length 123
% identity 91





```
PHYTEPSIN PRECURSOR (ASPARTIC PROTEINASE)
NCBI Description
                  >gi 100567 pir S19697 aspartic proteinase (EC 3.4.23.-)
                  precursor - barley >gi 18904_emb_CAA39602_ (X56136)
                  aspartic proteinase [Hordeum vulgare]
Seq. No.
                  306052
Seq. ID
                  uC-zmflb73028b09a1
Method
                  BLASTN
NCBI GI
                  g2326946
BLAST score
                  119
                  1.0e-60
E value
Match length
                  211
                  89
% identity
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29
                  306053
Seq. No.
                  uC-zmflb73028b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g283051
                  279
BLAST score
                  1.0e-24
E value
Match length
                  84
% identity
                  69
                  RNA-directed DNA polymerase (EC 2.7.7.49) - maize
NCBI Description
                  transposon (fragment)
                  306054
Seq. No.
                  uC-zmflb73028c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4584429
BLAST score
                  161
E value
                  7.0e-11
                  111
Match length
% identity
                   40
NCBI Description (AJ237751) aquaglyceroporin [Nicotiana tabacum]
Seq. No.
                   306055
Seq. ID
                  uC-zmflb73028d07b1
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  163
E value
                   3.0e-11
Match length
                   54
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >qi 2130146 pir S61419 thiamine biosynthetic enzyme thil-1
                   - maize >qi 596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
                   306056
Seq. No.
Seq. ID
                  uC-zmflb73028d11b1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g2773154
BLAST score 285
E value 2.0e-25
Match length 131
% identity 50



NCBI Description (AF039573) abscisic acid- and stress-inducible protein [Oryza sativa]

Seq. No. 306057

Seq. ID uC-zmflb73028e02b1

Method BLASTN
NCBI GI g168421
BLAST score 121
E value 8.0e-62
Match length 125
% identity 99

NCBI Description Maize auxin-binding protein (ABP) mRNA, complete cds

Seq. No. 306058

Seq. ID uC-zmflb73028e08b1

Method BLASTX
NCBI GI g1498395
BLAST score 172
E value 2.0e-12
Match length 76
% identity 51

NCBI Description (U60514) actin [Zea mays]

Seq. No. 306059

Seq. ID uC-zmflb73028f06b1

Method BLASTX
NCBI GI g113456
BLAST score 464
E value 2.0e-46
Match length 122
% identity 76

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)

>gi_22162_emb_CAA40781_ (X57556) adenine nucleotide

translocator [Zea mays]

Seq. No. 306060

Seq. ID uC-zmflb73028f07b1

Method BLASTN
NCBI GI g22149
BLAST score 69
E value 9.0e-31
Match length 109
% identity 92

NCBI Description Z.mays mRNA for alpha-tubulin

Seq. No. 306061

Seq. ID uC-zmflb73028f08b1

Method BLASTX
NCBI GI g2224915
BLAST score 155
E value 1.0e-10
Match length 48
% identity 62

NCBI Description (U95968) beta-expansin [Oryza sativa]

Seq. No. 306062

BLAST score

488

```
uC-zmflb73028g01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1170937
BLAST score
                   216
E value
                   5.0e-18
Match length
                   68
% identity
                   65
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
Seq. No.
                   306063
Seq. ID
                   uC-zmflb73028q03a1
Method
                   BLASTN
NCBI GI
                   q559531
BLAST score
                   80
E value
                   3.0e-37
Match length
                   196
% identity
                   85
NCBI Description
                  Z.mays mRNA for cysteine proteinase
Seq. No.
                   306064
Seq. ID
                  uC-zmflb73028h03b1
Method
                  BLASTX
NCBI GI
                   q4314378
BLAST score
                   142
E value
                   9.0e-09
Match length
                   85
% identity
                   42
NCBI Description
                  (AC006232) putative lipase [Arabidopsis thaliana]
Seq. No.
                   306065
Seq. ID
                  uC-zmflb73029a08b1
Method
                  BLASTN
NCBI GI
                   g393400
BLAST score
                   76
E value
                   7.0e-35
Match length
                  156
                   87
% identity
                  Z.mays mRNA for alpha-tubulin
NCBI Description
Seq. No.
                   306066
Seq. ID
                  uC-zmflb73029a09b1
Method
                  BLASTX
NCBI GI
                  g2737882
BLAST score
                  167
E value
                  8.0e-12
Match length
                  88
% identity
NCBI Description
                  (U46014) polyphenol oxidase [Saccharum sp.]
Seq. No.
                  306067
Seq. ID
                  uC-zmflb73029a10b1
Method
                  BLASTX
NCBI GI
                  g2369714
```

43390



```
2.0e-49
E value
Match length
                   106
% identity
                   88
NCBI Description
                   (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                   306068
Seq. ID
                  uC-zmflb73029b06a1
Method
                  BLASTX
NCBI GI
                  g3176660
BLAST score
                   219
E value
                   6.0e-18
Match length
                  103
% identity
                   48
NCBI Description
                   (AC004393) Similar to ERECTA receptor protein kinase
                  gb U47029 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                  306069
Seq. ID
                  uC-zmflb73029c10b1
Method
                  BLASTX
NCBI GI
                  g585273
BLAST score
                  233
E value
                  1.0e-20
Match length
                  125
% identity
                  53
NCBI Description MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR
Seq. No.
                  306070
Seq. ID
                  uC-zmflb73029f06b1
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  547
E value
                  4.0e-56
Match length
                  123
% identity
                  86
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  306071
Seq. ID
                  uC-zmflb73029f08b1
Method
                  BLASTX
NCBI GI
                  g123650
BLAST score
                  151
                  9.0e-11
E value
Match length
                  64
% identity
NCBI Description
                  HEAT SHOCK COGNATE 70 KD PROTEIN >gi 82245 pir S03250 heat
                  shock protein 70 (clone pMON9743) - garden petunia
                  >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70
                  [Petunia x hybrida]
Seq. No.
                  306072
Seq. ID
                  uC-zmflb73029g11b1
Method
                  BLASTX
```

NCBI GI g1184077 BLAST score 255 E value 6.0e-22 Match length 143 % identity 2



```
NCBI Description
                  (U42445) Cf-2.2 [Lycopersicon pimpinellifolium]
                  306073
Seq. No.
                  uC-zmflb73030a03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2737881
BLAST score
                  33
E value
                   4.0e-09
Match length
                  41
% identity
                   95
                  Saccharum sp. polyphenol oxidase mRNA, complete cds
NCBI Description
Seq. No.
                   306074
                  uC-zmflb73030a04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3176690
BLAST score
                  192
E value
                   3.0e-15
Match length
                  60
% identity
                   63
NCBI Description
                   (AC003671) Similar to ubiquitin ligase gb D63905 from S.
                   cerevisiae. EST gb R65295 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   306075
Seq. ID
                  uC-zmflb73030b02b1
Method
                  BLASTX
NCBI GI
                   g3193291
BLAST score
                   286
E value
                   2.0e-25
Match length
                  103
                   57
% identity
NCBI Description
                   (AF069298) Similar to DNA mismatch repair protein; T14P8.6
                   [Arabidopsis thaliana]
                   306076
Seq. No.
Seq. ID
                  uC-zmflb73030g05b1
Method
                  BLASTX
                  g4337178
                  295
                   2.0e-26
                  88
                   66
```

NCBI GI BLAST score E value Match length % identity

NCBI Description (AC006416) T31J12.5 [Arabidopsis thaliana]

Seq. No. 306077

Seq. ID uC-zmflb73030g09b1

Method BLASTX NCBI GI g2911049 BLAST score 170 E value 3.0e-12 Match length 82 % identity

NCBI Description (AL021961) glucosyltransferase -like protein [Arabidopsis

thaliana]

306078 Seq. No.

NCBI GI

BLAST score

q2062705

34

```
uC-zmflb73030g12b1
Seq. ID
                  BLASTN
Method
                  g3264604
NCBI GI
BLAST score
                  44
                  1.0e-15
E value
                  48
Match length
                  98
% identity
                  Zea mays ribosomal protein L25 mRNA, partial cds
NCBI Description
                  306079
Seq. No.
                  uC-zmflb73030h12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g322752
                  338
BLAST score
                  1.0e-31
E value
                  118
Match length
                  55
% identity
                  auxin-independent growth promoter - Nicotiana tabacum
NCBI Description
                  >gi 559921 emb CAA56570 (X80301) axi 1 [Nicotiana tabacum]
                  306080
Seq. No.
                  uC-zmflb73031a04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2984709
BLAST score
                  539
                   3.0e-55
E value
                  102
Match length
                   99
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                   306081
Seq. No.
Seq. ID
                   uC-zmf1b73031a07b1
Method
                   BLASTX
NCBI GI
                   g1762144
                   281
BLAST score
                   5.0e-25
E value
                   103
Match length
                   55
% identity
NCBI Description (U48435) putative cytochrome P450 [Solanum chacoense]
                   306082
Seq. No.
                   uC-zmflb73031b01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2497486
BLAST score
                   233
                   2.0e-19
E value
                   61
Match length
                   77
% identity
NCBI Description
                   URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
                   KINASE) >gi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis
                   thaliana]
                   306083
Seq. No.
Seq. ID
                   uC-zmflb73031d07b1
Method
                   BLASTN
```

43393



```
E value
                     2.0e-09
  Match length
                     34
                     100
  % identity
                    Human butyrophilin (BTF5) mRNA, complete cds
  NCBI Description
                     306084
  Seq. No.
  Seq. ID
                     uC-zmflb73031d10b1
  Method
                     BLASTX
  NCBI GI
                     g3036816
  BLAST score
                     188
  E value
                     5.0e-14
  Match length
                     155
                     36
  % identity
                    (AL022373) myosin-like protein [Arabidopsis thaliana]
  NCBI Description
                     306085
  Seq. No.
                     uC-zmflb73031e03b1
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g2245086
  BLAST score
                     169
  E value
                     6.0e-12
                     46
  Match length
                     76
  % identity
  NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                     306086
                     uC-zmflb73031g08a1
- Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g4539314
                     146
  BLAST score
  E value
                     2.0e-09
  Match length
                     63
  % identity
                     49
  NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]
                     306087
  Seq. No.
                     uC-zmflb73031h09b1
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g13709
  BLAST score
                     155
  E value
                     9.0e-82
  Match length
                     167
  % identity
                     98
  NCBI Description
                     Wheat mitochondrial trnQ-2 gene for transfer RNA-Gln (UUG)
                     306088
  Seq. No.
  Seq. ID
                     uC-zmflb73032a03b1
  Method
                     BLASTN
  NCBI GI
                     g168454
  BLAST score
                     295
```

E value 1.0e-165 Match length 371 % identity 20

NCBI Description Z.mays cell wall protein mRNA, complete cds

306089 Seq. No.

uC-zmflb73032a08b1 Seq. ID

43394

E value

Match length

1.0e-12 56

```
Method
                  BLASTX
NCBI GI
                   g3947688
BLAST score
                   333
                   4.0e-31
E value
                  127
Match length
                   53
% identity
NCBI Description (AJ131244) Sec24A protein [Homo sapiens]
                  306090
Seq. No.
                  uC-zmflb73032b12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2654226
                  198
BLAST score
                   2.0e-15
E value
                   98
Match length
                   44
% identity
                   (AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   306091
Seq. ID
                   uC-zmf1b73032c08b1
Method
                  BLASTN
NCBI GI
                   g169818
BLAST score
                   104
E value
                   2.0e-51
Match length
                   184
                   89
% identity
NCBI Description Rice 25S ribosomal RNA gene
                   306092
Seq. No.
                   uC-zmflb73032c11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2911067
BLAST score
                   600
                   2.0e-62
E value
                   158
Match length
% identity
NCBI Description
                  (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis
                   thaliana]
                   306093
Seq. No.
                   uC-zmflb73032d01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4586308
BLAST score
                   171
                   4.0e-12
E value
                   58
Match length
% identity
NCBI Description
                  (AB025102) protoporphyrinogen IX oxidase [Glycine max]
Seq. No.
                   306094
Seq. ID
                   uC-zmflb73032e05b1
Method
                   BLASTX
NCBI GI
                   g3047090
BLAST score
                   174
```



```
% identity
NCBI Description
                   (AF058826) T26D22.18 gene product [Arabidopsis thaliana]
Seq. No.
                   306095
Seq. ID
                   uC-zmflb73032f02b1
Method
                   BLASTX
NCBI GI
                   g4455171
BLAST score
                   161
E value
                   6.0e-11
Match length
                   43
% identity
                   (AL035521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   306096
Seq. ID
                  uC-zmflb73032g01b1
Method
                  BLASTX
NCBI GI
                   q729671
BLAST score
                   147
E value
                   2.0e-09
Match length
                   71
% identity
                   51
NCBI Description
                  HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]
Seq. No.
                   306097
Seq. ID
                  uC-zmflb73032h06b1
Method
                  BLASTX
NCBI GI
                  q4584521
BLAST score
                   496
E value
                   4.0e-50
Match length
                   133
% identity
                   68
NCBI Description
                   (AL049607) putative protein [Arabidopsis thaliana]
Seq. No.
                  306098
Seq. ID
                  uC-zmflb73032h09b1
Method
                  BLASTX
NCBI GI
                  g729671
BLAST score
                  227
E value
                   9.0e-19
Match length
                  70
% identity
                  71
NCBI Description
                  HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]
Seq. No.
                  306099
Seq. ID
                  uC-zmflb73033c07b1
Method
                  BLASTX
NCBI GI
                  q461987
BLAST score
                  197
E value
                  1.0e-15
Match length
                  79
% identity
                  53
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi 82042 pir JS0719 translation elongation factor eEF-1
                  alpha chain - carrot >gi_217913_dbj_BAA02205_ (D12709)
```

43396

elongation factor 1-alpha [Daucus carota]

```
Seq. ID
                   uC-zmflb73033d01b1
Method
                   BLASTN
NCBI GI
                   g1698669
BLAST score
                   132
E value
                   3.0e-68
Match length
                   155
% identity
                   98
NCBI Description
                   Zea mays S-like RNase (kin1) mRNA, complete cds
Seq. No.
                   306101
Seq. ID
                   uC-zmflb73033d10b1
Method
                   BLASTX
NCBI GI
                   g2569940
BLAST score
                   147
E value
                   2.0e-09
Match length
                   97
% identity
                   41
NCBI Description (Y15194) GRS protein [Arabidopsis thaliana]
Seq. No.
                   306102
Seq. ID
                   uC-zmflb73033d12b1
Method
                  BLASTN
NCBI GI
                   g211907
BLAST score
                   38
E value
                   5.0e-12
Match length
                   62
% identity
                   90
NCBI Description Chicken histone H4 protein gene, complete cds
Seq. No.
                   306103
Seq. ID
                  uC-zmflb73033g03b1
Method
                  BLASTN
NCBI GI
                  g2984708
BLAST score
                  163
E value
                  8.0e-87
Match length
                  215
                  94
% identity
NCBI Description
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
Seq. No.
                  306104
Seq. ID
                  uC-zmflb73033g04b1
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  215
E value
                  2.0e-17
Match length
                  53
% identity
                  79
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  306105
Seq. ID
                  uC-zmflb73033g08b1
```

Method BLASTN

NCBI GI g2997588 BLAST score 95 E value 2.0e-46 Match length 127



% identity NCBI Description 4

Zea mays glucose-6-phosphate/phosphate-translocator precursor (gpt) mRNA, nuclear gene encoding plastid

protein, complete cds

Seq. No. 306106

Seq. ID uC-zmflb73033h08a1

Method BLASTX
NCBI GI g1899175
BLAST score 359
E value 1.0e-34
Match length 80
% identity 85

NCBI Description (U90262) calcium-dependent calmodulin-independent protein

kinase CDPK [Cucurbita pepo]

Seq. No. 306107

Seq. ID uC-zmflb73034b07b2

Method BLASTX
NCBI GI g2345154
BLAST score 203
E value 6.0e-16
Match length 63
% identity 68

NCBI Description (AF015522) ribsomal protein S4 [Zea mays]

Seq. No. 306108

Seq. ID uC-zmflb73034c03b2

Method BLASTX
NCBI GI g4455331
BLAST score 150
E value 7.0e-10
Match length 57
% identity 44

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 306109

Seq. ID uC-zmflb73037c11b2

Method BLASTX
NCBI GI g547683
BLAST score 258
E value 6.0e-23
Match length 59
% identity 83

NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat

shock cognate protein 80 [Solanum lycopersicum]
>gi_445601_prf__1909348A heat shock protein hsp80

[Lycopersicon esculentum]

Seq. No. 306110

Seq. ID uC-zmflb73037e01b2

Method BLASTX
NCBI GI g4539351
BLAST score 138
E value 7.0e-09
Match length 47
% identity 64



NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 306111

Seq. ID uC-zmflb73037e10b2

Method BLASTX
NCBI GI g547683
BLAST score 176
E value 1.0e-18
Match length 64
% identity 72

NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi 170456 (M96549) heat

shock cognate protein 80 [Solanum lycopersicum]
>gi_445601_prf__1909348A heat shock protein hsp80

[Lycopersicon esculentum]

Seq. No. 306112

Seq. ID uC-zmflb73037e12b2

Method BLASTX
NCBI GI g417154
BLAST score 366
E value 3.0e-35
Match length 95
% identity 74

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 306113

Seq. ID uC-zmflb73037f08b2

Method BLASTX
NCBI GI g4204861
BLAST score 137
E value 1.0e-08
Match length 32
% identity 81

NCBI Description (U55860) heat shock protein 90 [Triticum aestivum]

Seq. No. 306114

Seq. ID uC-zmflb73037g01b2

Method BLASTX
NCBI GI g397396
BLAST score 325
E value 3.0e-30
Match length 93
% identity 75

NCBI Description (X66077) DNA-binding protein [Zea mays]

Seq. No. 306115

Seq. ID uC-zmflb73038c01b1

Method BLASTX
NCBI GI g2827524
BLAST score 161
E value 7.0e-11
Match length 37
% identity 81

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

NCBI GI

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306116
Seq. No.
                  uC-zmflb73038c03b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g940880
BLAST score
                  369
                  0.0e+00
E value
Match length
                  484
% identity
                  94
NCBI Description
                  Z.mays zag2 gene
Seq. No.
                  306117
                  uC-zmflb73038c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4587595
BLAST score
                  302
E value
                   2.0e-27
Match length
                  133
% identity
                   (AC006951) putative proline-rich protein APG [Arabidopsis
NCBI Description
                  thaliana]
                   306118
Seq. No.
                  uC-zmflb73038c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3645899
BLAST score
                   727
E value
                   3.0e-77
Match length
                   159
% identity
                   87
NCBI Description (U68408) 5' end not determined experimentally [Zea mays]
                   306119
Seq. No.
                   uC-zmflb73038d12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3334320
BLAST score
                   366
                   7.0e-35
E value
                   91
Match length
                   82
% identity
                   40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                   ribosome-associated protein p40 [Glycine max]
                   306120
Seq. No.
Seq. ID
                   uC-zmflb73038e08b1
Method
                   BLASTN
NCBI GI
                   g22149
BLAST score
                   129
                   1.0e-66
E value
Match length
                   129
                   100
% identity
NCBI Description Z.mays mRNA for alpha-tubulin
                   306121
Seq. No.
Seq. ID
                   uC-zmflb73038f05b1
Method
                   BLASTX
```

43400

g4099605

NCBI Description



```
BLAST score
E value
                   1.0e-30
Match length
                   134
% identity
                   47
NCBI Description
                   (U88836) translational activator GCN1 [Homo sapiens]
Seq. No.
                   306122
Seq. ID
                   uC-zmflb73038g01b1
Method
                   BLASTN
NCBI GI
                   g3450841
BLAST score
                   101
E value
                   2.0e-49
Match length
                   282
% identity
                   94
NCBI Description
                  Oryza sativa mitogen activated protein kinase kinase (MEK1)
                   mRNA, complete cds
Seq. No.
                   306123
Seq. ID
                   uC-zmflb73039a01b1
Method
                   BLASTX
NCBI GI
                   g595768
BLAST score
                   155
E value
                   2.0e-10
Match length
                   45
% identity
                   62
NCBI Description
                  (U13866) non-functional lacZ alpha peptide [Cloning vector]
Seq. No.
Seq. ID
                   uC-zmflb73039a09a2
Method
                   BLASTX
NCBI GI
                   g2435395
BLAST score
                   144
E value
                   3.0e-09
Match length
                   52
% identity
                   65
NCBI Description
                  (U63550) pectate lyase [Fragaria x ananassa]
Seq. No.
                   306125
Seq. ID
                   uC-zmflb73039b09b1
Method
                   BLASTX
NCBI GI
                   g478753
BLAST score
                   197
E value
                   1.0e-15
Match length
                   44
% identity
                   84
NCBI Description
                  tubulin alpha-4 chain - maize (fragment)
Seq. No.
                   306126
Seq. ID
                   uC-zmflb73039c06b1
Method
                   BLASTX
NCBI GI
                   g129591
BLAST score
                   206
E value
                   1.0e-16
Match length
                  83
% identity
                   53
```

PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226 (X16099) phenylalanine ammonia-lyase [Oryza sativa]

```
306127
Seq. No.
Seq. ID
                   uC-zmflb73039d09b1
Method
                   {\tt BLASTX}
NCBI GI
                   g3149952
BLAST score
                   190
E value
                   4.0e-30
Match length
                   89
                   78
% identity
NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]
```

Seq. No. 306128

Seq. ID uC-zmflb73039e02b1 Method BLASTN

NCBI GI g3821780 BLAST score 36 E value 1.0e-10 Match length 48 % identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 306129

Seq. ID uC-zmflb73039f11a2

Method BLASTX
NCBI GI g2589164
BLAST score 172
E value 3.0e-26
Match length 76
% identity 88

NCBI Description (D88452) aldehyde oxidase-2 [Zea mays]

Seq. No. 306130

Seq. ID uC-zmflb73039f12b1

Method BLASTN
NCBI GI g257040
BLAST score 37
E value 3.0e-11

Match length 69 % identity 88

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 306131

Seq. ID uC-zmflb73039g08a2

Method BLASTX
NCBI GI g3287683
BLAST score 189
E value 2.0e-14
Match length 104
% identity 25

NCBI Description (AC003979) Similar to apoptosis protein MA-3 gb D50465 from

Mus musculus. [Arabidopsis thaliana]

Seq. No. 306132

Seq. ID uC-zmflb73040a02b1

Method BLASTX
NCBI GI g4415937
BLAST score 245

E value

Match length

3.0e-35

99



```
E value
                   9.0e-21
Match length
                   139
                   37
% identity
NCBI Description
                   (AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   306133
Seq. ID
                  uC-zmflb73040b08b1
Method
                  BLASTN
NCBI GI
                   g4416300
BLAST score
                   127
E value
                   5.0e-65
                   235
Match length
% identity
                   93
                   Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
                   306134
Seq. No.
Seq. ID
                   uC-zmflb73040c01b1
Method
                   BLASTX
NCBI GI
                   g3337389
BLAST score
                   481
E value
                   5.0e-52
Match length
                   152
                   68
% identity
NCBI Description
                   (AC004682) pre-mRNA splicing factor (PRP16)(KIAA0224) [Homo
                   sapiens]
                   306135
Seq. No.
Seq. ID
                   uC-zmflb73040c11b1
Method
                   BLASTX
NCBI GI
                   g1170037
                   326
BLAST score
                   4.0e-30
E value
Match length
                   106
% identity
                   64
NCBI Description
                   GLUTATHIONE SYNTHETASE (GLUTATHIONE SYNTHASE) (GSH
                   SYNTHETASE) (GSH-S) >gi 758452 (U22359) glutathione
                   synthetase [Arabidopsis thaliana] >gi 1305491 (U53856)
                   glutathione synthetase [Arabidopsis thaliana]
Seq. No.
                   306136
Seq. ID
                   uC-zmflb73040d11b1
Method
                   BLASTX
NCBI GI
                   g4056486
BLAST score
                   207
E value
                   2.0e-16
Match length
                   90
% identity
NCBI Description
                   (AC005896) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   306137
Seq. ID
                   uC-zmflb73040f05b1
Method
                   BLASTX
NCBI GI
                   g1707642
BLAST score
                   368
```



```
% identity
                  (Y07748) TMK [Oryza sativa]
NCBI Description
                  306138
Seq. No.
                  uC-zmflb73040h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2832686
BLAST score
                  369
E value
                  3.0e-35
Match length
                  86
                  79
% identity
                  (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
                  306139
Seq. No.
                  uC-zmflb73041a08b1
Seq. ID
Method
                  BLASTX
                  g312179
NCBI GI
BLAST score
                  450
                  5.0e-45
E value
Match length
                  107
% identity
                   (X73151) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                   (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
                   glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                   >gi_1185554 (U45858) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays]
                   306140
Seq. No.
                   uC-zmflb73041c07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2062705
BLAST score
                   34
                   2.0e-09
E value
Match length
                   34
% identity
                   100
                  Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
                   306141
Seq. No.
                   uC-zmflb73041d12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g118104
BLAST score
                   436
                   3.0e-43
E value
                   103
Match length
                   82
% identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi_168461 (M55021) cyclophilin [Zea mays]
                   >qi 82914\overline{8} emb CAA48638 (X68678) cyclophilin [Zea mays]
```

306142 Seq. No.

uC-zmflb73041e08b1 Seq. ID

BLASTX Method NCBI GI q4510363 BLAST score 168 7.0e-12 E value

```
Match length
                  86
% identity
NCBI Description
                  (AC007017) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  306143
Seq. ID
                  uC-zmflb73042d08a2
Method
                  BLASTN
NCBI GI
                  g22513
BLAST score
                  74
E value
                  8.0e-34
Match length
                  168
% identity
                  88
NCBI Description Maize 316 bp insertion sequence 5' of waxy gene
                  306144
Seq. No.
Seq. ID
                  uC-zmflb73042e11a2
Method
                  BLASTN
NCBI GI
                  g168508
BLAST score
                  135
E value
                  6.0e-70
Match length .
                  167
                  95
% identity
NCBI Description Maize oleosin KD18 (KD18; L2) gene, complete cds
Seq. No.
                  306145
Seq. ID
                  uC-zmflb73043a08b1
Method
                  BLASTX
NCBI GI
                  g2511531
BLAST score
                  349
E value
                  4.0e-33
                  70
Match length
% identity
                  91
NCBI Description
                  (AF008120) alpha tubulin 1 [Eleusine indica]
                  >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
```

[Eleusine indica]

Seq. No. 306146

Seq. ID uC-zmflb73043f03b1

Method BLASTX NCBI GI g3264596 BLAST score 225 E value 8.0e-19 Match length 63 % identity

NCBI Description (AF057183) putative tonoplast aquaporin [Zea mays]

Seq. No. 306147

Seq. ID uC-zmflb73043h01b1

Method BLASTX NCBI GI g1710551 BLAST score 159 E value 3.0e-11 Match length 47 % identity 66

NCBI Description 60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728

(X95458) ribosomal protein L39 [Zea mays]

```
Seq. No.
                  306148
Seq. ID
                  uC-zmflb73043h02b1
Method
                  BLASTX
NCBI GI
                  g1710551
BLAST score
                  158
E value
                  7.0e-12
Match length
                  52
                  75
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728
                   (X95458) ribosomal protein L39 [Zea mays]
Seq. No.
                  306149
Seq. ID
                  uC-zmflb73044a04a2
Method
                  BLASTN
NCBI GI
                  g312180
BLAST score
                  35
E value
                  1.0e-10
Match length
                  79
% identity
                  86
NCBI Description
                  Z.mays GapC4 gene
Seq. No.
                  306150
Seq. ID
                  uC-zmflb73044a05a2
Method
                  BLASTN
NCBI GI
                  g3511235
BLAST score
                  33
E value
                  4.0e-09
Match length
                  41
% identity
                  95
NCBI Description
                  Zea mays starch branching enzyme IIb (ae) gene, complete
Seq. No.
                  306151
Seq. ID
                  uC-zmflb73044c10a2
Method
                  BLASTX
NCBI GI
                  q548770
BLAST score
                  204
E value
                  3.0e-16
Match length
                  54
                  76
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                  306152
Seq. ID
                  uC-zmflb73045b02a2
Method
                  BLASTX
NCBI GI
                  g2252632
BLAST score
                  146
E value
                  2.0e-09
```

Seq. No. 306153

Match length

% identity

Seq. ID uC-zmflb73045c05a2

40

43406

NCBI Description (U95973) Barley Mlo protein isolog [Arabidopsis thaliana]



Method BLASTX
NCBI GI g1946355
BLAST score 182
E value 2.0e-13
Match length 92
% identity 34
NCBI Description (U93215)

Description (U93215) maize transposon MuDR mudrA protein isolog
[Arabidopsis thaliana] >gi_2880040 (AC002340) maize

transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 306154

Seq. ID uC-zmflb73045e05a2

Method BLASTX
NCBI GI g417544
BLAST score 244
E value 6.0e-21
Match length 51
% identity 86

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD PROTEIN) (PSI-D) (PS I SUBUNIT 5) >gi 320209 pir A60695 photosystem I chain II precursor -

>gi_320209_pir__A60695 photosystem I chain II precursor cucumber >gi_625966_pir__JQ2132 photosystem I complex 20K
protein precursor - cucumber >gi_227772 prf 1710320A

photosystem I 20kD protein [Cucumis sativus]

Seq. No. 306155

Seq. ID uC-zmflb73045e08a2

Method BLASTX
NCBI GI g2160173
BLAST score 351
E value 3.0e-33
Match length 142
% identity 10

NCBI Description (AC000132) Similar to N. tabacum salt-inducible protein

(gb U08285). [Arabidopsis thaliana]

Seq. No. 306156

Seq. ID uC-zmflb73045f03a2

Method BLASTX
NCBI GI g3335173
BLAST score 144
E value 3.0e-09
Match length 59
% identity 49

NCBI Description (AF071202) ABC transporter MOAT-B [Homo sapiens]

Seq. No. 306157

Seq. ID uC-zmflb73045q10a2

Method BLASTX
NCBI GI g3378650
BLAST score 186
E value 7.0e-14
Match length 63
% identity 56

NCBI Description (X97606) abscisic acid activated [Medicago sativa]

Seq. No. 306158



```
uC-zmflb73046b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982303
BLAST score
                  274
E value
                  2.0e-24
Match length
                  97
% identity
                  56
NCBI Description
                  (AF051236) hypothetical protein [Picea mariana]
                  306159
Seq. No.
Seq. ID
                  uC-zmflb73046d10b1
Method
                  BLASTX
NCBI GI
                  g4507857
BLAST score
                  149
E value
                  4.0e-10
Match length
                  46
% identity
                  65
NCBI Description
                  Herpes virus-associated ubiquitin-specific protease
                  >gi 2501460 sp Q93009 UBPH HUMAN PROBABLE UBIQUITIN
                  CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE
                  HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP)
                  (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED
                  UBIQUITIN-SPECIFIC PROTEASE) >gi 1545952 emb CAA96580
                  (Z72499) herpesvirus associated ubiquitin-specific protease
                  (HAUSP) [Homo sapiens]
Seq. No.
                  306160
Seq. ID
                  uC-zmflb73047a12b1
Method
                  BLASTX
NCBI GI
                  g542175
BLAST score
                  200
E value
                  1.0e-15
Match length
                  68
                  62
% identity
NCBI Description
                  endoxyloglucan transferase - wheat >gi 469511 dbj BAA03924
                  (D16457) endo-xyloglucan transferase [Triticum aestivum]
Seq. No.
                  306161
Seq. ID
                  uC-zmflb73047d12b1
Method
                  BLASTX
NCBI GI
                  g2462925
BLAST score
                  187
E value
                  1.0e-14
Match length
                  60
% identity
NCBI Description
                  (AJ000053) GTP cyclohydrolase II /
                  3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                  thaliana]
Seq. No.
                  306162
Seq. ID
                  uC-zmflb73047f12b1
Method
                  BLASTX
NCBI GI
                  g3513727
BLAST score
                  189
```

43408

1.0e-14

74

55

E value Match length

% identity



```
NCBI Description
                  (AF080118) contains similarity to TPR domains (Pfam:
                  TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
                  kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis
                  thaliana] >gi_4539358_emb_CAB40052.1 (AL049525) putative
                  protein [Arabidopsis thaliana]
Seq. No.
                  306163
                  uC-zmflb73048a01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1326163
BLAST score
                  180
E value
                  2.0e-13
                  77
Match length
                  48
% identity
NCBI Description
                  (U54704) stress related protein PvSRP [Phaseolus vulgaris]
                  306164
Seq. No.
Seq. ID
                  uC-zmflb73048b09b1
Method
                  BLASTX
NCBI GI
                  g2274993
BLAST score
                  236
E value
                  1.0e-19
Match length
                  50
% identity
                  88
NCBI Description (AJ000230) unnamed protein product [Hordeum vulgare]
Seq. No.
                  306165
Seq. ID
                  uC-zmflb73048c02b1
Method
                  BLASTX
NCBI GI
                  g3249096
BLAST score
                  171
E value
                  3.0e-12
Match length
                  95
% identity
NCBI Description
                  (AC003114) Match to mRNA for importin alpha-like protein 4
                  (impa4) gb_Y14616 from A. thaliana. ESTs gb N96440,
                  gb_N37503, gb_N37498 and gb T42198 come from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  306166
                  uC-zmflb73048c09b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g998429
BLAST score
                  218
E value
                  1.0e-119
Match length
                  262
% identity
                  96
NCBI Description
                  GRF1=general regulatory factor [Zea mays, XL80, Genomic,
                  5348 nt]
Seq. No.
                  306167
Seq. ID
                  uC-zmflb73048c10b1
Method
                  BLASTN
```

NCBI GI g2642323 BLAST score 63 E value 6.0e-27

107

Match length



77

Match length

```
% identity
                  Zea mays profilin (PRO4) mRNA, complete cds
NCBI Description
                  306168
Seq. No.
                  uC-zmflb73048d04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2264369
BLAST score
                  245
E value
                  8.0e-21
```

61 % identity (AC002354) predicted protein of unknown function NCBI Description [Arabidopsis thaliana]

306169 Seq. No. Seq. ID uC-zmflb73048e03b1 Method BLASTX NCBI GI g458692 BLAST score 140 E value 8.0e-09 Match length 64 % identity

NCBI Description (U06631) homologous to mouse gene PC326:GenBank Accession Number M95564 [Homo sapiens]

Seq. No. 306170 uC-zmflb73048q01b1 Seq. ID Method BLASTN NCBI GI g777774

BLAST score 34 8.0e-10 E value Match length 50 % identity 92

Chicken heparan sulfate proteoglycan core protein gene, NCBI Description complete cds

Seq. No. 306171 uC-zmflb73048g05b1Seq. ID

Method BLASTX NCBI GI g82733 489 BLAST score E value 2.0e-49 124 Match length 81 % identity

ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937) NCBI Description ubiquitin fusion protein [Zea mays] >gi_902527 (U29161)

ubiquitin fusion protein [Zea mays]

>gi 1589388 prf 2211240B ubiquitin fusion protein [Zea

mays]

306172 Seq. No.

uC-zmflb73048h11b1 Seq. ID

Method BLASTX NCBI GI g3395432 BLAST score 277 E value 9.0e-25 Match length 85

% identity

86

NCBI Description Zea mays retrotransposon Cinful-2



```
% identity
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                  306173
Seq. No.
Seq. ID
                  uC-zmflb73049a09b1
                  BLASTX
Method
NCBI GI
                  g3126967
BLAST score
                   649
                   4.0e-68
E value
                   136
Match length
                   17
% identity
                   (AF061807) polyubiquitin [Elaeagnus umbellata]
NCBI Description
Seq. No.
                   306174
                   uC-zmflb73049b08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4115922
BLAST score
                   604
E value
                   7.0e-63
                   147
Match length
                   75
% identity
                   (AF118222) contains similarity to ubiquitin
NCBI Description
                   carboxyl-terminal hydrolase family 2 (Pfam:PF00443,
                   score=48.3, E=3.5e-13, N=2) and (Pfam:PF00442, Score=40.0
                   E=5.2e-08, N=1) [Arabidopsis thaliana]
                   306175
Seq. No.
Seq. ID
                   uC-zmflb73049b12b1
Method
                   BLASTN
NCBI GI
                   g22312
BLAST score
                   85
                   2.0e-40
E value
Match length
                   161
                   88
% identity
                   Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
                   306176
Seq. No.
Seq. ID
                   uC-zmflb73050a01b1
                   BLASTX
Method
                   g1350680
NCBI GI
BLAST score
                   267
                   1.0e-23
E value
Match length
                   105
% identity
                   55
NCBI Description
                   60S RIBOSOMAL PROTEIN L1
                   306177
Seq. No.
Seq. ID
                   uC-zmflb73050b02b1
Method
                   BLASTN
NCBI GI
                   g4206307
BLAST score
                   56
E value
                   1.0e-22
Match length
                   124
```

Method

NCBI GI

BLASTX

q4204793



```
306178
Seq. No.
Seq. ID
                  uC-zmflb73050b03b1
Method
                  BLASTX
NCBI GI
                  g3367596
BLAST score
                  164
E value
                  4.0e-11
Match length
                  64
                  47
% identity
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
                  306179
Seq. No.
Seq. ID
                  uC-zmflb73050c09b1
                  BLASTX
Method
NCBI GI
                  q4218120
BLAST score
                  232
E value
                   4.0e-37
Match length
                  97
                  79
% identity
                  (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  306180
Seq. No.
Seq. ID
                  uC-zmflb73050e01b1
Method
                  BLASTX
NCBI GI
                  g1498597
BLAST score
                  380
E value
                   1.0e-36
                  119
Match length
% identity
NCBI Description (U66105) phospholipid transfer protein [Zea mays]
Seq. No.
                  306181
Seq. ID
                  uC-zmflb73050e12b1
Method
                  BLASTX
NCBI GI
                   g2511531
BLAST score
                   648
                   5.0e-68
E value
Match length
                   126
% identity
                   96
                   (AF008120) alpha tubulin 1 [Eleusine indica]
NCBI Description
                   >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
                   [Eleusine indica]
Seq. No.
                  306182
Seq. ID
                  uC-zmflb73050g12b1
Method
                   BLASTX
NCBI GI
                   g2984709
BLAST score
                   509
                   1.0e-51
E value
Match length
                   104
% identity
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                   306183
                   uC-zmflb73051a03b1
Seq. ID
```



```
BLAST score
                   208
E value
                   6.0e-24
Match length
                   104
% identity
                   61
NCBI Description
                   (U52079) P-glycoprotein [Solanum tuberosum]
Seq. No.
                   306184
Seq. ID
                   uC-zmflb73051a05b1
Method
                   BLASTN
NCBI GI
                   q2352798
BLAST score
                   87
                   2.0e-41
E value
Match length
                   187
                   92
% identity
NCBI Description
                   Zea mays retinoblastoma-related protein 2b (RRB2b) mRNA,
                   partial cds
Seq. No.
                   306185
Seq. ID
                   uC-zmflb73051b03b1
Method
                   BLASTX
NCBI GI
                   g1785486
BLAST score
                   268
                   1.0e-23
E value
Match length
                   116
% identity
                   47
NCBI Description
                   (D14589) flavonoid 3',5'-hydroxylase [Eustoma russellianum]
Seq. No.
                   306186
Seq. ID
                   uC-zmflb73051c05b1
Method
                   BLASTX
                   q4139264
NCBI GI
BLAST score
                   139
E value
                   8.0e-09
Match length
                   41
% identity
                   71
NCBI Description
                  (AF111812) actin [Brassica napus]
Seq. No.
                   306187
Seq. ID
                   uC-zmflb73051e08a2
Method
                   BLASTX
NCBI GI
                   g4587589
BLAST score
                   353
E value
                   2.0e-33
Match length
                   96
% identity
NCBI Description
                   (AC007232) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   306188
Seq. ID
                   uC-zmflb73051e11b1
```

Method BLASTN
NCBI GI g4204858
BLAST score 103
E value 1.0e-50
Match length 175
% identity 91

NCBI Description Triticum aestivum heat shock protein 80 mRNA, complete cds



268

82

2.0e-27

E value

Match length

```
Seq. No.
Seq. ID
                  uC-zmflb73051f04a2
Method
                 BLASTX
NCBI GI
                   g3894197
BLAST score
                   454
E value
                   3.0e-45
Match length
                  110
% identity
                   71
NCBI Description
                  (AC005662) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   306190
Seq. ID
                  uC-zmflb73051g07b1
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                  36
E value
                   7.0e-11
Match length
                  36
% identity
                  100
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   306191
Seq. ID
                  uC-zmflb73051h07b1
Method
                  BLASTX
NCBI GI
                  q3258575
BLAST score
                  189
E value
                  1.0e-14
Match length
                  48
% identity
                   77
NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  306192
Seq. ID
                  uC-zmflb73051h10b1
Method
                  BLASTN
NCBI GI
                  a22272
BLAST score
                  91
E value
                  1.0e-43
Match length
                  91
% identity
                  100
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
Seq. No.
                  306193
Seq. ID
                  uC-zmflb73052a04b1
Method
                  BLASTN
NCBI GI
                  g949979
BLAST score
                  109
E value
                  2.0e-54
Match length
                  218
% identity
                  87
NCBI Description
                  Z.mays Glossy2 locus DNA
Seq. No.
                  306194
Seq. ID
                  uC-zmflb73052e10b1
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
```



```
% identity
NCBI Description
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
                   306195
Seq. No.
Seq. ID
                   uC-zmflb73052f02b1
Method
                   BLASTX
NCBI GI
                   g549063
BLAST score
                   269
E value
                   1.0e-23
Match length
                   85
% identity
                   61
NCBI Description
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
Seq. No.
                   306196
Seq. ID
                   uC-zmflb73052g03b1
Method
                   BLASTX
NCBI GI
                   g2499570
BLAST score
                   233
E value
                   2.0e-19
                   87
Match length
% identity
                   60
NCBI Description PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE
                   (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN
                   L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN
                   CARBOXYL METHYLTRANSFERASE) >gi_414332 (L07941)
                   L-isoaspartyl methyltransferase [Triticum aestivum]
Seq. No.
                   306197
Seq. ID
                   uC-zmflb73052g12b1
Method
                   BLASTX
NCBI GI
                   g2431771
BLAST score
                   259
E value
                   2.0e-22
Match length
                   108
% identity
                   56
NCBI Description (U62753) acidic ribosomal protein P2b [Zea mays]
Seq. No.
                   306198
Seq. ID
                   uC-zmflb73052h05b1
Method
                   BLASTX
NCBI GI
                   g3935183
BLAST score
                   336
E value
                   2.0e-31
Match length
                   153
% identity
NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]
Seq. No.
                   306199
Seq. ID
                   uC-zmflb73053a06b2
Method
                   BLASTX
NCBI GI
                   g542175
BLAST score
                   219
E value
                   2.0e-18
Match length
                   58
```

NCBI Description



```
% identity
NCBI Description
                  endoxyloglucan transferase - wheat >gi 469511 dbj BAA03924
                   (D16457) endo-xyloglucan transferase [Triticum aestivum]
                   306200
Seq. No.
Seq. ID
                  uC-zmflb73053a07b2
Method
                  BLASTN
NCBI GI
                  g1816587
                  84
BLAST score
E value
                  1.0e-39
Match length
                  163
                   98
% identity
NCBI Description
                  Zea mays LON2 protease (LON2) mRNA, complete cds
                   306201
Seq. No.
Seq. ID
                  uC-zmflb73053d06b2
Method
                  BLASTX
NCBI GI
                   g4539293
BLAST score
                   337
E value
                   1.0e-31
Match length
                  123
% identity
                   53
                   (AL049480) putative membrane transporter [Arabidopsis
NCBI Description
                  thaliana]
                   306202
Seq. No.
Seq. ID
                  uC-zmflb73053d11b2
Method
                  BLASTX
NCBI GI
                   g4455169
BLAST score
                  165
E value
                   1.0e-11
                  59
Match length
% identity
                  54
                   (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  306203
Seq. No.
Seq. ID
                  uC-zmflb73053e04b2
Method
                  BLASTX
NCBI GI
                  g3402685
BLAST score
                  180
E value
                   4.0e-13
                  82
Match length
% identity
                   45
NCBI Description
                  (AC004697) unknown protein [Arabidopsis thaliana]
                  306204
Seq. No.
Seq. ID
                  uC-zmflb73053f12b2
Method
                  BLASTX
NCBI GI
                  g128388
BLAST score
                  198
                   6.0e-16
E value
Match length
                  63
% identity
                  73
```

43416

(PHOSPHOLIPID TRANSFER PROTEIN) (PLTP)

NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)

>gi_82711_pir__A31779 phospholipid transfer protein 9C2



precursor - maize >gi_168576 (J04176) phospholipid transfer protein precursor [Zea mays]

Seq. No. 306205

Seq. ID uC-zmflb73053h12b2

Method BLASTX
NCBI GI g4582465
BLAST score 311
E value 1.0e-28
Match length 91
% identity 64

NCBI Description (AC007071) hypothetical protein [Arabidopsis thaliana]

Seq. No. 306206

Seq. ID uC-zmflb73054b04b1

Method BLASTX
NCBI GI g3046696
BLAST score 539
E value 3.0e-55
Match length 144
% identity 74

NCBI Description (AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No. 306207

Seq. ID uC-zmflb73054g06b1

Method BLASTN
NCBI GI g312180
BLAST score 59
E value 2.0e-24
Match length 139
% identity 85

NCBI Description Z.mays GapC4 gene

Seq. No. 306208

Seq. ID uC-zmflb73054h03b1

Method BLASTX
NCBI GI g4262154
BLAST score 376
E value 3.0e-36
Match length 112
% identity 63

NCBI Description (AC005275) putative protein phosphatase regulatory subunit

[Arabidopsis thaliana]

Seq. No. 306209

Seq. ID uC-zmflb73054h08b1

Method BLASTX
NCBI GI g135398
BLAST score 589
E value 4.0e-61
Match length 111
% identity 97

NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1

chain - maize >gi_22147_emb_CAA33734_ (X15704)

alphal-tubulin [Zea mays]

Seq. No. 306210

NCBI GI

E value

BLAST score

g1172635

539 4.0e-55



```
uC-zmflb73055a05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2286151
BLAST score
                   267
E value
                   1.0e-23
Match length
                   80
% identity
                   68
NCBI Description
                  (AF007580) translation initiation factor [Zea mays]
Seq. No.
                   306211
Seq. ID
                  uC-zmflb73055a08b1
Method
                  BLASTN
NCBI GI
                   q2921303
BLAST score
                   236
E value
                   1.0e-130
Match length
                   300
                   95
% identity
NCBI Description
                  Zea mays herbicide safener binding protein (SBP1) mRNA,
                  complete cds
Seq. No.
                  306212
Seq. ID
                  uC-zmflb73055c01b1
Method
                  BLASTX
NCBI GI
                  g4490316
BLAST score
                  189
E value
                  1.0e-16
Match length
                  67
% identity
                   64
NCBI Description
                  (AL035678) nucellin-like protein [Arabidopsis thaliana]
Seq. No.
                  306213
Seq. ID
                  uC-zmflb73055c03b1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  206
E value
                  6.0e-20
Match length
                  94
                  57
% identity
NCBI Description
                  PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  306214
Seq. ID
                  uC-zmflb73055c10b1
Method
                  BLASTX
NCBI GI
                  g4587584
BLAST score
                  596
E value
                  6.0e-62
Match length
                  148
% identity
NCBI Description
                  (AC007232) unknown protein [Arabidopsis thaliana]
Seq. No.
                  306215
Seq. ID
                  uC-zmflb73055f03b1
Method
                  BLASTX
```

43418



Match length 151 % identity 75

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice

homologue of Tat binding protein [Oryza sativa]

Seq. No. 306216

Seq. ID uC-zmflb73055f04b1

Method BLASTX
NCBI GI g3789942
BLAST score 406
E value 3.0e-49
Match length 130
% identity 20

NCBI Description (AF093505) polyubiquitin [Saccharum hybrid cultivar

H32-8560]

Seq. No. 306217

Seq. ID uC-zmflb73055f06b1

Method BLASTX
NCBI GI g417154
BLAST score 417
E value 4.0e-41
Match length 93
% identity 85

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 306218

Seq. ID uC-zmflb73055h09b1

Method BLASTX
NCBI GI g3913464
BLAST score 325
E value 3.0e-30
Match length 86
% identity 73

NCBI Description BETAINE-ALDEHYDE DEHYDROGENASE (BADH)

>gi_2244604_dbj_BAA21098_ (AB001348) betaine aldehyde

dehydrogenase [Oryza sativa]

Seq. No. 306219

Seq. ID uC-zmflb73055h10b1

Method BLASTX
NCBI GI g1498390
BLAST score 417
E value 4.0e-41
Match length 118
% identity 72

NCBI Description (U60511) actin [Zea mays]

Seq. No. 306220

Seq. ID uC-zmflb73056a02b1

Method BLASTX NCBI GI g3643604 BLAST score 210



```
E value
                  9.0e-17
Match length
                  125
% identity
                  (AC005395) receptor-like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  306221
                  uC-zmflb73056f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130442
BLAST score
                  375
E value
                  6.0e-36
                  151
Match length
                  47
% identity
                  hypothetical protein SPAC8A4.01c - fission yeast
NCBI Description
                  (Schizosaccharomyces pombe) (fragment)
                  >gi 1052534 emb CAA91511 (Z66569) unknown
                  [Schizosaccharomyces pombe]
Seq. No.
                  306222
Seq. ID
                  uC-zmflb73056f08b1
                  BLASTX
Method
                  g1168328
NCBI GI
BLAST score
                  174
                  2.0e-12
E value
Match length
                  91
                  43
% identity
NCBI Description
                  ACTIN-LIKE PROTEIN 3 >gi 629878 pir S48844 actin-like
                  protein - slime mold (Dictyostelium discoideum)
                  >gi 2130164 pir S69002 actin-like protein - slime mold
                   (Dictyostelium discoideum) >gi 563346 emb CAA86553
                   (Z46418) actin-like protein [Dictyostelium discoideum]
Seq. No.
                  306223
                  uC-zmflb73056h11b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2668745
BLAST score
                  142
E value
                  4.0e-74
Match length
                  281
% identity
NCBI Description Zea mays inorganic pyrophosphatase (IPP) mRNA, complete cds
Seq. No.
                  306224
Seq. ID
                  uC-zmflb73057a09b1
Method
                  BLASTX
NCBI GI
                  g4587584
BLAST score
                  447
E value
                  2.0e-44
Match length
                  172
```

% identity

NCBI Description (AC007232) unknown protein [Arabidopsis thaliana]

Seq. No. 306225

uC-zmflb73057c03a2 Seq. ID

Method BLASTX NCBI GI q629783

Method

NCBI GI

BLASTX

q3128168



```
BLAST score
E value
                  2.0e-22
Match length
                  58
                  81
% identity
                  ES43 protein - barley >gi_1345528_emb_CAA54682_ (X77575)
NCBI Description
                  ES43 [Hordeum vulgare]
Seq. No.
                  306226
Seq. ID
                  uC-zmflb73057h02b1
Method
                  BLASTX
NCBI GI
                  g1169528
BLAST score
                  290
E value
                  1.0e-26
                  57
Match length
                  95
% identity
NCBI Description
                  ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi 602253 (U17973)
                  enolase [Zea mays]
                  306227
Seq. No.
Seq. ID
                  uC-zmflb73058a10b1
Method
                  BLASTX
NCBI GI
                  g4646217
BLAST score
                  388
E value
                  1.0e-37
Match length
                 - 86
% identity
NCBI Description
                  (AC007290) putative phosphoprotein phosphatase [Arabidopsis
                  thaliana]
                  306228
Seq. No.
Seq. ID
                  uC-zmflb73058a12b1
Method
                  BLASTX
NCBI GI
                  g1706261
BLAST score
                  142
E value
                  4.0e-09
Match length
                  42
                  76
% identity
NCBI Description
                  CYSTEINE PROTEINASE 2 PRECURSOR >gi 2118129 pir $59598
                  cysteine proteinase 2 precursor - maize
                  >gi_644490_dbj_BAA08245 (D45403) cysteine proteinase [Zea
                  mays]
Seq. No.
                  306229
Seq. ID
                  uC-zmflb73058b09b1
Method
                  BLASTX
NCBI GI
                  g4138282
BLAST score
                  149
E value
                  5.0e-10
Match length
                  79
% identity
NCBI Description
                  (AJ011576) RNA-directed RNA polymerase [Nicotiana tabacum]
Seq. No.
                  306230
Seq. ID
                  uC-zmflb73058c05b1
```

E value

Match length

NCBI Description

% identity



```
BLAST score
                   1.0e-29
E value
                  118
Match length
                   54
% identity
                   (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   306231
                  uC-zmflb73058d05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3402685
BLAST score
                   416
                   6.0e-41
E value
Match length
                  117
% identity
                   68
                   (AC004697) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   306232
Seq. ID
                   uC-zmflb73058f10b1
Method
                   BLASTX
NCBI GI
                   g1890575
BLAST score
                   578
E value
                   8.0e-60
Match length
                   135
% identity
                   76
                   (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
NCBI Description
                   vulgare]
                   306233
Seq. No.
                   uC-zmflb73058h12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3021268
BLAST score
                   175
                   1.0e-12
E value
                   115
Match length
                   36
% identity
                  (AL022347) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   306234
Seq. ID
                   uC-zmflb73059a05b1
Method
                   BLASTX
NCBI GI
                   g2444178
BLAST score
                   324
E value
                   3.0e-31
Match length
                   119
% identity
                   66
                  (U94784) unconventional myosin [Helianthus annuus]
NCBI Description
                   306235
Seq. No.
                   uC-zmflb73059a10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g135398
BLAST score
                   568
                   7.0e-59
```

108

43422

TUBULIN ALPHA-1 CHAIN >gi 82731 pir S15773 tubulin alpha-1



chain - maize >gi_22147_emb_CAA33734_ (X15704)
alphal-tubulin [Zea mays]

Seq. No. 306236

Seq. ID uC-zmflb73059c01b1

Method BLASTX
NCBI GI g3413697
BLAST score 189
E value 3.0e-14
Match length 125
% identity 37

NCBI Description (AC004747) SF16-like protein, 5' partial [Arabidopsis

thaliana]

Seq. No. 306237

Seq. ID uC-zmflb73059c08a2

Method BLASTX
NCBI GI g4056421
BLAST score 171
E value 4.0e-12
Match length 45
% identity 67

NCBI Description (AC005322) Similar to gb_Z30094 basic transcripion factor

2, 44 kD subunit from Homo sapiens. EST gb W43325 comes

from this gene. [Arabidopsis thaliana]

Seq. No. 306238

Seq. ID uC-zmflb73059e02b1

Method BLASTX
NCBI GI g3776025
BLAST score 522
E value 3.0e-53
Match length 135
% identity 73

NCBI Description (AJ010474) RNA helicase [Arabidopsis thaliana]

Seq. No. 306239

Seq. ID uC-zmflb73059e05b1

Method BLASTX
NCBI GI g4512702
BLAST score 160
E value 2.0e-11
Match length 102
% identity 43

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 306240

Seq. ID uC-zmflb73059f04a2

Method BLASTN
NCBI GI g312178
BLAST score 93
F value 8 00-45

E value 8.0e-45 Match length 372 % identity 82

NCBI Description Z.mays GapC2 gene

Seq. No. 306241



uC-zmflb73059f04b1 Seq. ID Method BLASTN NCBI GI g4140643 133 BLAST score 1.0e-68 E value Match length 292 53 % identity NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence 306242 Seq. No. Seq. ID uC-zmflb73059h03b1 Method BLASTX NCBI GI g4416302 BLAST score 257 E value 3.0e-22 Match length 122 % identity 47 NCBI Description (AF105716) copia-type pol polyprotein [Zea mays] Seq. No. 306243 uC-zmflb73060c09b1 Seq. ID Method BLASTX NCBI GI g2827715 BLAST score 551 E value 1.0e-56 Match length 166 % identity 10 NCBI Description (AL021684) receptor protein kinase - like protein [Arabidopsis thaliana] 306244 Seq. No. Seq. ID uC-zmflb73060c10b1 Method BLASTX NCBI GI g282994 505 BLAST score 3.0e-51 E value Match length 112 % identity 84 Sip1 protein - barley >gi_167100 (M77475) seed imbibition NCBI Description protein [Hordeum vulgare] Seq. No. 306245 Seq. ID uC-zmflb73060d12b1 Method BLASTX NCBI GI g4220537 BLAST score 162 E value 5.0e-11 Match length 62 % identity 40 NCBI Description (AL035356) PsRT17-1 like protein [Arabidopsis thaliana] Seq. No. 306246 Seq. ID uC-zmflb73061b03a2

Method BLASTX NCBI GI g3914024 BLAST score 198



E value 2.0e-15
Match length 59
% identity 63
NCBI Description (R)-MAN

(R)-MANDELONITRILE LYASE ISOFORM 2 PRECURSOR

(HYDROXYNITRILE LYASE 2) ((R)-OXYNITRILASE 2) >gi_2773274

(AF040078) (R)-(+)-mandelonitrile lyase isoform MDL2 precursor [Prunus serotina] >gi 2773276 (AF040079)

(R)-(+)-mandelonitrile lyase isoform MDL2 precursor [Prunus

serotina]

306247

306248

Seq. No. Seq. ID

uC-zmflb73061b09b1

Method BLASTX
NCBI GI g3372233
BLAST score 155
E value 3.0e-10
Match length 107
% identity 38

NCBI Description (AF019248) RNA polymerase I, II and III 24.3 kDa subunit

[Arabidopsis thaliana]

Seq. No.

Seq. ID

uC-zmflb73061c10b1

Method BLASTX
NCBI GI g3540179
BLAST score 214
E value 4.0e-17
Match length 53
% identity 74

NCBI Description (AC004122) putative amino acid permease [Arabidopsis

thaliana]

306249

Seq. No.

Seq. ID

uC-zmflb73061d05a2

Method BLASTX
NCBI GI g629844
BLAST score 320
E value 9.0e-30
Match length 81
% identity 81

NCBI Description heat shock protein hsp70-5 - maize (fragment)

>gi_498775_emb_CAA55184_ (X78415) heat shock protein 70 kDa

[Zea mays]

Seq. No. 306250

Seq. ID uC-zmflb73061f06b1

Method BLASTX
NCBI GI g137460
BLAST score 326
E value 2.0e-30
Match length 81
% identity 80

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi_67952_pir__PXPZV9 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 69K chain - carrot >gi_167560 (J03769)

vacular H+-ATPase [Daucus carota]

Method

NCBI GI

BLAST score

BLASTN

36

g2062705



```
Seq. No.
                   306251
Seq. ID
                   uC-zmflb73061f12b1
Method
                   BLASTX
NCBI GI
                   g1181673
BLAST score
                   357
E value
                   4.0e-34
Match length
                   89
% identity
                   79
                   (U41652) heat shock protein cognate 70 [Sorghum bicolor]
NCBI Description
Seq. No.
                   306252
Seq. ID
                   uC-zmflb73062a11b1
Method
                   BLASTX
NCBI GI
                   q1491615
BLAST score
                   173
E value
                   3.0e-12
Match length
                   114
% identity
                   36
NCBI Description
                   (X99923) male sterility 2-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   306253
                                                      s." . "
Seq. ID
                   uC-zmflb73062c08b1
Method
                   BLASTN
NCBI GI
                   g2921303
BLAST score
                   111
E value
                   1.0e-55
Match length
                   219
% identity
                   88
NCBI Description
                   Zea mays herbicide safener binding protein (SBP1) mRNA,
                   complete cds
Seq. No.
                   306254
Seq. ID
                   uC-zmflb73062d02a1
Method
                   BLASTX
NCBI GI
                   g1321661
BLAST score
                   242
                   2.0e-20
E value
Match length
                   49
% identity
                   96
NCBI Description
                   (D45423) ascorbate peroxidase [Oryza sativa]
Seq. No.
                   306255
Seq. ID
                   uC-zmflb73062e05b1
Method
                   BLASTX
NCBI GI
                   g1653625
BLAST score
                   252
E value
                   2.0e-21
Match length
                   130
% identity
                   40
NCBI Description
                  (D90915) hypothetical protein [Synechocystis sp.]
Seq. No.
                   306256
Seq. ID
                   uC-zmflb73062f01b1
```



```
E value
                   7.0e-11
Match length
                   36
 % identity
                   100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
 Seq. No.
                   306257
 Seq. ID
                   uC-zmflb73062q03b1
Method
                   BLASTX
NCBI GI
                   g2497748
BLAST score
                   168
E value
                   7.0e-12
Match length
                   68
% identity
                   49
NCBI Description
                   NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4)
                   >gi 902058 (U29176) lipid transfer protein precursor [Oryza
                   sativa]
Seq. No.
                   306258
Seq. ID
                   uC-zmflb73062g08b1
Method
                   BLASTX
NCBI GI
                   g3551245
BLAST score
                   225
E value
                   2.0e-18
Match length
                   56
% identity
                   73
NCBI Description
                   (AB012702) P40-like protein [Daucus carota]
Seq. No.
                   306259
Seq. ID
                   uC-zmflb73063b05a1
Method
                   BLASTN
NCBI GI
                   g473602
BLAST score
                   50
E value
                   3.0e-19
Match length
                   94
% identity
                   88
NCBI Description
                   Zea mays W-22 histone H2A mRNA, complete cds
Seq. No.
                   306260
Seq. ID
                   uC-zmflb73063e01b1
Method
                   BLASTX
NCBI GI
                   g1663648
BLAST score
                   154
E value
                   4.0e-10
Match length
                   67
% identity
                   42
NCBI Description
                  (U75321) chromaffin granule ATPase II homolog [Mus
                  musculus]
Seq. No.
                  306261
Seq. ID
                  uC-zmflb73064a06b1
Method
                  BLASTX
```

NCBI GI g2914706 BLAST score 455 E value 2.0e-45 Match length 97

% identity

NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]

Method

NCBI GI

`~j\.

BLASTX

q2827663

```
Seq. No.
                   306262
Seq. ID
                   uC-zmflb73064b03a2
Method
                   BLASTN
NCBI GI
                   g22155
BLAST score
                   64
E value
                   9.0e-28
Match length
                   116
% identity
                   89
NCBI Description Z.mays mRNA for alpha-tubulin
Seq. No.
                   306263
Seq. ID
                   uC-zmflb73064b05b1
Method
                   BLASTX
NCBI GI
                   g4586244
BLAST score
                   420
E value
                   3.0e-41
Match length
                   138
% identity
                   55
NCBI Description
                  (AL049640) putative protein [Arabidopsis thaliana]
Seq. No.
                   306264
Seq. ID
                  uC-zmflb73064f04b1
Method
                  BLASTX
NCBI GI
                   g2827141
BLAST score
                   386
E value
                   2.0e-37
Match length
                  108
% identity
                   68
NCBI Description
                   (AF027173) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                  306265
Seq. ID
                  uC-zmflb73064g06b1
Method
                  BLASTX
NCBI GI
                  g541825
BLAST score
                  551
                  1.0e-56
E value
Match length
                  119
% identity
                  87
NCBI Description
                  protein kinase - spinach >gi_457711 emb CAA82993 (Z30332)
                  protein kinase [Spinacia oleracea]
Seq. No.
                  306266
Seq. ID
                  uC-zmflb73065b04b1
Method
                  BLASTX
NCBI GI
                  q2760349
BLAST score
                  165
E value
                  8.0e-12
Match length
                  42
% identity
NCBI Description
                 (U84969) ubiquitin [Arabidopsis thaliana]
Seq. No.
                  306267
Seq. ID
                  uC-zmflb73065c04b1
```

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BLAST score

Match length

E value

414

138

1.0e-40



```
BLAST score
E value
                       2.0e-18
     Match length
                       134
                       5
     % identity
                        (AL021637) membrane-associated salt-inducible-like protein
     NCBI Description
                        [Arabidopsis thaliana]
                       306268
     Seq. No.
                       uC-zmflb73065d11a1
     Seq. ID
                       BLASTN
     Method
     NCBI GI
                       q416146
     BLAST score
                       142
     E value
                       3.0e-74
     Match length
                       162
                       97
     % identity
                       Zea mays beta-6 tubulin (tub6) gene and mRNA, complete cds
     NCBI Description
     Seq. No.
                       306269
     Seq. ID
                       uC-zmflb73066a09b1
     Method
                       BLASTX
     NCBI GI
                       g2462826
     BLAST score
                       358
     E value
                       8.0e-34
     Match length
                       169
     % identity
                        52
                       (AF000657) unknown protein [Arabidopsis thaliana]
     NCBI Description
                       306270
     Seq. No.
     Seq. ID
                       uC-zmflb73066c01b1
                       BLASTX
     Method
     NCBI GI
                        g1168537
     BLAST score
                        674
     E value
                        6.0e-71
     Match length
                       138
                        90
     % identity
     NCBI Description
                       ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732
                       aspartic proteinase (EC 3.4.23.-) - rice
                        >gi 218143 dbj BAA02242 (D12777) aspartic proteinase
                        [Oryza satīva]
     Seq. No.
                        306271
     Seq. ID
                        uC-zmflb73066e10b1
     Method
                        BLASTX
     NCBI GI
                        q4160292
     BLAST score
                        602
     E value
                        1.0e-62
                       144
     Match length
     % identity
     NCBI Description
                       (Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]
                        306272
     Seq. No.
     Seq. ID
                       uC-zmflb73066f01b1
     Method
                        BLASTX
     NCBI GI
                        q1552379
```

43429



% identity (Y08155) pectin methylesterase [Silene latifolia ssp. alba] NCBI Description 306273 Seq. No. uC-zmflb73066f02b1 Seq. ID Method BLASTX NCBI GI q3510250 BLAST score 232 E value 3.0e-19 140 Match length % identity 36 (AC005310) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 306274 uC-zmflb73066f03b1 Seq. ID BLASTX Method NCBI GI g1421730 BLAST score 447 E value 2.0e-44 Match length 88 % identity 100 NCBI Description (U43082) RF2 [Zea mays] 306275 Seq. No. Seq. ID uC-zmflb73066h07b1 BLASTX Method NCBI GI g2895866 BLAST score 347 E value 9.0e-33 Match length 136 % identity 60 (AF045770) methylmalonate semi-aldehyde dehydrogenase NCBI Description [Oryza sativa] 306276 Seq. No. Seq. ID uC-zmflb73067f03b1 Method BLASTX NCBI GI g3080353 BLAST score 139 9.0e-09 E value 69 Match length % identity 42 NCBI Description (AL022580) cytochrome P450 [Arabidopsis thaliana] 306277 Seq. No. Seq. ID uC-zmflb73067h04b1 BLASTX Method NCBI GI q4262167 BLAST score 198 E value 2.0e-15 Match length 57 % identity 63 NCBI Description (AC005275) putative LRR receptor-linked protein kinase

Seq. No. 306278

Seq. ID uC-zmflb73068a01b1

[Arabidopsis thaliana]



```
Method
                  BLASTX
NCBI GI
                  g2384671
                  522
BLAST score
E value
                   3.0e-53
Match length
                  134
                   73
% identity
                   (AF012657) putative potassium transporter AtKT2p
NCBI Description
                   [Arabidopsis thaliana]
                  306279
Seq. No.
                  uC-zmflb73068b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913427
BLAST score
                  437
E value
                   2.0e-43
Match length
                  122
                   77
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767)
                   S-adenosylmethionine decarboxylase [Zea mays]
Seq. No.
                  306280
                  uC-zmflb73068c02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739371
BLAST score
                  211
E value
                  1.0e-16
                  52
Match length
                  79
% identity
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.
                  306281
Seq. ID
                  uC-zmflb73068c03b1
Method
                  BLASTX
NCBI GI
                  g1421730
BLAST score
                  230
E value
                  2.0e-24
Match length
                  143
% identity
                   48
NCBI Description (U43082) RF2 [Zea mays]
                  306282
Seq. No.
Seq. ID
                  uC-zmflb73068d01a1
Method
                  BLASTX
                  g3522956
NCBI GI
BLAST score
                  187
E value
                  3.0e-14
Match length
                  57
% identity
                  54
NCBI Description
                  (AC004411) putative pectinacetylesterase precursor
                   [Arabidopsis thaliana]
Seq. No.
                  306283
Seq. ID
                  uC-zmflb73068d01b1
```

Method BLASTX NCBI GI g3047082 BLAST score 363



```
E value
                  1.0e-34
Match length
                  112
                  59
% identity
                  (AF058914) similar to Vigna radiata pectinacetylesterase
NCBI Description
                  precursor (GB:X99348) [Arabidopsis thaliana]
Seq. No.
                  306284
Seq. ID
                  uC-zmflb73068d07b1
                  BLASTX
Method
NCBI GI
                  g3540219
                  435
BLAST score
                  5.0e-43
E value
                  148
Match length
                  56
% identity
NCBI Description (D87686) KIAA0017 protein [Homo sapiens]
                  306285
Seq. No.
                  uC-zmflb73068e05a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4469026
                  154
BLAST score
                  5.0e-10
E value
                  55
Match length
% identity
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]
                   306286
Seq. No.
                  uC-zmflb73068f10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2288999
BLAST score
                  178
                   3.0e-13
E value
                   83
Match length
% identity
                   48
                   (AC002335) electron transfer flavoprotein ubiquinone
NCBI Description
                   oxidoreductase isolog [Arabidopsis thaliana]
                   306287
Seq. No.
Seq. ID
                   uC-zmflb73068g12b1
Method
                   BLASTX
                   g3451069
NCBI GI
BLAST score
                   212
E value
                   6.0e-17
Match length
                   144
% identity
                   (AL031326) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   306288
Seq. No.
Seq. ID
                   uC-zmflb73068h06b1
```

Method BLASTX
NCBI GI g3860277
BLAST score 422
E value 1.0e-41
Match length 114
% identity 71

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >qi 4314394 gb AAD15604 (AC006232) putative

Seq. No.

Seq. ID

306294

uC-zmflb73070b11b1



ribosomal protein L10A [Arabidopsis thaliana]

```
Seq. No.
                  306289
Seq. ID
                  uC-zmflb73069a04b1
Method
                  BLASTX
NCBI GI
                  g1621268
BLAST score
                  231
                  4.0e-19
E value
Match length
                  71
% identity
                  68
NCBI Description (Z81012) unknown [Ricinus communis]
                  306290
Seq. No.
Seq. ID
                  uC-zmflb73069c07b1
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  166
E value
                  3.0e-88
Match length
                  259
% identity
                  92
NCBI Description
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
Seq. No.
                  306291
Seq. ID
                  uC-zmflb73069g10a1
Method
                  BLASTN
NCBI GI
                  g602605
BLAST score
                  37
E value
                  1.0e-11
Match length
                  94
% identity
                  83
NCBI Description
                  Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
Seq. No.
                  306292
Seq. ID
                  uC-zmflb73069h05b1
Method
                  BLASTX
NCBI GI
                  g2117937
BLAST score
                  554
                  7.0e-57
E value
Match length
                  140
                  79
% identity
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                  barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
Seq. No.
                  306293
Seq. ID
                  uC-zmflb73069h09b1
Method
                  BLASTX
NCBI GI
                  g3212869
BLAST score
                  155
E value
                  2.0e-10
Match length
                  71
% identity
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
```

43433

Match length

46



```
Method
NCBI GI
                   g4204283
BLAST score
                   571
E value
                   7.0e-59
Match length
                   155
% identity
                   75
NCBI Description
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   306295
Seq. ID
                  uC-zmflb73070c10b1
Method
                  BLASTN
NCBI GI
                   g1504051
BLAST score
                   249
E value
                   1.0e-138
Match length
                   436
% identity
                   90
NCBI Description
                  Zea mays mRNA for Calcium-dependent protein kinase,
                  complete cds
                   306296
Seq. No.
Seq. ID
                  uC-zmflb73070d02b1
Method
                  BLASTX
NCBI GI
                  q4416302
BLAST score
                   408
E value
                   5.0e-50
Match length
                  115
% identity
                   86
NCBI Description
                  (AF105716) copia-type pol polyprotein [Zea mays]
Seq. No.
                   306297
Seq. ID
                  uC-zmflb73070d03b1
Method
                  BLASTX
NCBI GI
                   g4587597
BLAST score
                   180
E value
                   4.0e-13
Match length
                   81
% identity
                   41
NCBI Description
                   (AC006951) putative MAP kinase phosphatase [Arabidopsis
                  thaliana]
Seq. No.
                   306298
Seq. ID
                  uC-zmflb73070d04b1
Method
                  BLASTX
NCBI GI
                  g1001955
BLAST score
                   419
E value
                   4.0e-41
Match length
                  124
% identity
                  72
NCBI Description
                  (U19099) unknown protein [Lycopersicon chilense ]
Seq. No.
                  306299
                  uC-zmflb73070g02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827536
BLAST score
                  175
E value
                  2.0e-12
```



```
% identity
                   (AL021633) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  306300
Seq. No.
Seq. ID
                  uC-zmflb73070g03b1
Method
                  BLASTX
NCBI GI
                  g1181673
BLAST score
                  442
E value
                  1.0e-47
Match length
                  134
                  74
% identity
                  (U41652) heat shock protein cognate 70 [Sorghum bicolor]
NCBI Description
Seq. No.
                  306301
Seq. ID
                  uC-zmflb73070g09b1
Method
                  BLASTX
NCBI GI
                  g122007
BLAST score
                  257
E value
                  3.0e-22
Match length
                  80
% identity
                   68
NCBI Description
                  HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
                  >gi_20448_emb_CAA37828 (X53831) H2A histone protein (AA 1
                  - 149) [Petroselinum crispum]
Seq. No.
                   306302
                  uC-zmflb73070q12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1877482
BLAST score
                   421
E value
                  2.0e-41
Match length
                  102
% identity
                   80
NCBI Description
                  (U89271) short-chain alcohol dehydrogenase [Tripsacum
                  dactyloides]
                  306303
Seq. No.
Seq. ID
                  uC-zmflb73071a01b3
Method
                  BLASTX
NCBI GI
                  g4455338
BLAST score
                  387
E value
                  3.0e-37
Match length
                  119
% identity
                   64
NCBI Description
                  (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                  306304
Seq. ID
                  uC-zmflb73071b04b3
Method
                  BLASTX
NCBI GI
                  g4559377
```

BLAST score 215 E value 3.0e-17 Match length 69

% identity 57

NCBI Description (AC006526) putative photomorphogenesis repressor protein

COP1 [Arabidopsis thaliana]

Match length

NCBI Description

% identity

130



```
Seq. No.
                   306305
Seq. ID
                   uC-zmflb73071e05b3
Method
                   BLASTN
NCBI GI
                   g575959
BLAST score
                   43
E value
                   8.0e-15
Match length
                   71
% identity
                   92
NCBI Description
                   Z.mays (Black Mexican Sweet) mRNA for
                   1-acyl-glycerol-3-phosphate acyltransferase (putative)
Seq. No.
                   306306
Seq. ID
                   uC-zmflb73071g03b3
Method
                   BLASTX
NCBI GI
                   g1402878
BLAST score
                   257
E value
                   3.0e-22
Match length
                   97
% identity
                   49
NCBI Description (X98130) unknown [Arabidopsis thaliana]
Seq. No.
                   306307
Seq. ID
                   uC-zmflb73071g04b3
Method
                   BLASTX
                   g1346765
NCBI GI
BLAST score
                   724
E value
                   8.0e-77
Match length
                   174
% identity
                   77
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP1
NCBI Description
                   >gi_1084368_pir__S52371 phosphoprotein phosphatase (EC
3.1.3.16) PP1 - kidney bean >gi_2129870_pir__S60053
                   phosphoprotein phosphatase 1 - kidney bean
                   >gi_667049_emb_CAA88254_ (Z48221) protein phosphatase PP1
                   [Phaseolus vulgaris]
Seq. No.
                   306308
Seq. ID
                   uC-zmflb73071q10b3
Method
                   BLASTX
NCBI GI
                   g1769901
BLAST score
                   285
                   2.0e-25
E value
Match length
                   139
% identity
NCBI Description
                   (X95737) proline transporter 1 [Arabidopsis thaliana]
                   >gi_2088642 (AF002109) proline transporter 1 [Arabidopsis
                   thaliana]
Seq. No.
                   306309
Seq. ID
                   uC-zmflb73071g12b3
Method
                   BLASTX
NCBI GI
                   g3641838
BLAST score
                   352
E value
                   2.0e-33
```

(AL023094) putative protein (fragment) [Arabidopsis

Match length

NCBI Description

% identity

66 71



thaliana]

```
306310
Seq. No.
Seq. ID
                  uC-zmflb73071h02b3
Method
                  BLASTX
NCBI GI
                  g2944417
BLAST score
                  165
                  9.0e-12
E value
                  83
Match length
% identity
                  48
NCBI Description (AF049881) peroxidase FLXPER4 [Linum usitatissimum]
                  306311
Seq. No.
Seq. ID
                  uC-zmflb73072a01a1
Method
                  BLASTX
NCBI GI
                  g1362086
BLAST score
                  173
E value
                  2.0e-12
                  37
Match length
% identity
                  86
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919_pir__S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 886471 emb CAA58474 (X83499) methionine synthase
                  [Catharanthus roseus]
Seq. No.
                  306312
Seq. ID
                  uC-zmflb73072d10a1
Method
                  BLASTX
NCBI GI
                  q4220489
BLAST score
                  197
E value
                  2.0e-15
Match length
                  54
% identity
NCBI Description
                  (AC006069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  306313
Seq. ID
                  uC-zmflb73073a05a1
Method
                  BLASTN
NCBI GI
                  q1181332
BLAST score
                  113
E value
                  6.0e-57
Match length
                  248
% identity
                  85
NCBI Description Z.mays CRH mRNA
Seq. No.
                  306314
Seq. ID
                  uC-zmflb73073a06b3
Method
                  BLASTX
NCBI GI
                  g2739385
BLAST score
                  250
E value
                  2.0e-21
```

(AC002505) putative beta-1,3-glucanase [Arabidopsis



thaliana]

```
      Seq. No.
      306315

      Seq. ID
      uC-zmflb73073a08b3

      Method
      BLASTX

      NCBI GI
      g4309734
```

BLAST score 227 E value 2.0e-24 Match length 98 % identity 54

NCBI Description (AC006439) putative 26S proteosome regulatory subunit 8

[Arabidopsis thaliana]

Seq. No. 306316

Seq. ID uC-zmflb73073e06b3

Method BLASTX
NCBI GI g4204859
BLAST score 245
E value 6.0e-21
Match length 72
% identity 72

NCBI Description (U55859) heat shock protein 80 [Triticum aestivum]

Seq. No. 306317

Seq. ID uC-zmflb73073f04b3

Method BLASTX
NCBI GI g2842494
BLAST score 462
E value 3.0e-46
Match length 120
% identity 79

NCBI Description (AL021749) prohibitin-like protein [Arabidopsis thaliana]

>gi_4097688 (U66591) prohibitin 1 [Arabidopsis thaliana]
>gi_4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]

Seq. No. 306318

Seq. ID uC-zmflb73073f08b3

Method BLASTX
NCBI GI g4160441
BLAST score 145
E value 5.0e-09
Match length 71
% identity 49

NCBI Description (AF098674) lateral suppressor protein [Lycopersicon

esculentum]

Seq. No. 306319

Seq. ID uC-zmflb73073h01b3

Method BLASTX
NCBI GI g3377509
BLAST score 257
E value 2.0e-22
Match length 94
% identity 63

NCBI Description (AF056027) auxin transport protein REH1 [Oryza sativa]

Seq. No. 306320



```
Seq. ID uC-zmflb73073h05b3
Method BLASTX
NCBI GI g135398
BLAST score 288
E value 4.0e-50
```

Match length 119 % identity 84

NCBI Description TUBULIN ALPHA-1 CHAIN >gi 82731 pir S15773 tubulin alpha-1

chain - maize >gi 22147 emb CAA33734 (X15704)

alpha1-tubulin [Zea mays]

Seq. No. 306321

Seq. ID uC-zmflb73075a10a1

Method BLASTX
NCBI GI g3287693
BLAST score 158
E value 1.0e-10
Match length 43
% identity 70

NCBI Description (AC003979) Similar to LIM17 gene product gb 1653769 from

the genome of Synechocystis sp. gb_D90916. [Arabidopsis

thaliana]

Seq. No. 306322

Seq. ID uC-zmflb73075e03a1

Method BLASTN
NCBI GI g2463566
BLAST score 382
E value 0.0e+00
Match length 406
% identity 99

NCBI Description Zea mays mRNA for squalene synthase, complete cds

Seq. No. 306323

Seq. ID uC-zmflb73076a11b2

Method BLASTX
NCBI GI g123620
BLAST score 330
E value 6.0e-31
Match length 92
% identity 72

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950

heat shock cognate protein 70 - tomato

>gi 19258_emb_CAA37971_ (X54030) heat shock protein cognate

70 [Lycopersicon esculentum]

Seq. No. 306324

Seq. ID uC-zmflb73076d12b2

Method BLASTX
NCBI GI g3128208
BLAST score 191
E value 1.0e-14
Match length 54
% identity 59

NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No. 306325

Seq. ID

Method

NCBI GI



```
uC-zmflb73076e07b2
Seq. ID
                  BLASTX
Method
                  g2583120
NCBI GI
                  301
BLAST score
                  2.0e-27
E value
                  132
Match length
                  48
% identity
                   (AC002387) putative receptor-like protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  306326
Seq. No.
                  uC-zmflb73076e08b2
Seq. ID
Method
                  BLASTX
                  g3046695
NCBI GI
                  238
BLAST score
                  7.0e-20
E value
                  83
Match length
                  59
% identity
NCBI Description (AL022224) putative protein [Arabidopsis thaliana]
Seq. No.
                  306327
                  uC-zmflb73076e10b2
Seq. ID
                  BLASTN
Method
NCBI GI
                   g558364
                   184
BLAST score
                   4.0e-99
E value
                   328
Match length
                   90
% identity
                  Z.mays mRNA for ADP-glucose pyrophosphorylase
NCBI Description
                   306328
Seq. No.
                   uC-zmflb73076f02b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q231683
                   286
BLAST score
                   1.0e-25
E value
                   72
Match length
% identity
                   68
                   CALNEXIN HOMOLOG PRECURSOR >gi 421825 pir_JN0597
NCBI Description
                   calnexin-like protein - Arabidopsis thaliana
                   >gi 16211 emb CAA79144 (Z18242) calnexin homolog
                   [Arabidopsis thaliana]
Seq. No.
                   306329
                   uC-zmflb73076f03b2
Seq. ID
                   BLASTX
Method
                   q3036805
NCBI GI
BLAST score
                   349
E value
                   6.0e-33
                   88
Match length
% identity
                   (ALO22373) thaumatin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   306330
```

43440

uC-zmflb73076h10b2

BLASTN

g444046



```
BLAST score
E value
                   2.0e-48
Match length
                   265
% identity
                   90
NCBI Description
                   Z.mays OBF1 mRNA for ocs-element binding factor
Seq. No.
                   306331
Seq. ID
                   uC-zmflb73077a02b2
Method
                   BLASTX
NCBI GI
                   q3600039
BLAST score
                   646
E value
                   1.0e-67
Match length
                   160
% identity
                   69
NCBI Description
                   (AF080119) similar to Schizosaccharomyces pombe isp4
                   protein (GB:D14061) [Arabidopsis thaliana]
Seq. No.
                   306332
Seq. ID
                   uC-zmflb73077a06b2
Method
                   BLASTX
NCBI GI
                   g893294
BLAST score
                   167
E value
                   2.0e-14
Match length
                   58
% identity
                   78
NCBI Description
                  (L43362) 4-coumarate:CoA ligase isoform 2 [Oryza sativa]
Seq. No.
                   306333
Seq. ID
                  uC-zmflb73077b12b2
Method
                  BLASTX
NCBI GI
                   g2511531
BLAST score
                   656
E value
                   8.0e-69
Match length
                   125
% identity
                   (AF008120) alpha tubulin 1 [Eleusine indica]
NCBI Description
                  >gi_3163944_emb_CAA06618 (AJ005598) alpha-tubulin 1
                   [Eleusine indica]
Seq. No.
                  306334
Seq. ID
                  uC-zmflb73077c01b2
Method
                  BLASTX
NCBI GI
                  g1498597
BLAST score
                  329
E value
                  8.0e-31
Match length
                  91
                  75
% identity
NCBI Description
                  (U66105) phospholipid transfer protein [Zea mays]
```

Seq. ID uC-zmflb73077c05a1

Method BLASTX NCBI GI g4204297 BLAST score 238 E value 5.0e-20 Match length 51 % identity 84

Method

NCBI GI

BLASTX

q4582488



```
NCBI Description (AC003027) ADK1 [Arabidopsis thaliana]
 Seq. No.
                   306336
 Seq. ID
                   uC-zmflb73077c07b2
Method
                   BLASTX
NCBI GI
                   g2924247
BLAST score
                   182
E value
                   2.0e-13
Match length
                   66
 % identity
                   61
NCBI Description
                  (Y07782) expansin [Oryza sativa]
 Seq. No.
                   306337
 Seq. ID
                   uC-zmflb73077d04a1
Method
                   BLASTN
NCBI GI
                   g1498052
BLAST score
                   85
E value
                   4.0e-40
Match length
                   114
 % identity
                   92
NCBI Description Zea mays ribosomal protein S8 mRNA, complete cds
Seq. No.
                   306338
Seq. ID
                   uC-zmflb73077d04b2
Method
                   BLASTX
NCBI GI
                   g1498053
BLAST score
                   414
E value
                   1.0e-40
Match length
                   97
% identity
                   84
NCBI Description
                   (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                   306339
Seq. ID
                   uC-zmflb73077d09b2
Method
                   BLASTX
NCBI GI
                   g1498597
BLAST score
                   394
E value
                   2.0e-38
Match length
                   96
% identity
                   79
NCBI Description
                   (U66105) phospholipid transfer protein [Zea mays]
Seq. No.
                   306340
Seq. ID
                   uC-zmflb73077d11a1
Method
                   BLASTN
NCBI GI
                   g22144
BLAST score
                   49
E value
                   8.0e-19
Match length
                   89
% identity
                   89
NCBI Description
                   Maize anaerobically regulated gene for fructose
                   bisphosphate aldolase (EC 4.1.2.13)
Seq. No.
                   306341
Seq. ID
                   uC-zmflb73077e01b2
```

43442

```
BLAST score
                  190
E value
                  4.0e-17
Match length
                  77
% identity
                  70
NCBI Description
                  (AL021768) putative protein [Arabidopsis thaliana]
Seq. No.
                  306342
Seq. ID
                  uC-zmflb73077e05b2
Method
                  BLASTX
NCBI GI
                  g2494223
BLAST score
                  288
E value
                  7.0e-26
Match length
                  78
% identity
                  65
NCBI Description
                  DYNEIN LIGHT CHAIN 1, CYTOPLASMIC >gi 1209059 (U32855)
                  cytoplasmic dynein light chain 1 [Drosophila melanogaster]
                  >gi_4097197 (U48846) 8kd dynein light chain [Drosophila
                  melanogaster] >gi_4097201 (U48848) 8kd dynein light chain
                  [Drosophila melanogaster]
Seq. No.
                  306343
Seq. ID
                  uC-zmflb73077f03b2
Method
                  BLASTX
NCBI GI
                  g1710521
BLAST score
                  401
E value
                  5.0e-39
Match length
                  84
% identity
                  89
NCBI Description
                  60S RIBOSOMAL PROTEIN L24 >gi 1154859_emb_CAA63960
                  (X94296) L24 ribosomal protein [Hordeum vulgare]
Seq. No.
                  306344
```

Seq. ID uC-zmflb73077f07b2

Method BLASTX NCBI GI q533775 BLAST score 155 E value 1.0e-23 Match length 82

% identity 76

NCBI Description (U09989) H(+)-transporting ATPase [Zea mays]

Seq. No.

306345

Seq. ID uC-zmflb73078c09b2 Method BLASTX

NCBI GI q2984709 BLAST score 395 E value 2.0e-38 Match length 79 % identity

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No.

306346

Seq. ID uC-zmflb73078d02b2

Method BLASTX NCBI GI g2828012 BLAST score 250 E value 5.0e-41

Match length 113 % identity 76

NCBI Description (AF036891) starch synthase I precursor [Zea mays]

Seq. No. Seq. ID

306347

Method

uC-zmflb73078d04b2

NCBI GI

BLASTX g135417

BLAST score E value 266 5.0e-25

Match length % identity

123 62

NCBI Description

TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin alpha-3 chain - maize >gi_22150_emb_CAA44861_ (X63176) Alpha-tubulin #3 [Zea mays] >gi_485377 (M60171) alpha-3

tubulin [Zea mays]

Seq. No.

306348

Seq. ID

uC-zmflb73078e06b2

Method NCBI GI

BLASTN q2921303

BLAST score E value 131 1.0e-67

Match length % identity

215 90

NCBI Description

Zea mays herbicide safener binding protein (SBP1) mRNA,

complete cds

Seq. No.

306349

Seq. ID Method

uC-zmflb73078e08b2

Method NCBI GI BLASTX g115771

BLAST score

810

E value Match length

6.0e-87

% identity

154 99

NCBI Description

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) $>gi_82682$ _pir__S04453 chlorophyll

a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No.

306350

Seq. ID

uC-zmflb73078f06b2

Method NCBI GI

BLASTX g1170937

BLAST score

176

E value

9.0e-13

Match length % identity

35 89

NCBI Description

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No.

306351

Seq. ID

uC-zmflb73078g01b2



```
Method
                   BLASTN
NCBI GI
                   g22320
BLAST score
                   105
E value
                   3.0e-52
Match length
                   169
% identity
                   91
NCBI Description Maize H1 mRNA for H1 histone
Seq. No.
                   306352
Seq. ID
                  uC-zmflb73078h01b2
Method
                   BLASTX
                   g135417
                   421
                   2.0e-41
                   86
                   86
```

NCBI GI BLAST score E value Match length % identity

TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin alpha-3 chain - maize >gi_22150_emb_CAA44861_ (X63176) NCBI Description Alpha-tubulin #3 [Zea mays] >gi 485377 (M60171) alpha-3

tubulin [Zea mays]

Seq. No. 306353 Seq. ID uC-zmflb73078h02b2 Method BLASTX NCBI GI g3024018 BLAST score 291 E value 8.0e-27

Match length 73 % identity 78

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

3,5

initiation factor 5A [Zea mays]

Seq. No. 306354

Seq. ID uC-zmflb73079d06b2

Method BLASTX NCBI GI g1350680 BLAST score 217 E value 2.0e-17 Match length 77 % identity 53

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 306355

Seq. ID uC-zmflb73079f01b2

Method BLASTX NCBI GI g2130122 BLAST score 511 E value 5.0e-52 Match length 113 % identity 90

NCBI Description cyclin III - maize >gi 516548 (U10076) cyclin IIIZm [Zea

mays]

Seq. No. 306356

Seq. ID uC-zmflb73079g02b2

```
Method
                   BLASTX
NCBI GI
                   q3061308
BLAST score
                   184
E value
                   1.0e-13
Match length
                   94
% identity
                   37
NCBI Description
                  (AB006074) topoisomerase III [Mus musculus]
Seq. No.
                   306357
Seq. ID
                   uC-zmflb73079h01b2
Method
                   BLASTX
NCBI GI
                   g2146740
BLAST score
                   210
E value
                   8.0e-17
Match length
                   61
% identity
                   69
NCBI Description
                   inner mitochondrial membrane protein - Arabidopsis thaliana
                   >gi 603056 (U18126) inner mitochondrial membrane protein
                   [Arabidopsis thaliana]
Seq. No.
                   306358
Seq. ID
                  uC-zmflb73080a03b2
Method
                  BLASTN
NCBI GI
                   g575959
BLAST score
                   52
E value
                   2.0e-20
Match length
                   140
% identity
                   84
NCBI Description
                  Z.mays (Black Mexican Sweet) mRNA for
                   1-acyl-glycerol-3-phosphate acyltransferase (putative)
Seq. No.
                   306359
Seq. ID
                  uC-zmflb73080a05b2
Method
                  BLASTX
NCBI GI
                   q1705667
BLAST score
                  234
E value
                   7.0e-20
Match length
                  72
% identity
                   65
NCBI Description
                  SERINE CARBOXYPEPTIDASE-LIKE PRECURSOR
                  >gi 409582_dbj_BAA04511_ (D17587) serine
                  carboxypeptidase-like protein [Oryza sativa]
Seq. No.
                  306360
Seq. ID
                  uC-zmflb73080a08b2
Method
                  BLASTX
NCBI GI
                  q399940
BLAST score
                  342
E value
                  5.0e-32
```

Match length 105 % identity 65

NCBI Description MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR

> >gi 100004 pir S25005 heat shock protein, 70K - kidney bean >gi 22636 emb CAA47345 (X66874) 70 kDa heat shock

protein [Phaseolus vulgaris]

Seq. No. 306361

Method

NCBI GI

BLASTN

g1906603



```
Seq. ID
                   uC-zmflb73080a09a1
Method
                   BLASTN
NCBI GI
                   g575959
BLAST score
                   38
E value
                   3.0e-12
Match length
                   50
% identity
                   94
NCBI Description
                   Z.mays (Black Mexican Sweet) mRNA for
                   1-acyl-glycerol-3-phosphate acyltransferase (putative)
Seq. No.
                   306362
Seq. ID
                   uC-zmflb73080b04b2
Method
                   BLASTN
NCBI GI
                   g1181672
BLAST score
                   44
E value
                   1.0e-15
Match length
                   87
% identity
                   89
NCBI Description
                  Sorghum bicolor heat shock protein 70 cognate (hsc70) mRNA,
                   partial cds
                   306363
Seq. No.
Seq. ID
                   uC-zmflb73080c05b2
Method
                   BLASTX
NCBI GI
                   q3080420
BLAST score
                   147
E value
                   2.0e-12
Match length
                   76
% identity
                   61
NCBI Description
                   (AL022604) putative sugar transporter protein [Arabidopsis
                   thaliana]
                   306364
Seq. No.
Seq. ID
                  uC-zmflb73080d03b2
Method
                  BLASTX
NCBI GI
                   g2392895
BLAST score
                  164
E value
                   2.0e-11
Match length
                  52
% identity
                   58
NCBI Description
                   (AF017056) brassinosteroid insensitive 1 [Arabidopsis
                  thaliana]
Seq. No.
                  306365
Seq. ID
                  uC-zmflb73080d05b2
Method
                  BLASTX
NCBI GI
                  g1076678
BLAST score
                  293
E value
                  2.0e-26
Match length
                  71
% identity
                  85
NCBI Description
                  ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.
                  306366
Seq. ID
                  uC-zmflb73080d07b2
```

43447



BLAST score 200
E value 1.0e-108
Match length 432
% identity 91
NCRI Description 700 mag.

NCBI Description Zea mays ACCase gene, intron containing colonist1 and colonist2 retrotransposons and reverse transcriptase

pseudogene, complete sequence.
306367

Seq. No. 306367

Seq. ID uC-zmflb73080g10b2

Method BLASTX
NCBI GI g2462753
BLAST score 584
E value 2.0e-60
Match length 177
% identity 65

NCBI Description (AC002292) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 306368

Seq. ID uC-zmflb73080h01b2

Method BLASTX
NCBI GI g2961285
BLAST score 224
E value 2.0e-18
Match length 90
% identity 47

NCBI Description (Y16848) cinnamyl alcohol dehydrogenase-like protein,

subunit b [Arabidopsis thaliana]

Seq. No. 306369

Seq. ID uC-zmflb73080h02b2

Method BLASTX
NCBI GI g4467104
BLAST score 314
E value 6.0e-29
Match length 118
% identity 51

NCBI Description (AL035538) cinnamyl-alcohol dehydrogenase ELI3-1

[Arabidopsis thaliana]

Seq. No. 306370

Seq. ID uC-zmflb73080h11a1

Method BLASTN
NCBI GI g3004949
BLAST score 224
E value 1.0e-123
Match length 259
% identity 97

NCBI Description Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,

complete cds

Seq. No. 306371

Seq. ID uC-zmflb73082b02a2

Method BLASTN NCBI GI g559533

BLAST score 34



```
4.0e-10
E value
Match length
                   74
% identity
                   86
NCBI Description
                   Z.mays mRNA for defense-related protein
                   306372
Seq. No.
Seq. ID
                   uC-zmflb73083a03b2
Method
                   BLASTX
NCBI GI
                 - q585452
BLAST score
                   166
E value
                   7.0e-12
Match length
                   31
                   90
% identity
                   MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 59 KD ISOFORM
NCBI Description
                   PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME)
                   ({\tt NAD-ME}) \ \ {\tt >gi\_1076666\_pir\_A53318} \ \ {\tt malate\ dehydrogenase}
                   (decarboxylating) (EC 1.1.1.39) 59K chain precursor,
                   mitochondrial - potato >gi 438131 emb CAA80547 (Z23002)
                   precursor of the 59kDa subunit of the mitochondrial
                   NAD+-dependent malic enzyme [Solanum tuberosum]
                   306373
Seq. No.
Seq. ID
                   uC-zmflb73083c10a1
Method
                   BLASTX
NCBI GI
                   q3096920
BLAST score
                   277
E value
                   3.0e-25
Match length
                   65
                   72
% identity
NCBI Description
                   (AL023094) putative ketoacyl-CoA synthase [Arabidopsis
                   thaliana]
Seq. No.
                   306374
Seq. ID
                   uC-zmflb73083d08b2
Method
                   BLASTX
NCBI GI
                   g1644291
BLAST score
                   340
E value
                   5.0e-32
Match length
                   105
% identity
                   63
NCBI Description
                   (273295) receptor-like protein kinase [Catharanthus roseus]
Seq. No.
                   306375
Seq. ID
                   uC-zmflb73083e03b2
Method
                   BLASTX
NCBI GI
                   g4336747
BLAST score
                   154
E value
                   5.0e-10
                   135
Match length
% identity
                   31
NCBI Description
                  (AF104924) unconventional myosin heavy chain [Zea mays]
```

Seq. ID uC-zmflb73083f01b2

Method BLASTN MCBI GI g2737881

BLAST score 87



```
2.0e-41
E value
Match length
                  139
% identity
                  91
                  Saccharum sp. polyphenol oxidase mRNA, complete cds
NCBI Description
                  306377
Seq. No.
                  uC-zmflb73083f12b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2495256
BLAST score
                  360
E value
                  2.0e-34
Match length
                  97
                  72
% identity
                  STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 HOMOLOG (HMG
NCBI Description
                  PROTEIN) >gi_481756_pir__S39242 HMG protein - Madagascar
                  periwinkle >gi_433872_emb_CAA82251 (Z28410) HMG protein
                   [Catharanthus roseus]
                   306378
Seq. No.
Seq. ID
                  uC-zmf1b73083q06b2
Method
                  BLASTN
NCBI GI
                  q433040
BLAST score
                   116
E value
                   1.0e-58
                   179
Match length
% identity
                   92
                  Zea mays W-22 clone PREM-1A retroelement PREM-1, partial
NCBI Description
                   sequence
Seq. No.
                   306379
                   uC-zmflb73083h12b2
Seq. ID
Method
                   BLASTX
                   g1279640
NCBI GI
BLAST score
                   210
E value
                   7.0e-17
Match length
                   89
% identity
                   48
                  (X92204) NAM [Petunia x hybrida]
NCBI Description
                   306380
Seq. No.
                   uC-zmflb73084a05b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4512663
BLAST score
                   386
                   3.0e-37
E value
Match length
                   173
% identity
                   40
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4544470 gb AAD22377.1 AC006580 9 (AC006580)
```

hypothetical protein [Arabidopsis thaliana]

306381 Seq. No.

Seq. ID uC-zmflb73084c07b2

BLASTX Method NCBI GI g4262233 BLAST score 176 E value 1.0e-12

```
59
Match length
                  58
% identity
                  (AC006200) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  306382
Seq. No.
                  uC-zmflb73084d07b2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g413792
BLAST score
                  44
E value
                  9.0e-16
Match length
                  168
                  82
% identity
                  Cloning vector lambda EMBL3 SP6/T7, left arm
NCBI Description
Seq. No.
                   306383
                  uC-zmflb73084e09b2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2959781
BLAST score
                   151
E value
                   3.0e-10
Match length
                   48
                   65
% identity
NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]
                   306384
Seq. No.
                   uC-zmflb73085a07b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2984709
BLAST score
                   386
                   2.0e-37
E value
Match length
                   87
% identity
                   86
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                   306385
                   uC-zmflb73085b12a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4558553
BLAST score
                   278
                   7.0e-25
E value
Match length
                   102
                   57
% identity
                  (AC007138) putative potassium channel [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   306386
                   uC-zmflb73085c02a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g82307
BLAST score
                   201
E value
                   8.0e-16
```

43451

Myb oncoprotein homolog {clone 306} [Antirrhinum majus=snapdragons, J1:522, flowers, Peptide, 316 aa]

myb protein 306 - garden snapdragon >gi 256828_bbs_115017

106

49

Match length

NCBI Description

% identity



```
306387
Seq. No.
                  uC-zmflb73085c02b2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g282963
BLAST score
                  190
E value
                   1.0e-24
                  72
Match length
                   75
% identity
                  transforming protein (myb) homolog (clone myb.Ph2) - garden
NCBI Description
                   petunia >gi_20561_emb_CAA78387_ (Z13997) protein 2 [Petunia
                   x hybrida]
                   306388
Seq. No.
                   uC-zmflb73085c04b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4204265
BLAST score
                   162
                   1.0e-21
E value
Match length
                   87
% identity
                   57
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                   306389
                   uC-zmflb73085g02b2
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1944204
                   52
BLAST score
                   3.0e-20
E value
                   56
Match length
                   98
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                   306390
Seq. No.
                   uC-zmflb73085g08b2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1944204
BLAST score
                   56
                   1.0e-22
E value
Match length
                   68
                   96
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                   306391
Seq. No.
                   uC-zmflb73086a06b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2109457
BLAST score
                   256
                   3.0e-22
E value
                   76
Match length
                   66
% identity
                  (AF001501) chitinase [Oryza sativa]
NCBI Description
```

Seq. ID uC-zmflb73086b01b2

Method BLASTN NCBI GI g3821780 BLAST score 36



4.0e-11 E value Match length 36 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No.

306393 uC-zmflb73086e10b2 Seq. ID

Method BLASTX NCBI GI g1351136 BLAST score 901 E value 2.0e-97 Match length 168 % identity 99

SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) NCBI Description

>gi 514946 (L22296) UDP-glucose:D-fructose

2-glucosyl-transferase [Zea mays] >gi 533252 (L33244)

sucrose synthase 2 [Zea mays]

Seq. No. 306394

Seq. ID uC-zmflb73086g03b2

Method BLASTX NCBI GI g1362162 BLAST score 160 E value 7.0e-11 Match length 64 52 % identity

beta-glucosidase BGQ60 precursor - barley >gi 804656 NCBI Description

(L41869) beta-glucosidase [Hordeum vulgare]

306395 Seq. No.

Seq. ID uC-zmflb73086h09b2

BLASTX Method NCBI GI g2586087 BLAST score 220 E value 7.0e-18 Match length 117

% identity

NCBI Description (U72724) receptor kinase-like protein [Oryza sativa]

Seq. No.

Seq. ID uC-zmflb73086h10b2

Method BLASTX NCBI GI g123620 BLAST score 168 E value 5.0e-12 Match length 88 % identity 47

HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950 NCBI Description

heat shock cognate protein 70 - tomato

>gi 19258 emb CAA37971 (X54030) heat shock protein cognate

70 [Lycopersicon esculentum]

306397 Seq. No.

Seq. ID uC-zmflb73088a10b2

Method BLASTN NCBI GI g1698669 BLAST score 189



1.0e-102 E value 265 Match length % identity 94 Zea mays S-like RNase (kin1) mRNA, complete cds NCBI Description Seq. No. Seq. ID uC-zmflb73088b11b2 Method BLASTX NCBI GI q3193222 BLAST score 294 E value 1.0e-26 Match length 73 75 % identity (AF068687) malate dehydrogenase [Glycine max] NCBI Description 306399 Seq. No. Seq. ID uC-zmflb73088c01a1 Method BLASTX NCBI GI g4190952 BLAST score 242 1.0e-20 E value 79 Match length % identity 54 NCBI Description (AB022689) similar to hsr203J [Lycopersicon esculentum] Seq. No. 306400 Seq. ID uC-zmflb73088c08b2 Method BLASTN NCBI GI g2921303 BLAST score 245 E value 1.0e-135 Match length 373 92 % identity Zea mays herbicide safener binding protein (SBP1) mRNA, NCBI Description complete cds 306401 Seq. No. uC-zmflb73088d08b2 Seq. ID BLASTX Method NCBI GI g3786005 BLAST score 248 3.0e-21E value Match length 107 49 % identity (AC005499) putative phosphoethanolamine NCBI Description cytidylyltransferase [Arabidopsis thaliana]

rge" -

Seq. No. 306402

Seq. ID uC-zmflb73088g01b2

Method BLASTN
NCBI GI g3342801
BLAST score 53
E value 4.0e-21
Match length 192

Match length 192 % identity 83

NCBI Description Zea mays strain W64A x A182E putative cytosolic

6-phosphogluconate dehydrogenase (pdh2) mRNA, complete cds

43454

% identity

89

```
306403
Seq. No.
Seq. ID
                  uC-zmflb73088g03b2
Method
                  BLASTX
                  g135398
NCBI GI
BLAST score
                  441
E value
                  7.0e-44
Match length
                  92
                  90
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 82731 pir S15773 tubulin alpha-1
NCBI Description
                  chain - maize >gi_22147_emb_CAA33734_ (X15704)
                  alpha1-tubulin [Zea mays]
                  306404
Seq. No.
                  uC-zmflb73088h07b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3342802
BLAST score
                  611
E value
                  1.0e-63
Match length
                  123
% identity
                  98
                  (AF061838) putative cytosolic 6-phosphogluconate
NCBI Description
                  dehydrogenase [Zea mays]
Seq. No.
                  306405
                  uC-zmf1b73090f05a2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g128191
BLAST score
                  266
                  7.0e-26
E value
Match length
                  106
% identity
                  63
                  NITRATE REDUCTASE (NAD(P)H) >gi 66210 pir RDBHNP nitrate
NCBI Description
                  reductase (NAD(P)H) (EC 1.6.6.2) - barley
                  >gi 19065 emb CAA42739 (X60173) nitrate reductase
                  (NAD(P)H) [Hordeum vulgare]
Seq. No.
                  306406
Seq. ID
                  uC-zmflb73090f11a2
Method
                  BLASTN
NCBI GI
                  g416146
BLAST score
                  64
E value
                  9.0e-28
Match length
                  184
% identity
                  83
NCBI Description Zea mays beta-6 tubulin (tub6) gene and mRNA, complete cds
Seq. No.
                  306407
                  uC-zmflb73091e05b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  485
E value
                  8.0e-49
Match length
                  104
```

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]



```
306408
Seq. No.
                   uC-zmf1b73091e12b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4102839
                   499
BLAST score
                   2.0e-50
E value .
Match length
                   170
% identity
                   56
NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]
                   306409
Seq. No.
Seq. ID
                   uC-zmflb73091g03b2
                   BLASTX
Method
NCBI GI
                   q729882
                   229
BLAST score
                   6.0e-21
E value
Match length
                   99
                   59
% identity
                   CASEIN KINASE II BETA' CHAIN (CK II)
NCBI Description
                   >gi 1076300 pir S47968 casein kinase II (EC 2.7.1.-) beta
                   chain CKB2 - Arabidopsis thaliana >gi 467975 (U03984)
                   casein kinase II beta subunit CKB2 [Arabidopsis thaliana]
                   >gi_2245122_emb_CAB10544_ (Z97343) unnamed protein product
                   [Arabidopsis thaliana]
                   306410
Seq. No.
Seq. ID
                   uC-zmflb73091g06b2
Method
                   BLASTX
NCBI GI
                   g3668090
BLAST score
                   348
E value
                   9.0e-33
Match length
                   132
% identity
                   50
NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]
                   306411
Seq. No.
Seq. ID
                   uC-zmflb73091q09a1
Method
                   BLASTX
NCBI GI
                   g3287693
BLAST score
                   583
E value
                   2.0e-60
Match length
                   124
% identity
NCBI Description
                   (AC003979) Similar to LIM17 gene product gb 1653769 from
                   the genome of Synechocystis sp. gb D90916. [Arabidopsis
                   thaliana]
                   306412
Seq. No.
Seq. ID
                   uC-zmflb73092a01b2
```

Method

BLASTX

NCBI GI g4160292
BLAST score 237
E value 1.0e-19
Match length 58
% identity 67

NCBI Description (Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]



```
306413
Seq. No.
Seq. ID
                  uC-zmflb73092a07b2
Method
                  BLASTX
NCBI GI
                  g135411
BLAST score
                  480
E value
                  2.0e-48
Match length
                  101
% identity
                  89
                  TUBULIN ALPHA-2 CHAIN >gi 82732 pir S15772 tubulin alpha-2
NCBI Description
                  chain - maize >gi 22148 emb CAA33733 (X15704)
                  alpha2-tubulin [Zea mays]
                  306414
Seq. No.
Seq. ID
                  uC-zmflb73092a09b2
                  BLASTX
Method
NCBI GI
                  g137460
BLAST score
                  149
E value
                  9.0e-20
Match length
                  73
                  77
% identity
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                  SUBUNIT) >gi_67952_pir__PXPZV9 H+-transporting ATPase (EC
                  3.6.1.35), vacuolar, 69K chain - carrot >gi 167560 (J03769)
                  vacular H+-ATPase [Daucus carota]
                  306415
Seq. No.
Seq. ID
                  uC-zmflb73092c09b2
Method
                  BLASTX
NCBI GI
                  g3297813
BLAST score
                  229
E value
                  7.0e-19
Match length
                  157
% identity
                  38
NCBI Description
                  (AL031032) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  306416
                  uC-zmflb73092c10b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g531389
BLAST score
                  374
E value
                  7.0e-36
Match length
                  153
% identity
                  48
NCBI Description
                  (U12626) copia-like retrotransposon Hopscotch polyprotein
                  [Zea mays]
```

Seq. ID uC-zmflb73092d07a1

Method BLASTX NCBI GI q4375834 BLAST score 165 E value 1.0e-11 Match length 88 % identity

NCBI Description (AL021713) putative protein [Arabidopsis thaliana]

Seq. No. 306418

43457

Seq. ID

306423

uC-zmflb73093b04b2

3,



```
uC-zmflb73092e05b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2961343
BLAST score
                   166
E value
                   1.0e-11
                   57
Match length
% identity
                   60
NCBI Description
                   (AL022140) symbiosis-related like protein [Arabidopsis
                   thaliana] -
                   306419
Seq. No.
                   uC-zmflb73092f11b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g135417
BLAST score
                   255
E value
                   3.0e-30
                   79
Match length
% identity
                   85
                   TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin alpha-3 chain - maize >gi_22150_emb_CAA44861_ (X63176)
NCBI Description
                   Alpha-tubulin #3 [Zea mays] >gi 485377 (M60171) alpha-3
                   tubulin [Zea mays]
Seq. No.
                   306420
Seq. ID
                   uC-zmflb73092h01b2
Method
                   BLASTN
NCBI GI
                   q248338
BLAST score
                   51
E value
                   5.0e-20
Match length
                   138
                   85
% identity
NCBI Description polyubiquitin [maize, Genomic, 3439 nt]
Seq. No.
                   306421
Seq. ID
                   uC-zmflb73092h03b2
Method
                   BLASTX
NCBI GI
                   q1345587
BLAST score
                   165
E value
                   2.0e-12
Match length
                   81
% identity
                   60
                   14-3-3-LIKE PROTEIN GF14-6 >gi 998430 bbs_164522 (S77133)
NCBI Description
                   GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261
                   aa] [Zea mays]
                   306422
Seq. No.
Seq. ID
                   uC-zmf1b73093a08b2
                   BLASTX
Method
NCBI GI
                   g2984709
BLAST score
                   499
                   1.0e-50
E value
                   98
Match length
% identity
                   (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
```

Seq. ID

306428

uC-zmflb73093f11b2



```
Method
                  BLASTX
NCBI GI
                  g3868758
                  269
BLAST score
                  7.0e-24
E value
                  75
Match length
                  71
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                                     · .
Seq. No.
                  306424
                  uC-zmflb73093c06b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135411
BLAST score
                  150
E value
                  6.0e-22
Match length
                  66
% identity
                  88
                  TUBULIN ALPHA-2 CHAIN >gi 82732 pir S15772 tubulin alpha-2
NCBI Description
                  chain - maize >gi_22148_emb_CAA33733_ (X15704)
                  alpha2-tubulin [Zea mays]
                  306425
Seq. No.
Seq. ID
                  uC-zmflb73093c09b2
Method ~
                  BLASTX
NCBI GI
                  g2832623
BLAST score
                  264
E value
                   6.0e-23
Match length
                  82
% identity
                   62
                  (AL021711) protein kinase - like protein [Arabidopsis
NCBI Description
                  thaliana]
                   306426
Seq. No.
Seq. ID
                  uC-zmflb73093c10b2
                  BLASTX
Method
NCBI GI
                  g1168536
BLAST score
                  248
E value
                   2.0e-21
Match length
                  83
% identity
                   66
                  PHYTEPSIN PRECURSOR (ASPARTIC PROTEINASE)
NCBI Description
                  >gi_100567_pir__S19697 aspartic proteinase (EC 3.4.23.-)
                  precursor - barley >gi_18904_emb_CAA39602_ (X56136)
                  aspartic proteinase [Hordeum vulgare]
Seq. No.
                  306427
                  uC-zmf1b73093d02b2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3249105
BLAST score
                  194
                   4.0e-15
E value
Match length
                  89
% identity
                  (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                   (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
```



Method BLASTN
NCBI GI g22332
BLAST score 299
E value 1.0e-167
Match length 442
% identity 93

NCBI Description Z.mays HRGP gene

Seq. No.

306429 uC-zmflb73093f12a1

Seq. ID uC-zmflb
Method BLASTX
NCBI GI g4432832
BLAST score 159
E value 8.0e-11
Match length 50
% identity 64

NCBI Description (AC006283) similar to protein Htf9C [Arabidopsis thaliana]

Seq. No.

Seq. ID uC-zmflb73093g12b2

306430

Method BLASTX
NCBI GI g902584
BLAST score 710
E value 3.0e-75
Match length 152
% identity 15

NCBI Description (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea

mays]

Seq. No. 306431

Seq. ID uC-zmflb73093h10a1

Method BLASTN
NCBI GI g4185305
BLAST score 59
E value 1.0e-24
Match length 222
% identity 86

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 306432

Seq. ID uC-zmflb73094a08b2

Method BLASTX
NCBI GI g3702620
BLAST score 220
E value 6.0e-18
Match length 120
% identity 50

NCBI Description (Y17329) calnexin [Pisum sativum]

Seq. No. 306433

Seq. ID uC-zmflb73094a11b2

Method BLASTX NCBI GI g2341061 BLAST score 255



```
E value
                    3.0e-22
                    76
Match length
                    70
% identity
                    (U73459) translational initiation factor eIF-4A [Zea mays]
NCBI Description
                    306434
Seq. No.
Seq. ID
                    uC-zmflb73094b07a1
Method
                    BLASTX
NCBI GI
                    g3860247
BLAST score
                    150
                    2.0e-20
E value
                    70
Match length
                    74
% identity
NCBI Description
                    (AC005824) unknown protein [Arabidopsis thaliana]
                    306435
Seq. No.
Seq. ID
                    uC-zmflb73094b11b2
                    BLASTX
Method
NCBI GI
                    g401161
BLAST score
                    648
E value
                    5.0e-68
Match length
                    125
% identity
                    98
                    TUBULIN ALPHA-5 CHAIN >gi_322879_pir_ S28982 tubulin alpha-5 chain - maize >gi_22156_emb_CAA44862_ (X6317 alpha-tubulin #5 [Zea mays] >gi_450293 (L27815)
NCBI Description
                                                                        (X63177)
                    alpha-tubulin [Zea mays] >gi 45\overline{2}474 (U05258) alpha-tubulin
                    [Zea mays]
Seq. No.
                    306436
Seq. ID
                    uC-zmflb73094d07b2
Method
                    BLASTX
NCBI GI
                    g3309243
BLAST score
                    552
E value
                    1.0e-56
Match length
                    136
                    78
% identity
                    (AF073507) aconitase-iron regulated protein 1 [Citrus
NCBI Description
                    limon]
                    306437
Seq. No.
Seq. ID
                    uC-zmflb73094g02b2
Method
                    BLASTN
NCBI GI
                    g22346
BLAST score
                    114
                    4.0e-57
E value
Match length
                    250
                    87
% identity
NCBI Description
                    Maize In2-1 mRNA
Seq. No.
                    306438
Seq. ID
                    uC-zmflb73094g07b2
Method
                    BLASTX
NCBI GI
                    g3342800
BLAST score
                    227
E value
                    1.0e-18
Match length
                    62
```

NCBI Description

```
% identity
                  (AF061837) putative cytosolic 6-phosphogluconate
NCBI Description
                  dehydrogenase [Zea mays]
                  306439
Seq. No.
Seq. ID
                  uC-zmflb73094h05b2
                  BLASTX
Method
NCBI GI
                  g3096949
                  153
BLAST score
                  4.0e-21
E value
                  90
Match length
                  62
% identity
                   (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic
                  nucleotide-gated cation channel [Arabidopsis thaliana]
                  306440
Seq. No.
                  uC-zmflb73094h07b2
Seq. ID
Method
                  BLASTX
                   g3860277
NCBI GI
                  174
BLAST score
E value
                   1.0e-12
                  73
Match length
                   55
% identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >qi 4314394 gb AAD15604 (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
                   306441
Seq. No.
                   uC-zmflb73094h08b2
Seq. ID
                   BLASTX
Method
                   g3004950
NCBI GI
                   295
BLAST score
                   6.0e-27
E value
                   98
Match length
                   65
% identity
                  (AF037061) tonoplast intrinsic protein; ZmarPi [Zea mays]
NCBI Description
                   306442
Seq. No.
Seq. ID
                   uC-zmflb73095c05b1
                   BLASTX
Method
                   q4455350
NCBI GI
BLAST score
                   350
                   3.0e - 33
E value
Match length
                   115
% identity
                   61
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   306443
Seq. No.
Seq. ID
                   uC-zmflb73095c11b1
                   BLASTX
Method
                   q2104949
NCBI GI
                   174
BLAST score
E value
                   2.0e-12
Match length
                   40
% identity
```

-50

43462

(U96716) MAP kinase-like protein [Selaginella lepidophylla]



```
306444
Seq. No.
                   uC-zmflb73095d03a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4586249
                   190
BLAST score
                   2.0e-14
E value
Match length
                   106
% identity *
                   (AL049640) putative pollen surface protein [Arabidopsis
NCBI Description
                   thaliana]
                   306445
Seq. No.
                   uC-zmflb73095f04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244831
BLAST score
                   181
E value
                   9.0e-21
Match length
                   100
 % identity
                   64
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   306446
                   uC-zmflb73095h12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4580461
BLAST score
                   257
E value
                   2.0e-22
Match length
                   89
 % identity
                   56
 NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
                   306447
 Seq. No.
                   uC-zmflb73096c12b1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g135411
                   587
 BLAST score
                   6.0e-61
 E value
                   113
 Match length
                   96
 % identity
                   TUBULIN ALPHA-2 CHAIN >gi_82732_pir__S15772 tubulin alpha-2
 NCBI Description
                   chain - maize >gi_22148_emb_CAA33733 (X15704)
                   alpha2-tubulin [Zea mays]
                   306448
 Seq. No.
                   uC-zmflb73096d02b1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1703446
 BLAST score
                   186
                   2.0e-14
 E value
                   67
 Match length
 % identity
                   L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
 NCBI Description
                   >gi 1076292_pir__S53127 asparaginase - Arabidopsis thaliana
```

thaliana]

>gi 735918 emb CAA84367 (Z34884) asparaginase [Arabidopsis

% identity

67

```
306449
Seq. No.
Seq. ID
                  uC-zmflb73096e02b1
Method
                  BLASTN
NCBI GI
                  g1906603
BLAST score
                  49
                  2.0e-18
E value
Match length
                  109
% identity
                  86
                  Zea mays ACCase gene, intron containing colonist1 and
NCBI Description
                  colonist2 retrotransposons and reverse transcriptase
                  pseudogene, complete sequence
Seq. No.
                  306450
Seq. ID
                  uC-zmflb73096f06a1
Method
                  BLASTN
NCBI GI
                  g435542
BLAST score
                  101
E value
                  6.0e-50
Match length
                  161
% identity
                  91
NCBI Description
                  Z.mays mRNA for calmodulin
Seq. No.
                  306451
Seq. ID
                  uC-zmflb73096f08b1
Method
                  BLASTX
NCBI GI
                  q544242
BLAST score
                  188
E value
                   4.0e-26
Match length
                  110
% identity
                   65
                  ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
NCBI Description
                  >gi 485498 pir S33533 heat shock protein 90 homolog
                  precursor - barley >gi 22652 emb CAA48143 (X67960) GRP94
                  homologue [Hordeum vulgare]
Seq. No.
                   306452
Seq. ID
                  uC-zmflb73096q01b1
Method
                  BLASTX
NCBI GI
                  q4335745
                  198
BLAST score
E value
                   2.0e-15
                  99
Match length
                   42
% identity
                   (AC006284) putative hydrolase (contains an
NCBI Description
                  esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
                   306453
Seq. No.
Seq. ID
                  uC-zmflb73096g06b1
Method
                  BLASTX
NCBI GI
                  g2688830
BLAST score
                  329
E value
                  1.0e-30
Match length
                  100
```

NCBI Description (AF000952) putative sugar transporter [Prunus armeniaca]



```
306454
Seq. No.
Seq. ID
                  uC-zmflb73096h02b1
Method
                  BLASTX
NCBI GI
                  g3201623
BLAST score
                  186
E value
                  5.0e-14
Match length
                  109
% identity
                  41
NCBI Description
                  (AC004669) shaqqy-like kinase dzeta [Arabidopsis thaliana]
Seq. No.
                  306455
Seq. ID
                  uC-zmflb73096h04b1
Method
                  BLASTX
NCBI GI
                  g232033
BLAST score
                  166
E value
                  7.0e-12
Match length
                  71
% identity
                  56
NCBI Description
                  ELONGATION FACTOR 1 BETA' >gi_479830_pir_ S35501
                  translation elongation factor eEF-1 beta chain - wheat
                  >gi_218341_dbj_BAA02436_ (D13147) elongation factor 1 beta'
                  [Triticum aestivum]
Seq. No.
                  306456
Seq. ID
                  uC-zmflb73097a01b1
Method
                  BLASTX
NCBI GI
                  q3914431
BLAST score
                  142
E value
                  3.0e-14
Match length
                  69
% identity
                  65
NCBI Description
                  PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)
                   (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)
                  >gi_2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha
                  subunit [Spinacia oleracea]
Seq. No.
                  306457
Seq. ID
                  uC-zmflb73097b06b1
Method
                  BLASTX
NCBI GI
                  g2244750
BLAST score
                  348
E value
                  6.0e-33
Match length
                  123
% identity
                  61
NCBI Description
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                  >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
                  306458
Seq. No.
Seq. ID
                  uC-zmflb73097d01b1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1708236
BLAST score 212
E value 6.0e-17
Match length 81
% identity 59

NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)



(3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >qi 2129617 pir JC4567 hydroxymethylglutaryl-CoA synthase

(EC 4.1.3.5) - Arabidopsis thaliana

>gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA

synthase [Arabidopsis thaliana]

Seq. No. 306459

Seq. ID uC-zmflb73097d04b1

Method BLASTN NCBI GI q22292 BLAST score 60 E value 3.0e-25 231 Match length % identity 83

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 306460

Seq. ID uC-zmflb73097e08b1

Method BLASTX NCBI GI g2511574 BLAST score 267 E value 2.0e-23 Match length 65 % identity

(Y13176) multicatalytic endopeptidase [Arabidopsis NCBI Description

thaliana] >gi_3421075 (AF043520) 20S proteasome subunit

PAB1 [Arabidopsis thaliana]

Seq. No. 306461

uC-zmflb73097e11b1 Seq. ID

Method BLASTN NCBI GI q2331300 BLAST score 42 E value 2.0e-14 Match length 62 92 % identity

Zea mays ribosomal protein S4 type I (rps4) mRNA, complete NCBI Description

cds

306462 Seq. No.

Seq. ID uC-zmflb73097h12b1

BLASTX Method NCBI GI g3281853 BLAST score 182 E value 1.0e-13 Match length 43 % identity

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 306463

uC-zmflb73098a02b1 Seq. ID

Method BLASTX NCBI GI g730450 BLAST score 251 E value 7.0e-29

Match length

NCBI Description

% identity

70

70



```
Match length
                   91
% identity
                   60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
NCBI Description
                   >gi_480649_pir__S37134 cold-induced protein BnC24B - rape
>gi_398922_emb_CAA80343_ (Z22620) cold induced protein
                   (BnC24B) [Brassica napus]
Seq. No.
                   306464
Seq. ID
                   uC-zmflb73098a03b1
Method
                   BLASTX
NCBI GI
                   q1890575
BLAST score
                   154
                   3.0e-10
E value
Match length
                   54
% identity
                   61
NCBI Description
                   (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
                   vulgare]
Seq. No.
                   306465
Seq. ID
                   uC-zmflb73098a04b1
Method
                   BLASTN
NCBI GI
                   q22091
BLAST score
                   200
E value
                   1.0e-109
Match length
                   256
% identity
                   95
NCBI Description
                   Z.diploperennis gene for hydroxyproline-rich glycoprotein
Seq. No.
                   306466
Seq. ID
                   uC-zmflb73098a06b1
Method
                   BLASTN
NCBI GI
                   g1944204
BLAST score
                   33
E value
                   3.0e-09
Match length
                   45
% identity
                   93
                   Oryza sativa mRNA for RicMT, complete cds
NCBI Description
Seq. No.
                   306467
Seq. ID
                   uC-zmflb73098a12b1
Method
                   BLASTN
NCBI GI
                   g1944204
BLAST score
                   43
E value
                   5.0e-15
Match length
                   63
% identity
                   92
NCBI Description
                   Oryza sativa mRNA for RicMT, complete cds
Seq. No.
                   306468
Seq. ID
                   uC-zmflb73098b10b1
Method
                   BLASTX
NCBI GI
                   g82080
BLAST score
                   259
E value
                   2.0e-22
```

chlorophyll a/b-binding protein type III precursor - tomato



>gi_226872_prf__1609235A chlorophyll a/b binding protein
[Lycopersicon esculentum]

306469 Seq. No. uC-zmflb73098c08b1 Seq. ID BLASTX Method NCBI GI g2829915 BLAST score 262 9.0e-23 E value 153 Match length 12 % identity (AC002291) Hypothetical protein [Arabidopsis thaliana] NCBI Description 306470 Seq. No. uC-zmflb73098f01b1 Seq. ID BLASTX Method NCBI GI g417745 BLAST score 412 2.0e-40 E value 110 Match length 74 % identity ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE NCBI Description HYDROLASE) (ADOHCYASE) >gi 170773 (L11872) S-adenosyl-L-homocysteine hydrolase [Triticum aestivum] 306471 Seq. No. uC-zmflb73098f09b1 Seq. ID BLASTX Method NCBI GI g3822403 158 BLAST score 1.0e-10 E value 58 Match length % identity 48 NCBI Description (AF087932) hydroperoxide lyase [Arabidopsis thaliana] 306472 Seq. No. Seq. ID uC-zmflb73098g01b1 BLASTX Method NCBI GI g1181331 BLAST score 191 6.0e-15 E value 75 Match length % identity NCBI Description (X77569) calnexin [Zea mays] 306473 Seq. No. Seq. ID uC-zmflb73098g05b1 BLASTX Method NCBI GI g729671 199 BLAST score 1.0e-21 E value 88 Match length

NCBI Description HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]

% identity

Seq. No.

Seq. ID uC-zmflb73098g08b1

306474

43468



Method BLASTX
NCBI GI g3850588
BLAST score 364
E value 8.0e-35
Match length 125
% identity 51

NCBI Description (AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding

domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come

from this gene. [Arabidopsis thaliana]

Seq. No. 306475

Seq. ID uC-zmflb73098h01b1

Method BLASTX
NCBI GI g2914706
BLAST score 152
E value 2.0e-10
Match length 47
% identity 62

NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No. 306476

Seq. ID uC-zmflb73099a09b1

Method BLASTX
NCBI GI g3098603
BLAST score 268
E value 8.0e-24
Match length 91
% identity 58

NCBI Description (AF052191) katanin p60 subunit [Strongylocentrotus

purpuratus]

Seq. No. 306477

Seq. ID uC-zmflb73099a10b1

Method BLASTX
NCBI GI g4062934
BLAST score 272.
E value 5.0e-24
Match length 92
% identity 65

NCBI Description (D88272) formate dehydrogenase [Hordeum vulgare]

Seq. No. 306478

Seq. ID uC-zmflb73099a11b1

Method BLASTX
NCBI GI g113460
BLAST score 147
E value 2.0e-09
Match length 80
% identity 46

NCBI Description ADP, ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2)

(ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)

>gi_100851_pir__S16568 ADP,ATP carrier protein precursor maize >gi_22164_emb_CAA41812_ (X59086) adenine nucleotide

translocator [Zea mays]

Seq. No. 306479

Method

NCBI GI

BLAST score

BLASTX

g3395938 276

```
Seq. ID
                   uC-zmf1b73099e04b1
Method
                   BLASTX
NCBI GI
                   g3522938
BLAST score
                   252
E value
                   2.0e-21
Match length
                   151
% identity
                   42
NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]
Seq. No.
                   306480
Seq. ID
                   uC-zmflb73099e05b1
                   BLASTX
Method
NCBI GI
                   q4581508
BLAST score
                   393
E value
                   5.0e-38
Match length
                   118
% identity
                   64
NCBI Description
                   (AL049558) putative phosphatidylinositol-kinase
                    [Schizosaccharomyces pombe]
Seq. No.
                   306481
Seq. ID
                   uC-zmflb73099f10b1
Method
                   BLASTX
NCBI GI
                   g548770
BLAST score
                   162
E value
                   4.0e-11
Match length
                   119
% identity
                   37
                   60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
NCBI Description
                   ribosomal protein L3 [Oryza sativa]
Seq. No.
                   306482
Seq. ID
                   uC-zmflb73099g11b1
Method
                   BLASTX
NCBI GI
                   g2662343
BLAST score
                   409
E value
                   4.0e-60
Match length
                   152
% identity
                   82
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   306483
Seq. ID
                   uC-zmflb73099h09b1
Method
                   BLASTN
NCBI GI
                   g577824
BLAST score
                   97
                   3.0e-47
E value
Match length
                   224
% identity
                   87
NCBI Description Z.mays gene for H2B histone (gH2B3)
Seq. No.
                   306484
Seq. ID
                   uC-zmflb73100b01b1
```



2.0e-24 E value Match length 98 % identity 55 (AF076924) polypyrimidine tract-binding protein homolog NCBI Description [Arabidopsis thaliana] 306485 Seq. No. Seq. ID uC-zmflb73100f12b1 Method BLASTX NCBI GI g3599491 BLAST score 303 E value 1.0e-27 Match length 112 % identity 54 (AF085149) putative aminotransferase [Capsicum chinense] NCBI Description Seq. No. 306486 uC-zmflb73100h08b1 Seq. ID Method BLASTX NCBI GI q1723614 BLAST score 265 E value 4.0e-23 Match length 139 % identity NCBI Description RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE D (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) >gi_2121009_pir__S60168 hypothetical protein X - Zymomonas mobilis >gi_1143378_dbj_BAA09443_ (D50832) homologue of E. coli ClpB5' ORF [Zymomonas mobilis] Seq. No. 306487 Seq. ID uC-zmflb73101g07a1 Method BLASTN NCBI GI g22185 BLAST score 33 E value 3.0e-09 Match length 65 % identity Z.mays mRNA for b-32 protein, putative regulatory factor of NCBI Description zein expression (clone b-32.120) 306488 Seq. No. uC-zmflb73105f09a1 Seq. ID BLASTX Method NCBI GI q4336349 BLAST score 252

E value 9.0e-26 Match length 80 % identity

(AF082871) arsenate resistance protein ARS2 [Homo sapiens] NCBI Description

306489 Seq. No.

Seq. ID uC-zmflb73107a09a2

BLASTN Method NCBI GI g1220422 BLAST score 62 E value 8.0e-27



```
Match length
                    118
                    92
 % identity
                   Zea mays ubiquitin (MUB14) mRNA, 3' end
 NCBI Description
                    306490
 Seq. No.
                    uC-zmflb73107b01a2
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1498053
BLAST score
                    144
                    4.0e-09
 E value
 Match length
                    41
                    73
 % identity
                   (U64436) ribosomal protein S8 [Zea mays]
 NCBI Description
                    306491
 Seq. No.
 Seq. ID
                    uC-zmflb73108a08a1
                    BLASTN
 Method
 NCBI GI
                    g4416300
 BLAST score
                    41
 E value
                    9.0e-14
 Match length
                    77
 % identity
                    88
                    Zea mays chromosome 4 22 kDa zein-associated intercluster
 NCBI Description
                    region, complete sequence
                    306492
 Seq. No.
 Seq. ID
                    uC-zmflb73108e06a1
 Method
                    BLASTX
 NCBI GI
                    g4584542
 BLAST score
                    148
                    2.0e-09
 E value
 Match length
                    75
 % identity
 NCBI Description (AL049608) putative protein [Arabidopsis thaliana]
                    306493
 Seq. No.
 Seq. ID
                    uC-zmflb73108f09a1
 Method
                    BLASTX
 NCBI GI
                    g3461817
                    270
 BLAST score
 E value
                    7.0e-24
 Match length
                    59
 % identity
 NCBI Description
                   (AC004138) unknown protein [Arabidopsis thaliana]
                    306494
 Seq. No.
 Seq. ID
                    uC-zmflb73110d05a1
 Method
                    BLASTX
 NCBI GI
                    g4056507
 BLAST score
                    190
```

E value 2.0e-14 Match length 59 % identity

NCBI Description (AC005896) putative RNA binding protein [Arabidopsis

thaliana]

Seq. No. 306495



uC-zmflb73110g09a1 Seq. ID Method BLASTX NCBI GI g3702336 BLAST score 151 E value 6.0e-10 55 Match length % identity 51 NCBI Description (AC005397) putative 3-methyl-2-oxobutanoate hydroxy-methyl-transferase [Arabidopsis thaliana] Seq. No. 306496 uC-zmflb73111h01a1 Seq. ID Method BLASTN NCBI GI q168569 BLAST score 65 E value 3.0e-28 Match length 65 100 % identity NCBI Description Zea mays putative phenylalanine ammonia lyase mRNA, partial 306497 Seq. No. Seq. ID uC-zmflb73112f11a1 Method BLASTX NCBI GI q4582435 BLAST score 355 E value 1.0e-33 Match length 94 69 % identity NCBI Description (AC007196) putative selenium-binding protein [Arabidopsis thaliana] Seq. No. 306498 Seq. ID uC-zmflb73112h09a1 Method BLASTN NCBI GI g1895083 BLAST score 38 5.0e-12 E value Match length 42 98 % identity Zea mays golgi associated protein se-wap41 mRNA, complete NCBI Description 306499 Seq. No. Seq. ID uC-zmflb73113a02a2 Method BLASTN NCBI GI g4416300 BLAST score 82 8.0e-39 E value Match length 114 % identity 93

Zea mays chromosome 4 22 kDa zein-associated intercluster NCBI Description

region, complete sequence

Seq. No. 306500

Seq. ID uC-zmflb73113c03a2

Method BLASTX

E value

Match length

3.0e-09

77



```
NCBI GI
                  g1705812
                  145
BLAST score
                  4.0e-09
E value
                  44
Match length
                  61
% identity
                  ACIDIC CHITINASE PRECURSOR >gi_1150686_emb_CAA92207_
NCBI Description
                  (Z68123) acidic chitinase [Vitis vinifera]
                306501
Seq. No.
Seq. ID
                  uC-zmflb73113c09a2
                  BLASTX
Method
NCBI GI
                  g3935173
BLAST score
                  190
                  3.0e-14
E value
                  78
Match length
% identity
                  51
NCBI Description (AC004557) F17L21.16 [Arabidopsis thaliana]
                  306502
Seq. No.
Seq. ID
                  uC-zmflb73114a02b1
Method
                  BLASTX
NCBI GI
                  g1653897
BLAST score
                  160
E value
                  2.0e-11
Match length
                  63
                  46
% identity
                  (D90917) dihydroxyacid dehydratase [Synechocystis sp.]
NCBI Description
Seq. No.
                  306503
Seq. ID
                  uC-zmflb73114a07b1
                  BLASTX
Method
NCBI GI
                  g4512685
BLAST score
                  165
E value
                  1.0e-11
Match length
                   62
                   47
% identity
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4559325 gb AAD22987.1 AC007087 6 (AC007087)
                  hypothetical protein [Arabidopsis thaliana]
                  306504
Seq. No.
Seq. ID
                  uC-zmflb73114b03a2
Method
                  BLASTN
NCBI GI
                  g1698669
BLAST score
                  48
E value
                  2.0e-18
Match length
                  52
% identity
                   98
NCBI Description Zea mays S-like RNase (kin1) mRNA, complete cds
                   306505
Seq. No.
Seq. ID
                  uC-zmflb73114b03b1
Method
                  BLASTX
NCBI GI
                  q129591
BLAST score
                  143
```



% identity PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226 NCBI Description (X16099) phenylalanine ammonia-Tyase [Oryza sativa] Seq. No. 306506 Seq. ID uC-zmflb73114b05a2 BLASTN Method NCBI GI q168541 BLAST score 36 E value 1.0e-10 Match length 48 % identity 94 NCBI Description Zea mays putative proteolipid subunit of vacuolar H+ ATPase mRNA, partial cds 306507 Seq. No. Seq. ID uC-zmflb73114b10b1 Method BLASTN NCBI GI g2921303 BLAST score 220 E value 1.0e-120 Match length 328 92 % identity NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA, complete cds Seq. No. 306508 Seq. ID uC-zmflb73114c01b1 Method BLASTX NCBI GI q2499708 BLAST score 198 E value 2.0e-15 Match length 82 % identity 50 NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1020409_dbj_BAA11135 (D73410) phospholipase D [Zea mays] Seq. No. 306509 Seq. ID uC-zmflb73114c03b1 Method BLASTN NCBI GI g22292 BLAST score 36 E value 5.0e-11 Match length 60 % identity 90 NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 306510

Seq. ID uC-zmflb73114c10b1

Method BLASTX NCBI GI g2829918 BLAST score 149 E value 4.0e-10 Match length 60 % identity 57



NCBI Description (AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No. 306511

Seq. ID uC-zmflb73114d10b1

Method BLASTN
NCBI GI g551482
BLAST score 33
E value 4.0e-09
Match length 89
% identity 84

NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA,

complete cds

Seq. No. 306512

Seq. ID uC-zmflb73114d12b1

Method BLASTX
NCBI GI g1621268
BLAST score 183
E value 1.0e-13
Match length 74
% identity 54

NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 306513

Seq. ID uC-zmflb73114e04a2

Method BLASTX
NCBI GI g2842531
BLAST score 201
E value 1.0e-15
Match length 60
% identity 63

NCBI Description (AB004291) gamma-subunit of enolase [Gallus gallus]

Seq. No. 306514

Seq. ID uC-zmflb73114f09b1

Method BLASTX
NCBI GI g1076791
BLAST score 148
E value 1.0e-09
Match length 60
% identity 55

NCBI Description calcium-binding protein - maize >gi_2119370_pir__S58170

Calreticulin precursor - maize >gi 577612 emb CAA86728_

(Z46772) calcium-binding protein [Zea mays]

>gi_927572_emb_CAA61939_ (X89813) Calreticulin precursor
[Zea mays] >gi_1587033_prf__2205314A calreticulin [Zea

mays]

Seq. No. 306515

Seq. ID uC-zmflb73114g07b1

Method BLASTN
NCBI GI g22336
BLAST score 70
E value 2.0e-31

Match length 102 % identity 94



NCBI Description Maize mRNA for an 18kDa heat shock protein

Seq. No. 306516

Seq. ID uC-zmflb73114g09b1

Method BLASTX
NCBI GI g129881
BLAST score 145
E value 3.0e-15
Match length 72

% identity 59

NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE

ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))

(PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)

(PPI-PFK) >qi 482294 pir A36094

pyrophosphate--fructose-6-phosphate 1-phosphotransferase

(EC 2.7.1.90) alpha chain - potato (cv. Kennebec)

>gi_169538 (M55190) pyrophosphate-fructose 6-phosphate
1-phosphotransferase alpha-subunit [Solanum tuberosum]

Seq. No. 306517

Seq. ID uC-zmflb73114g10b1

Method BLASTX
NCBI GI g951172
BLAST score 390
E value 6.0e-38
Match length 107
% identity 71

NCBI Description (U31521) MADS box protein [Zea mays]

>gi_1001934_emb_CAA56504_ (X80206) ZAG2 [Zea mays]

Seq. No. 306518

Seq. ID uC-zmflb73114h05b1

Method BLASTN
NCBI GI g2909845
BLAST score 77
E value 1.0e-35
Match length 161
% identity 88

NCBI Description Zea mays (S)-adenosyl-L-methionine:delta 24-sterol

methyltransferase mRNA, complete cds

Seq. No. 306519

Seq. ID uC-zmflb73114h09b1

Method BLASTX
NCBI GI g2529680
BLAST score 195
E value 2.0e-15
Match length 71
% identity 58

NCBI Description (AC002535) putative protein disulfide-isomerase precursor

[Arabidopsis thaliana]

Seq. No. 306520

Seq. ID uC-zmflb73116a05b2

Method BLASTX NCBI GI g4490323 BLAST score 312



E value 1.0e-28 Match length 114 % identity 51

NCBI Description (AJ131464) nitrate transporter [Arabidopsis thaliana]

Seq. No. 30652

Seq. ID uC-zmflb73116a07b2

Method BLASTX
NCBI GI g2511531
BLAST score 453
E value 4.0e-45
Match length 104
% identity 83

NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]

>gi 3163944 emb CAA06618 (AJ005598) alpha-tubulin 1

[Eleusine indica]

Seq. No. 306522

Seq. ID uC-zmflb73116f01b2

Method BLASTX
NCBI GI g283496
BLAST score 201
E value 2.0e-15
Match length 175
% identity 8

NCBI Description ubiquitin TU20 - Tetrahymena pyriformis (SGC5)

>gi_578547_emb_CAA43387_ (X61053) ubiquitin [Tetrahymena

pyriformis]

Seq. No. 306523

Seq. ID uC-zmflb73116f11b2

Method BLASTN
NCBI GI g22507
BLAST score 113
E value 8.0e-57
Match length 242
% identity 33

NCBI Description Maize (strain W64A) mRNA for cell wall glycoprotein

Seq. No. 306524

Seq. ID uC-zmflb73116g04b2

Method BLASTX
NCBI GI 94539452
BLAST score 145
E value 6.0e-09
Match length 52
% identity 63

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No. 306525

Seq. ID uC-zmflb73116h04b2

Method BLASTX
NCBI GI g4587615
BLAST score 148
E value 1.0e-09
Match length 51



% identity (AC006951) putative acyl-CoA synthetase [Arabidopsis NCBI Description thaliana] 306526 Seq. No. uC-zmflb73117a05b2 Seq. ID BLASTX Method NCBI GI g4379198

BLAST score 227 E value 5.0e-19 Match length 66 % identity 73

(V00730) alpha-crystallin [Mus musculus] NCBI Description

306527 Seq. No. uC-zmflb73117b05b2 Seq. ID Method BLASTX g4510426 NCBI GI BLAST score 222

E value 2.0e-18 Match length 72 65 % identity

NCBI Description (AC006929) hypothetical protein [Arabidopsis thaliana]

Seq. No. 306528

uC-zmflb73117c01b2 Seq. ID

Method BLASTX g135398 NCBI GI BLAST score 757 E value 1.0e-80 Match length 141 % identity 100

NCBI Description TUBULIN ALPHA-1 CHAIN >gi 82731 pir S15773 tubulin alpha-1

chain - maize >gi_22147_emb_CAA33734_ (X15704)

alphal-tubulin [Zea mays]

Seq. No. 306529

uC-zmflb73117c12b2 Seq. ID

Method BLASTX NCBI GI g115815 BLAST score 235 E value 8.0e-39 Match length 120 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll

a/b-binding protein precursor - maize

>gi_22355_emb_CAA39376_ (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays]

Seq. No. 306530

Seq. ID uC-zmflb73117d07b2

Method BLASTX NCBI GI g1173234 BLAST score 189 E value 3.0e-14 Match length 89

BLAST score

Match length

% identity

E value

118

157

94

7.0e-60

```
% identity
NCBI Description
                   40S RIBOSOMAL PROTEIN S25 >gi 481909 pir S40089 ribosomal
                   protein S25 - tomato >gi 43\overline{5}6\overline{7}9 emb \overline{CAA541}32 (X76714)
                   ribosomal protein S25 [Lycopersicon esculentum]
                   >gi 1584836 prf 2123431A ribosomal protein S25
                   [Lycopersicon esculentum]
Seq. No.
                   306531
Seq. ID
                   uC-zmflb73117d08a1
Method
                   BLASTX
NCBI GI
                   g2827561
BLAST score
                   317
E value
                   3.0e-29
Match length
                   88
% identity
NCBI Description
                   (AL021635) predicted protein [Arabidopsis thaliana]
                   >gi 3292809 emb CAA19799 (AL031018) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   306532
Seq. ID
                   uC-zmflb73117d11b2
Method
                   BLASTN
NCBI GI
                   q2062705
BLAST score
                   36
E value
                   3.0e-11
Match length
                   36
                   100
% identity
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
                   306533
Seq. No.
Seq. ID
                   uC-zmflb73117e08a1
Method
                   BLASTX
NCBI GI
                   g3790441
BLAST score
                   223
E value
                   2.0e-18
Match length
                   63
% identity
                   (AF030515) chaperonin 60 alpha subunit [Canavalia lineata]
NCBI Description
Seq. No.
                   306534
Seq. ID
                   uC-zmflb73117h01b2
Method
                   BLASTX
NCBI GI
                   g1839188
BLAST score
                   193
E value
                   9.0e-15
Match length
                   116
% identity
                   41
NCBI Description
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
Seq. No.
                   306535
Seq. ID
                   uC-zmflb73118a12b1
Method
                   BLASTN
NCBI GI
                   g4590325
```



NCBI Description Zea mays 101 kDa heat shock protein (HSP101) mRNA, partial 306536 Seq. No. Seq. ID uC-zmflb73118c07b1 Method BLASTX NCBI GI g3004950 BLAST score 236 E value 4.0e-20 49 Match length 96

NCBI Description (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]

Seq. No. 306537

% identity

Seq. ID uC-zmflb73118d08b1

Method BLASTX NCBI GI g3395431 BLAST score 146 E value 2.0e-09 72 Match length % identity 46

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

306538 Seq. No.

Seq. ID uC-zmflb73118f07b1

Method BLASTN NCBI GI g551482 BLAST score 154 E value 3.0e-81 306 Match length 92 % identity

NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA,

complete cds

Seq. No. 306539

Seq. ID uC-zmflb73118f10b1

Method BLASTX NCBI GI g479413 BLAST score 186 2.0e-20 E value Match length 98 61 % identity

NCBI Description myosin-like protein - Arabidopsis thaliana

306540 Seq. No.

Seq. ID uC-zmflb73118g09b1

Method BLASTX NCBI GI g1707007 BLAST score 362 E value 1.0e-34 Match length 111 57 % identity

NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No. 306541

Seq. ID uC-zmflb73118g12b1

Method BLASTX



```
q3785989
 NCBI GI
 BLAST score
                    438
 E value
                    2.0e-43
 Match length
                    107
 % identity
                    78
 NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
                    306542
 Seq. No.
                    uC-zmflb73118h03b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g123620
                    342
 BLAST score
                    3.0e-32
 E value
                    111
 Match length
  % identity
                    65
                    HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir__S14950
 NCBI Description
                    heat shock cognate protein 70 - tomato
                    >gi 19258_emb_CAA37971_ (X54030) heat shock protein cognate
                    70 [Lycopersicon esculentum]
                    306543
  Seq. No.
 Seq. ID
                    uC-zmflb73119b11b1
                    BLASTN
 Method
                    g1905943
 NCBI GI
 BLAST score
                    34
                    6.0e-10
 E value
Match length
                    74
  % identity
                    86
  NCBI Description Sorghum bicolor MADS box transcription factor SbMADS1 mRNA,
                    complete cds
                    306544
  Seq. No.
  Seq. ID
                    uC-zmflb73119c08b1
  Method
                    BLASTX
  NCBI GI
                    g4206306
  BLAST score
                    187
  E value
                    6.0e-19
  Match length
                    137
  % identity
  NCBI Description (AF049110) prpol [Zea mays]
                    306545
  Seq. No.
                    uC-zmflb73119e01b1
  Seq. ID
                    BLASTX
  Method
                    q1498120
  NCBI GI
  BLAST score
                    474
                    1.0e-47
  E value
  Match length
                    149
  % identity
```

NCBI Description (D85416) sulfate transporter [Arabidopsis thaliana]

Seq. No. 306546

Seq. ID uC-zmflb73119e03b1

Method BLASTX
NCBI GI g3600039
BLAST score 173
E value 2.0e-12



```
Match length
                  38
% identity
                  (AF080119) similar to Schizosaccharomyces pombe isp4
NCBI Description
                  protein (GB:D14061) [Arabidopsis thaliana]
                  306547
Seq. No.
Seq. ID
                  uC-zmflb73119f11b1
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  500
                  1.0e-50
E value
Match length
                  94
% identity
                  100
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                  306548
Seq. No.
Seq. ID
                  uC-zmflb73119h08b1
                  BLASTX
Method
NCBI GI
                  g2914700
BLAST score
                  591
E value
                  2.0e-61
Match length
                  151
                  79
% identity
NCBI Description
                  (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
                  thaliana]
                  306549
Seq. No.
Seq. ID
                  uC-zmf1b73120c10b1
Method
                  BLASTX
NCBI GI
                  g2181180
BLAST score
                  196
E value
                  5.0e-15
                  88
Match length
                  44
% identity
NCBI Description (Z84377) xylosidase [Aspergillus niger]
                  306550
Seq. No.
Seq. ID
                  uC-zmflb73120c12b1
Method
                  BLASTX
NCBI GI
                  g2500980
BLAST score
                  172
E value
                  3.0e-12
Match length
                  49
% identity
NCBI Description
                  GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS)
                  >gi 1076718 pir S51684 glutamate--tRNA ligase (EC
                  6.1.1.17) precursor - barley >gi 603849 emb CAA58505
                  (X83523) glutamate--tRNA ligase [Hordeum vulgare]
Seq. No.
                  306551
Seq. ID
                  uC-zmflb73120d04b1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4262167
BLAST score 500
E value 1.0e-50
Match length 157
% identity 61



NCBI Description (AC005275) putative LRR receptor-linked protein kinase [Arabidopsis thaliana]

Seq. No. 306552

Seq. ID uC-zmflb73120e08b1

Method BLASTX
NCBI GI g3421378
BLAST score 197
E value 2.0e-29
Match length 120
% identity 56

NCBI Description (AF080249) kinesin-like heavy chain [Arabidopsis thaliana]

Seq. No. 306553

Seq. ID uC-zmflb73120f12b1

Method BLASTX
NCBI GI g3860250
BLAST score 150
E value 4.0e-16
Match length 56
% identity 82

NCBI Description (AC005824) putative chloroplast prephenate dehydratase

[Arabidopsis thaliana]

Seq. No. 306554

Seq. ID uC-zmflb731215c10a1

Method BLASTX
NCBI GI g4056615
BLAST score 165
E value 1.0e-11
Match length 65
% identity 48

NCBI Description (AF067401) Scl1 protein [Oryza sativa]

Seq. No. 306555

Seq. ID uC-zmflb731215e06a1

Method BLASTX
NCBI GI g4539386
BLAST score 241
E value 2.0e-20
Match length 111
% identity 50

NCBI Description (AL035526) extensin-like protein [Arabidopsis thaliana]

Seq. No. 306556

Seq. ID uC-zmflb731215g12a1

Method BLASTN
NCBI GI g3132824
BLAST score 63
E value 6.0e-27
Match length 109
% identity 90

NCBI Description Zea mays putative cytosine-5 DNA methyltransferase (ZMET1)

gene, complete cds

Seq. No. 306557

Seq. ID uC-zmflb73121a03b2



```
Method
                  BLASTX
NCBI GI
                  g1465735
BLAST score
                  316
                   9.0e-30
E value
Match length
                   66
                  83
% identity
NCBI Description
                   (U44133) violaxanthin de-epoxidase precursor [Arabidopsis
                   thaliana] >gi 3063441 (AC003981) F22013.3 [Arabidopsis
                  thaliana]
                  306558
Seq. No.
Seq. ID
                  uC-zmflb73121a12a1
Method
                  BLASTN
NCBI GI
                  g2232016
BLAST score
                  189
E value
                  1.0e-102
Match length
                  330
                   92
% identity
NCBI Description Zea mays viviparous-14 (vp14) mRNA, complete cds
                  306559
Seq. No.
Seq. ID
                  uC-zmflb73121g06a1
Method
                  BLASTX
NCBI GI
                  g2224915
BLAST score
                  194
E value
                  2.0e-15
Match length
                  70
% identity
                  53
NCBI Description
                  (U95968) beta-expansin [Oryza sativa]
                  306560
Seq. No.
Seq. ID
                  uC-zmflb73122a03a1
Method
                  BLASTN
NCBI GI
                  q18035
BLAST score
                  48
                  2.0e-18
E value
Match length
                  96
% identity
                  88
NCBI Description
                  Z.mays chloroplast rbcL gene for ribulose bisphosphate
                  carboxylase
                  306561
Seq. No.
Seq. ID
                  uC-zmflb73122a10b2
Method
                  BLASTX
NCBI GI
                  g2326229
BLAST score
                  284
E value
                  2.0e-25
Match length
                  78
                  76
% identity
NCBI Description
                  (AF012888) tousled-like kinase 1 [Zea mays]
Seq. No.
                  306562
```

Seq. ID uC-zmflb73122b12b2

Method BLASTX NCBI GI g2094888 BLAST score 163 E value 3.0e-11

```
Match length 69
% identity 43
NCBI Description Cucumber Basic Protein, A Blue Copper Protein
Seq. No. 306563
Seq. ID uC-zmflb73122f07b2
Method BLASTN
```

Method BLASIN
NCBI GI g3851527
BLAST score 53
E value 5.0e-21
Match length 93
% identity 89

NCBI Description Hordeum vulgare cultivar Bomi starch branching enzyme IIb (sbeIIb) gene, nuclear gene encoding plastid protein,

partial cds

Seq. No. 306564

Seq. ID uC-zmflb731230c05a1

Method BLASTX
NCBI GI g3668088
BLAST score 231
E value 3.0e-19
Match length 76
% identity 53

NCBI Description (AC004667) G9a-like protein [Arabidopsis thaliana]

Seq. No. 306565

Seq. ID uC-zmflb731234h10a1

Method BLASTX
NCBI GI g2982318
BLAST score 170
E value 4.0e-12
Match length 45
% identity 84

NCBI Description (AF051244) probable 60S ribosomal protein L15 [Picea

mariana]

Seq. No. 306566

Seq. ID uC-zmflb73124a03b1

Method BLASTN
NCBI GI g998429
BLAST score 76
E value 1.0e-34
Match length 122
% identity 98

NCBI Description GRF1=general regulatory factor [Zea mays, XL80, Genomic,

5348 nt]

Seq. No. 306567

Seq. ID uC-zmflb73124b09b1

Method BLASTX
NCBI GI g3927830
BLAST score 219
E value 2.0e-18
Match length 93
% identity 63

NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]



```
306568
Seq. No.
Seq. ID
                  uC-zmflb73124c02a1
Method
                  BLASTN
NCBI GI
                  g313135
BLAST score
                  187
E value
                  1.0e-101
                  288
Match length
                  99
% identity
NCBI Description Z.mays mRNA for porin
Seq. No.
                  306569
Seq. ID
                  uC-zmflb73124d11a1
Method
                  BLASTX
                  g1865677'
NCBI GI
BLAST score
                  571
E value
                  5.0e-59
Match length
                  123
% identity
                  86
NCBI Description
                  (Y08568) trehalose-6-phosphate synthase [Arabidopsis
                  thaliana]
Seq. No.
                  306570
Seq. ID
                  uC-zmflb73124e02a1
Method
                  BLASTX
NCBI GI
                  g1931645
BLAST score
                  145
E value
                  3.0e-09
Match length
                  47
% identity
                  64
NCBI Description (U95973) Fe(II) transporter isolog [Arabidopsis thaliana]
                  306571
Seq. No.
Seq. ID
                  uC-zmflb73124h07a1
Method
                  BLASTX
NCBI GI
                  q461498
BLAST score
                  152
E value
                  8.0e-10
Match length
                  37
% identity
                  78
NCBI Description
                  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
                  TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                  (ALAAT-2) >gi_320619_pir_s28429 alanine transaminase (EC
                  2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421)
                  alanine aminotransferase [Panicum miliaceum]
                  306572
Seq. ID
                  uC-zmflb73125a01b2
Method
                  BLASTX
                  g3063455
```

Seq. No.

NCBI GI BLAST score 399 E value 8.0e-39 Match length 101 % identity

NCBI Description (AC003981) F22013.17 [Arabidopsis thaliana]

Seq. No. 306573

Seq. ID

Method

NCBI GI



```
uC-zmflb73125a08b2
Seq. ID
                  BLASTX
Method
                  g2829889
NCBI GI
BLAST score
                  198
                  2.0e-15
E value
                  59
Match length
% identity
                  71
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  306574
                  uC-zmflb73125a11b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2792220
BLAST score
                  204
E value
                  6.0e-16
Match length
                  126
                  40
% identity
NCBI Description (AF032688) NBS-LRR type resistance protein [Oryza sativa]
Seq. No.
                  306575
                  uC-zmflb73125d03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1353193
BLAST score
                  173
E value
                  4.0e-13
Match length
                  64
                  64
% identity
                  O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268
NCBI Description
                  O-methyltransferase (EC 2.1.1.-) - maize >gi 404070
                  (L14063) O-methyltransferase [Zea mays]
                  306576
Seq. No.
                  uC-zmflb73125d03b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1353193
BLAST score
                  223
                  1.0e-18
E value
                  57
Match length
% identity
                  77
                  O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268
NCBI Description
                  O-methyltransferase (EC 2.1.1.-) - maize >gi 404070
                   (L14063) O-methyltransferase [Zea mays]
                  306577
Seq. No.
                  uC-zmflb73125h12a1
Seq. ID
Method
                  BLASTX
                  g4455177
NCBI GI
BLAST score
                  203
                  2.0e-16
E value
Match length
                  77
% identity
                  66
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
                  306578
Seq. No.
```

43488

uC-zmflb73126a07b1

BLASTX

g2662343



306580

306581

```
BLAST score
                   5.0e-28
E value
Match length
                   69
% identity
                   87
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   306579
Seq. No.
Seq. ID
                   uC-zmflb73126b02b1
Method
                   BLASTX
NCBI GI
                   g1101025
BLAST score
                   162
                   1.0e-11
E value
Match length
                   51
```

NCBI Description (U37794) alpha-tubulin [Eucalyptus globulus]

uC-zmflb73126c02b1 Seq. ID Method BLASTX NCBI GI g2160178 BLAST score 158 2.0e-10 E value Match length 81 40 % identity

% identity

Seq. No.

(AC000132) No definition line found [Arabidopsis thaliana] NCBI Description

Seq. No. uC-zmflb73126c07b1 Seq. ID Method BLASTX NCBI GI g417154 BLAST score 577 E value 1.0e-59 Match length 117

% identity 95 NCBI Description

HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

306582 Seq. No.

uC-zmflb73126f05a1 Seq. ID

Method BLASTX NCBI GI g1711615 296 BLAST score E value 1.0e-26 95 Match length % identity 65

HIGH AFFINITY SULPHATE TRANSPORTER 1 NCBI Description

>gi 1085847 pir S51763 high affinity sulphate transporter - Stylosanthes hamata >gi 607184 emb CAA57710 (X82255) high affinity sulphate transporter [Stylosanthes hamata]

306583 Seq. No.

Seq. ID uC-zmflb73126h10b1

BLASTX Method NCBI GI g135398 BLAST score 163



1.0e-11 E value Match length 45 71 % identity TUBULIN ALPHA-1 CHAIN >gi 82731 pir S15773 tubulin alpha-1 NCBI Description chain - maize >gi_22147_emb_CAA33734_ (X15704) alpha1-tubulin [Zea mays] 306584 Seq. No. Seq. ID uC-zmflb73127b12b2 Method BLASTX NCBI GI q4455192 BLAST score 234 2.0e-19 E value Match length 75 % identity NCBI Description (AL035440) putative protein [Arabidopsis thaliana] 306585 Seq. No. Seq. ID uC-zmflb73127c01b2 BLASTX Method g3548804 NCBI GI BLAST score 368 4.0e-35 E value 116 Match length 57 % identity NCBI Description (AC005313) unknown protein [Arabidopsis thaliana] Seq. No. 306586 uC-zmf1b73127e11b2 Seq. ID Method BLASTX NCBI GI g2459529 BLAST score 416 E value 1.0e-40 Match length 123 63 % identity NCBI Description (U65642) acyl-ACP thioesterase [Myristica fragrans] Seq. No. 306587 Seq. ID uC-zmflb73128a10b1 Method BLASTX NCBI GI g3912917 BLAST score 163 E value 2.0e-11 Match length 36 % identity 89 (AF001308) putative NAK-like ser/thr protein kinase NCBI Description [Arabidopsis thaliana] 306588 Seq. No. uC-zmflb73128e04b1Seq. ID BLASTX Method NCBI GI g3913653 BLAST score 446 E value 4.0e-44 Match length 86 95 % identity

43490

NCBI Description FERREDOXIN--NADP REDUCTASE, EMBRYO ISOZYME PRECURSOR (FNR)



>gi_1778686_dbj_BAA13417_ (D87547) precursor ferredoxin-NADP+ oxidoreductase [Oryza sativa]

 Seq. No.
 306589

 Seq. ID
 uC-zmflb73128e08b1

 Method
 BLASTX

 NCBI GI
 g116374

 BLAST score
 250

E value 2.0e-21
Match length 87
% identity 60

NCBI Description CHALCONE SYNTHASE WHP1 (NARINGENIN-CHALCONE SYNTHASE WHP1)

(WHITE POLLEN) >gi_66555_pir__SYZMW1 naringenin-chalcone synthase (EC 2.3.1.74) whp1 - maize >gi_22512_emb_CAA42763_

(X60204) chalcone synthase [Zea mays]

Seq. No. 306590

Seq. ID uC-zmflb73128g09b1

Method BLASTX
NCBI GI g1931652
BLAST score 207
E value 1.0e-16
Match length 57
% identity 70

NCBI Description (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog

[Arabidopsis thaliana]

Seq. No. 306591

Seq. ID uC-zmflb73129a10b1

Method BLASTN
NCBI GI g1864000
BLAST score 67
E value 2.0e-29
Match length 111
% identity 93

NCBI Description Maize DNA for Fd III, complete cds

Seq. No. 306592

Seq. ID uC-zmflb73129c05b1

Method BLASTX
NCBI GI g3219164
BLAST score 138
E value 7.0e-09
Match length 33
% identity 76

NCBI Description (AB006210) glutamine amidotransferase/cyclase [Arabidopsis

thaliana]

Seq. No. 306593

Seq. ID uC-zmflb73129f03b1

87

Method BLASTN
NCBI GI g168419
BLAST score 82
E value 4.0e-38
Match length 190

% identity

NCBI Description Maize (Z.mays) aldolase mRNA, complete cds



```
Seq. No.
                  306594
Seq. ID
                  uC-zmflb73129f06b1
Method
                  BLASTX
NCBI GI
                  g4371296
BLAST score
                  349
E value
                  4.0e-33
Match length
                  111
% identity
                  63
NCBI Description
                  (AC006260) putative receptor protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  306595
Seq. ID
                  uC-zmflb73130f03a1
Method
                  BLASTN
NCBI GI
                  g4160401
BLAST score
                  46
E value
                  9.0e-17
Match length
                  98
                  87
% identity
NCBI Description Zea mays eIF-5 gene, exons 1-2
Seq. No.
                  306596
Seq. ID
                  uC-zmflb73130g03b2
Method
                  BLASTX
NCBI GI
                  g4309698
BLAST score
                  307
E value
                  4.0e-28
Match length
                  117
% identity
                  59
NCBI Description
                  (AC006266) putative glucosyltransferase [Arabidopsis
                  thaliana]
Seq. No.
                  306597
Seq. ID
                  uC-zmflb73130g11b2
Method
                  BLASTX
NCBI GI
                  g2829881
BLAST score
                  160
E value
                  8.0e-11
Match length
                  116
% identity
                  37
NCBI Description
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  306598
Seq. ID
                  uC-zmflb73131c04b2
                  BLASTN
                  g596077
                  71
                  9.0e-32
```

Method NCBI GI BLAST score E value Match length 83 % identity 96

NCBI Description Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA,

complete cds

306599 Seq. No.

Seq. ID uC-zmflb73131c09a1

Method BLASTX



```
NCBI GI
                   g951427
BLAST score
                   282
E value
                   3.0e-25
Match length
                   111
% identity
                   49
NCBI Description
                   (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus
                   communis]
Seq. No.
                   306600
Seq. ID
                   uC-zmflb73131c10b2
Method
                   BLASTX
NCBI GI
                   g4567305
BLAST score
                   251
E value
                   1.0e-38
Match length
                   149
                   52
% identity
NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   306601
Seq. ID
                   uC-zmflb73131e01b2
Method
                   BLASTX
NCBI GI
                   g4455338
BLAST score
                   257
                   5.0e-22
E value
Match length
                   89
% identity
                   55
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                   306602
Seq. ID
                   uC-zmflb73131f01b2
Method
                   BLASTX
NCBI GI
                   g3183368
BLAST score
                   321
E value
                   9.0e-30
Match length
                   85
% identity
                   69
NCBI Description
                   HYPOTHETICAL 64.0 KD PROTEIN C20G4.05C IN CHROMOSOME I
                   >gi 2330761 emb CAB11255 (Z98600) hypothetical protein
                   [Schizosaccharomyces pombe]
Seq. No.
                   306603
Seq. ID
                   uC-zmflb73131f10a1
Method
                   BLASTN
NCBI GI
                   g20558
BLAST score
                   36
E value
                   8.0e-11
Match length
                   56
% identity
                   91
NCBI Description Petunia mRNA for heat shock protein hsp70
Seq. No.
                   306604
Seq. ID
                   uC-zmflb73131g05b2
Method
                   BLASTX
NCBI GI
                   g2505874
BLAST score
                   175
```

E value 8.0e-13

Match length 98



```
% identity
                  (Y12776) putative kinase [Arabidopsis thaliana]
NCBI Description
                  306605
Seq. No.
Seq. ID
                  uC-zmflb73131h04b2
Method
                  BLASTX
                  q1621483
NCBI GI
BLAST score
                  168
                  2.0e-12
E value
                  57
Match length
% identity
                  60
                  (D85871) reverse transcriptase [Oryza sativa]
NCBI Description
                  306606
Seq. No.
                  uC-zmflb73131h08a1
Seq. ID
Method
                  BLASTN
                  q623203
NCBI GI
BLAST score
                  90
                  3.0e-43
E value
Match length
                  90
% identity
                  100
                  Zea mays (clone pCIB808) encoding maize nitrite reductase
NCBI Description
                  (NiR) cDNA to mRNA, partial cds
Seq. No.
                  306607
Seq. ID
                  uC-zmflb73131h09b2
Method
                  BLASTX
NCBI GI
                  g4455208
BLAST score
                  271
E value
                  2.0e-33
                  120
Match length
% identity
                  55
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  306608
Seq. No.
Seq. ID
                  uC-zmflb73132a03b1
Method
                  BLASTX
NCBI GI
                  q1667389
BLAST score
                  215
E value
                  1.0e-17
Match length
                  66
% identity
NCBI Description
                  (Y09238) 3-hydroxy-3-methylglutaryl coenzyme A reductase
                   [Zea mays]
                  306609
Seq. No.
Seq. ID
                  uC-zmflb73132a08b1
Method
                  BLASTX
NCBI GI
                  g4204283
BLAST score
                  244
                  3.0e-21
E value
Match length
                  67
% identity
                  67
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 306610

Seq. ID uC-zmflb73132b10b1



```
Method
                  BLASTN
NCBI GI
                  g416146
                  83
BLAST score
                  4.0e-39
E value
Match length
                  115
% identity
                  94
NCBI Description Zea mays beta-6 tubulin (tub6) gene and mRNA, complete cds
Seq. No.
                  306611
Seq. ID
                  uC-zmflb73132c03b1
Method
                  BLASTX
NCBI GI
                  g2282584
BLAST score
                  168
E value
                  3.0e-12
Match length
                  34
                  97
% identity
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]
Seq. No.
                  306612
Seq. ID
                  uC-zmflb73132d04b1
Method
                  BLASTX
NCBI GI
                  g135398
BLAST score
                  273
E value
                  2.0e-24
Match length
                  51
                  96
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 82731 pir S15773 tubulin alpha-1
NCBI Description
                  chain - maize >gi_22147_emb_CAA33734_ (X15704)
                  alpha1-tubulin [Zea mays]
Seq. No.
                  306613
Seq. ID
                  uC-zmflb73132g01b1
Method
                  BLASTX
NCBI GI
                  a466160
BLAST score
                  183
E value
                  2.0e-13
Match length
                  52
% identity
                  69
NCBI Description
                  HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
                  >gi 630771 pir S44903 ZK652.3 protein - Caenorhabditis
                  elegans >gi 289769 (L14429) putative [Caenorhabditis
                  elegans]
Seq. No.
                  306614
Seq. ID
                  uC-zmflb73132q03b1
Method
                  BLASTX
NCBI GI
                  q1418331
BLAST score
                  334
E value
                  4.0e-31
Match length
                  150
% identity
                  49
                  (X95909) receptor like protein kinase [Arabidopsis
NCBI Description
```

thaliana]

Seq. No.

306615

Seq. ID

uC-zmflb73132h03b1

Method BLASTX



```
NCBI GI
                    q3297819
 BLAST score
                    249
                    7.0e-22
 E value
 Match length
                    64
                    77
 % identity
 NCBI Description
                    (AL031032) protein kinase-like protein [Arabidopsis
                    thaliana]
Seq. No.
                    306616
 Seq. ID
                    uC-zmflb73134a03b1
 Method
                    BLASTX
 NCBI GI
                    q4510368
 BLAST score
                    364
 E value
                    1.0e-34
 Match length
                    109
 % identity
                    65
                    (AC007017) putative transcription factor E2F5 [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    306617
 Seq. ID
                    uC-zmflb73134a06b1
 Method
                    BLASTX
 NCBI GI
                    g2809249
 BLAST score
                    201
 E value
                    3.0e-17
 Match length
                    84
 % identity
                    46
 NCBI Description (AC002560) F21B7.18 [Arabidopsis thaliana]
 Seq. No.
                    306618
 Seq. ID
                    uC-zmflb73134e12b1
 Method
                    BLASTX
 NCBI GI
                    g3402722
 BLAST score
                    242
 E value
                    9.0e-21
 Match length
                    79
 % identity
                    58
 NCBI Description
                   (AC004261) CPDK-related protein [Arabidopsis thaliana]
 Seq. No.
                    306619
 Seq. ID
                    uC-zmflb73134g01b1
 Method
                    BLASTX
 NCBI GI
                    g1657621
 BLAST score
                    352
 E value
                    3.0e-33
                    92
 Match length
                    72
 % identity
 NCBI Description
                    (U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236)
                    putative acyl-coA dehydrogenase [Arabidopsis thaliana]
                    306620
 Seq. No.
 Seq. ID
                    uC-zmflb73134g04a2
 Method
                    BLASTX
```

Method BLASTX
NCBI GI g1172994
BLAST score 210
E value 3.0e-17
Match length 53



% identity NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L22 >gi_1363592_pir__S58591 ribosomal protein L22 - maize chloroplast >gi 902261 emb CAA60325 (X86563) ribosomal protein L22 [Zea mays] Seq. No. 306621 uC-zmflb73134h03b1 Seq. ID Method BLASTX NCBI GI g3087888 BLAST score 240 E value 2.0e-20 98 Match length 49 % identity NCBI Description (X94302) hexokinase [Solanum tuberosum] Seq. No. 306622 Seq. ID uC-zmflb73135c06b2 Method BLASTX NCBI GI g399940 BLAST score 553 E value 7.0e-57 Match length 127 % identity 83 NCBI Description MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR >gi 100004 pir S25005 heat shock protein, 70K - kidney bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock protein [Phaseolus vulgaris] Seq. No. 306623 Seq. ID uC-zmflb73135d11b2 Method BLASTX NCBI GI g1262906 BLAST score 258 E value 1.0e-22 Match length 80 % identity NCBI Description (U51569) chalcone synthase [Sorghum bicolor] Seq. No. 306624 Seq. ID uC-zmflb73135e02b2 Method BLASTN NCBI GI q312180 BLAST score 34 E value 2.0e-09 Match length 66 % identity NCBI Description Z.mays GapC4 gene

Seq. No. 306625

Seq. ID uC-zmflb73135g12b2

Method BLASTX
NCBI GI g4559384
BLAST score 246
E value 7.0e-21
Match length 61
% identity 70



```
NCBI Description (AC006526) unknown protein [Arabidopsis thaliana]
                    306626
  Seq. No.
  Seq. ID
                    uC-zmflb73136a05b1
 Method
                    BLASTX
 NCBI GI
                    g3928088
 BLAST score
                    197
 E value
                    8.0e-19
                    87
 Match length
  % identity
                    56
 NCBI Description (AC005770) putative peroxidase [Arabidopsis thaliana]
                    306627
 Seq. No.
 Seq. ID
                    uC-zmflb73136a07b1
 Method
                    BLASTX
 NCBI GI
                    g4160292
 BLAST score
                    212
 E value
                    7.0e-17
 Match length
                    41
 % identity
                    83
 NCBI Description
                   (Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]
Seq. No.
                    306628
 Seq. ID
                    uC-zmflb73136b06a1
 Method
                    BLASTN
 NCBI GI
                    g3004949
 BLAST score
                    169
 E value
                    3.0e-90
 Match length
                    214
                    95
 % identity
 NCBI Description
                    Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,
                    complete cds
                    306629
 Seq. No.
 Seq. ID
                    uC-zmflb73136d05b1
 Method
                    BLASTX
 NCBI GI
                    g2462763
 BLAST score
                    210
                    5.0e-25
 E value
 Match length
                    136
 % identity
                    60
 NCBI Description
                   (AC002292) Highly similar to auxin-induced protein
                    (aldo/keto reductase family) [Arabidopsis thaliana]
 Seq. No.
                    306630
 Seq. ID
                    uC-zmflb73136d12a1
 Method
                    BLASTX
 NCBI GI
                    g1172861
 BLAST score
                    146
 E value
                    8.0e-10
 Match length
                    50
 % identity
 NCBI Description
                    RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR
                    (RUBISCO LARGE SUBUNIT) >gi 1363613 pir S58560
```

Ribulose bisphosphate carboxylase [Zea mays]

ribulose-bisphosphate carboxylase ($\overline{\text{EC}}$ 4.1.1.39) large chain

- maize chloroplast >gi 18036 emb CAA78027 (Z11973)



>gi_902230_emb_CAA60294_ (X86563) rubisco large subunit
[Zea mays]

Seq. No. 306631

Seq. ID uC-zmflb73136e04b1

Method BLASTX
NCBI GI g2809251
BLAST score 152
Te value 7.0e-10
Match length 54
% identity 52

NCBI Description (AC002560) F21B7.20 [Arabidopsis thaliana]

Seq. No. 306632

Seq. ID uC-zmflb73136h01b1

Method BLASTN
NCBI GI g3132309
BLAST score 73
E value 2.0e-33
Match length 77

% identity 99

NCBI Description Zea mays mRNA for phosphoenolpyruvate carboxylase, complete

cds

Seq. No. 306633

Seq. ID uC-zmflb73136h02b1

Method BLASTX
NCBI GI g4220482
BLAST score 145
E value 3.0e-09
Match length 56
% identity 50

NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 306634

Seq. ID uC-zmflb73136h03b1

Method BLASTN
NCBI GI g551482
BLAST score 240
E value 1.0e-132
Match length 458
% identity 94

NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA,

complete cds

Seq. No. 306635

Seq. ID uC-zmflb73136h11b1

Method BLASTX
NCBI GI g3859548
BLAST score 596
E value 8.0e-62
Match length 122
% identity 91

NCBI Description (AF097182) protein phosphatase 2A catalytic subunit [Oryza

sativa]

Seq. No. 306636

Seq. No.

Seq. ID

Method



```
uC-zmflb73137a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115538
                  239
BLAST score
E value
                   6.0e-20
Match length
                  174
% identity
                  34
NCBI Description
                   (AB012116) UDP-glycose:flavonoid glycosyltransferase [Vigna
                  mungo]
Seq. No.
                  306637
Seq. ID
                  uC-zmflb73137a09a1
Method
                  BLASTN
NCBI GI
                  g1841501
BLAST score
                  49
E value
                  1.0e-18
Match length
                  262
% identity
                  82
NCBI Description
                  Z.mays mRNA for glutathione-dependent formaldehyde
                  dehydrogenase
Seq. No.
                  306638
Seq. ID
                  uC-zmflb73137c04b1
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
                  100
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  306639
Seq. ID
                  uC-zmflb73137g06b1
Method
                  BLASTX
NCBI GI
                  q3122071
BLAST score
                  153
E value
                  2.0e-22
Match length
                  80
                  70
% identity
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi_2130148_pir S66339 translation elongation factor eEF-1
                  alpha chain - maize >gi 1321656 dbj BAA08249 (D45408)
                  alpha subunit of tlanslation elongation factor 1 [Zea mays]
Seq. No.
                  306640
Seq. ID
                  uC-zmflb73137g12a1
Method
                  BLASTX
NCBI GI
                  g3482916
BLAST score
                  237
E value
                  6.0e-20
Match length
                  78
% identity
NCBI Description
                  (AC003970) Hypothetical protein [Arabidopsis thaliana]
```

uC-zmflb73137h03b1

306641

BLASTX

NCBI GI

E value

BLAST score

Match length

g3152609

6.0e-34

357

136



```
NCBI GI
                  g3395938
BLAST score
                  200
                  2.0e-15
E value
                  50
Match length
% identity
                  80
                  (AF076924) polypyrimidine tract-binding protein homolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  306642
Seq. ID
                  uC-zmflb73138b03a1
Method
                  BLASTX
NCBI GI
                  g2982243
BLAST score
                  165
E value
                  2.0e-11
Match length
                  44
                  66
% identity
NCBI Description
                  (AF051204) hypothetical protein [Picea mariana]
Seq. No.
                  306643
Seq. ID
                  uC-zmflb73138h10a1
Method
                  BLASTN
                                                                    ή¢.
NCBI GI
                  g498772
BLAST score
                  71
                  7.0e-32
E value
Match length
                  221
                  84
% identity
                  Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
NCBI Description
Seq. No.
                  306644
Seq. ID
                  uC-zmflb73138h11a1
Method
                  BLASTN
NCBI GI
                  g498772
BLAST score
                  79
                  1.0e-36
E value
Match length
                  158
% identity
                  88
NCBI Description
                  Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
Seq. No.
                  306645
Seq. ID
                  uC-zmflb73139a01b1
Method
                  BLASTX
NCBI GI
                  g135398
BLAST score
                  344
E value
                  1.0e-32
Match length
                  75
% identity
                  88
NCBI Description
                  TUBULIN ALPHA-1 CHAIN >gi 82731 pir S15773 tubulin alpha-1
                  chain - maize >gi 22147 emb CAA33734 (X15704)
                  alpha1-tubulin [Zea mays]
Seq. No.
                  306646
Seq. ID
                  uC-zmf1b73139a02b1
Method
                  BLASTX
```

```
% identity
NCBI Description
                   (AC004482) putative Su(var)3-9 protein [Arabidopsis
                  thaliana]
Seq. No.
                  306647
Seq. ID
                  uC-zmflb73139a08b1
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  333
E value
                  3.0e-31
Match length
                  71
% identity
                  90
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  306648
Seq. No.
Seq. ID
                  uC-zmflb73139b06b1
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  76
E value
                  1.0e-34
                  96 -
Match length
                  95
% identity
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
                  306649
Seq. No.
Seq. ID
                  uC-zmflb73139c05b1
Method
                  BLASTX
NCBI GI
                  g478753
BLAST score
                  197
                  8.0e-16
E value
Match length
                  44
% identity
                  84
NCBI Description tubulin alpha-4 chain - maize (fragment)
Seq. No.
                  306650
Seq. ID
                  uC-zmflb73139c09b1
Method
                  BLASTX
NCBI GI
                  g397396
BLAST score
                  189
E value
                  2.0e-14
Match length
                  53
% identity
                  70
NCBI Description (X66077) DNA-binding protein [Zea mays]
                  306651
Seq. No.
Seq. ID
                  uC-zmflb73139f08b1
Method
                  BLASTX
NCBI GI
                  g4079800
BLAST score
                  189
E value
                  7.0e-15
Match length
                  45
```

% identity NCBI Description

(AF052503) S-phase-specific ribosomal protein [Oryza sativa]

306652

80

Seq. No.



uC-zmflb73139g03b1 Seq. ID Method BLASTX NCBI GI g2499946 BLAST score 376 3.0e-36 E value Match length 116 % identity 68 URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE NCBI Description PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi 747980 (U22260) UMP synthase [Nicotiana tabacum] Seq. No. 306653 Seq. ID uC-zmflb73139g10b1 Method BLASTX NCBI GI g1890575 BLAST score 149 E value 1.0e-09 Match length 72 % identity 42 NCBI Description (X93174) xyloglucan endotransglycosylase (XET) [Hordeum vulgare] 306654 Seq. No. Seq. ID uC-zmflb73139h03b1 Method BLASTX NCBI GI g3193306 BLAST score 163 E value 7.0e-24Match length 115 % identity 57 NCBI Description (AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana] Seq. No. 306655 uC-zmflb73139h12b1 Seq. ID Method BLASTX NCBI GI g2739168 BLAST score 333 5.0e-31 E value Match length 113 % identity NCBI Description (AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum] Seq. No. 306656 Seq. ID uC-zmflb73140b06b1 Method BLASTX NCBI GI q4204232 BLAST score 151

E value 1.0e-09 Match length 64 % identity 53

NCBI Description (AF035378) MADS-box protein 1 [Lolium temulentum]

Seq. No. 306657

Seq. ID Method

```
uC-zmflb73140e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3695059
BLAST score
                  379
E value
                  2.0e-61
Match length
                  164
                  72
% identity
                   (AF064787) rac GTPase activating protein 1 [Lotus
NCBI Description
                  japonicus]
Seq. No.
                  306658
Seq. ID
                  uC-zmflb73141b04b1
Method
                  BLASTX
NCBI GI
                  g3717946
BLAST score
                  194
E value
                   6.0e-15
Match length
                  77
% identity
                  55
                  (AJ005901) vag1 [Arabidopsis thaliana]
NCBI Description
                   306659
Seq. No.
Seq. ID
                  uC-zmflb73142a01b1
Method
                  BLASTX
NCBI GI
                   q1169528
BLAST score
                  257
                  2.0e-28
E value
Match length
                  113
% identity
                   68
                  ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi 602253 (U17973)
                   enolase [Zea mays]
Seq. No.
                   306660
Seq. ID
                  uC-zmflb73142c03b1
Method
                   BLASTX
NCBI GI
                   q1778093
BLAST score
                   156
E value
                   3.0e-10
Match length
                   75
                   43
% identity
NCBI Description
                   (U64902) putative sugar transporter; member of major
                   facilitative superfamily; integral membrane protein [Beta
                   vulgaris]
Seq. No.
                   306661
Seq. ID
                   uC-zmf1b73142c04b1
Method
                   BLASTX
NCBI GI
                   g4586586
BLAST score
                   325
E value
                   4.0e-30
Match length
                   123
% identity
                   59
NCBI Description
                  (AB024997) bZIP DNA binding protein [Cicer arietinum]
Seq. No.
                   306662
```

43504

uC-zmflb73142f06b1

BLASTX

```
NCBI GI
                  g2511531
BLAST score
                  142
E value
                  5.0e-09
                  50
Match length
% identity
                  60
NCBI Description
                  (AF008120) alpha tubulin 1 [Eleusine indica]
                  >gi_3163944_emb_CAA06618 (AJ005598) alpha-tubulin 1
                  [Eleusine indica]
Seq. No.
                  306663
Seq. ID
                  uC-zmflb73142f10b1
Method
                  BLASTX
NCBI GI
                  g2627181
BLAST score
                  654
E value
                  5.0e-72
Match length
                  171
% identity
                  73
NCBI Description (D89619) cycloartenol synthase [Pisum sativum]
Seq. No.
                  306664
Seq. ID
                  uC-zmflb73142g05b1
Method
                  BLASTX
NCBI GI
                  g4512659
BLAST score
                  224
E value
                  3.0e-18
Match length
                  156
                  38
% identity
NCBI Description
                  (AC006931) putative protein kinase [Arabidopsis thaliana]
                  >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative
                  protein kinase [Arabidopsis thaliana]
                  306665
Seq. No.
Seq. ID
                  uC-zmflb73142g06b1
Method
                  BLASTX
NCBI GI
                  g3283996
BLAST score
                  229
E value
                  8.0e-19
Match length
                  158
% identity
NCBI Description
                  (AF072908) calcium-dependent protein kinase [Nicotiana
                  tabacum]
Seq. No.
                  306666
Seq. ID
                  uC-zmflb73142g07b1
Method
                  ELASTN
NCBI GI
                  g433043
BLAST score
                  33
E value
                  3.0e-09
Match length
                  45
% identity
                  93
```

NCBI Description Zea mays W-22 clone PREM-1E retroelement PREM-1, partial sequence

sequen

Seq. No. 306667

Seq. ID uC-zmflb73143a09b1

Method BLASTX NCBI GI g130186



BLAST score 326 E value 4.0e-30 Match length 167 % identity 37

NCBI Description PHYTOCHROME A >gi 82715 pir JQ0382 phytochrome A - maize

Seq. No. 306668

Seq. ID uC-zmflb73143b07b1

Method BLASTX
NCBI GI g2306981
BLAST score 524
E value 2.0e-53
Match length 130
% identity 75

NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No. 306669

Seq. ID uC-zmflb73143b11b1

Method BLASTX
NCBI GI g4099919
BLAST score 229
E value 5.0e-22
Match length 79
% identity 67

NCBI Description (U91981) pollen allergen homolog [Triticum aestivum]

Seq. No. 306670

Seq. ID uC-zmflb73143c03b1

Method BLASTX
NCBI GI g135411
BLAST score 206
E value 1.0e-16
Match length 51
% identity 69

NCBI Description TUBULIN ALPHA-2 CHAIN >qi 82732 pir S15772 tubulin alpha-2

chain - maize >gi_22148_emb_CAA33733_ (X15704)

alpha2-tubulin [Zea mays]

Seq. No. 306671

Seq. ID uC-zmflb73143c05b1

Method BLASTX
NCBI GI g1619602
BLAST score 274
E value 4.0e-24
Match length 74
% identity 72

NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 306672

Seq. ID uC-zmflb73143e02b1

Method BLASTX
NCBI GI g1262382
BLAST score 553
E value 7.0e-57
Match length 111
% identity 85

NCBI Description (X96749) myb7 [Oryza sativa]

43506

. . .



Seq. No. 306673

Seq. ID uC-zmflb73143f01b1

Method BLASTX
NCBI GI g4538968
BLAST score 202
E value 9.0e-16
Match length 78

NCBI Description (AL049488) putative protein kinase [Arabidopsis thaliana]

Seq. No. 306674

% identity

Seq. ID uC-zmflb73143f02b1

Method BLASTX
NCBI GI g135097
BLAST score 143
E value 4.0e-12
Match length 53
% identity 74

NCBI Description CYSTEINYL-TRNA SYNTHETASE (CYSTEINE--TRNA LIGASE) (CYSRS)

>gi_68549_pir__YYEC cysteine--tRNA ligase (EC 6.1.1.16) -

Escherichia coli >gi_41206_emb_CAA41983_ (X59293) cysteinyl-tRNA synthetase [Escherichia coli] >gi_145692 (M59381) transfer RNA-Cys synthetase [Escherichia coli] >gi 1773207 (U82664) cysteinyl-tRNA synthetase [Escherichia

coli] >gi_1786737 (AE000158) cysteine tRNA synthetase [Escherichia coli] >gi 227964_prf__1714234A Cys-tRNA

synthetase [Escherichia coli]

Seq. No. 306675

Seq. ID uC-zmflb73143f11b1

Method BLASTX
NCBI GI g2511531
BLAST score 225
E value 2.0e-18
Match length 90
% identity 57

NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]

>gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1

[Eleusine indica]

Seq. No. 306676

Seq. ID uC-zmflb73144b04b1

Method BLASTN
NCBI GI g22354
BLAST score 80
E value 6.0e-37
Match length 176

% identity 87
NCBI Description Zea mays L. mRNA for light-harvesting chlorophyll a/b

binding protein

Seq. No. 306677

Seq. ID uC-zmflb73144b09b1

Method BLASTX NCBI GI g2500107 BLAST score 152

Match length

NCBI Description

% identity

156

53



```
E value
                  4.0e-10
Match length
                  40
% identity
                  80
NCBI Description
                  DNA REPAIR PROTEIN RAD51 HOMOLOG >gi 1143810 (U22441)
                  LeRAD51 [Solanum lycopersicum]
Seq. No.
                  306678
Seq. ID
                  uC-zmflb73144c03b1
Method
                  BLASTX
NCBI GI
                  g2369714
BLAST score
                  148
E value
                  2.0e-09
Match length
                  114
                  36
% identity
NCBI Description
                  (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                  306679
Seq. ID
                  uC-zmflb73144c12b1
Method
                  BLASTX
NCBI GI
                  g2058280
BLAST score
                  203
E value
                  2.0e-16
Match length
                  53
% identity
                  75
NCBI Description
                  (X97381) atran3 [Arabidopsis thaliana]
                  306680
Seq. No.
Seq. ID
                  uC-zmflb73144g02b1
Method
                  BLASTN
                  g1698669
NCBI GI
BLAST score
                  64
E value
                  2.0e-27
Match length
                  128
% identity
                  88
NCBI Description
                  Zea mays S-like RNase (kin1) mRNA, complete cds
Seq. No.
                  306681
Seq. ID
                  uC-zmflb73145a03b1
Method
                  BLASTX
NCBI GI
                  g2618860
BLAST score
                  158
                  2.0e-10
E value
Match length
                  148
% identity
                  28
NCBI Description
                  (AF017113) HPr(Ser-P) phosphatase [Bacillus subtilis]
                  >gi 2636010 emb CAB15502 (Z99121) similar to
                  phosphoglycolate phosphatase [Bacillus subtilis]
Seq. No.
                  306682
Seq. ID
                  uC-zmflb73145a06b1
Method
                  BLASTX
NCBI GI
                  g1770060
BLAST score
                  408
E value
                  1.0e-39
```

(Z75208) hypothetical protein [Bacillus subtilis]





>gi 2635301 emb CAB14796 (Z99118) similar to hypothetical proteins [Bacillus subtilis]

306683 Seq. No.

Seq. ID uC-zmflb73145a08b1

Method BLASTX NCBI GI g1805445 BLAST score 330 E value 2.0e-30 Match length 175 % identity 38

NCBI Description (D50453) homologue of alkaline phosphatase synthesis

transcriptional regulatory protein PhoP of B. subtilis [Bacillus subtilis] >gi 2632676 emb CAB12183 (Z99106) similar to two-component response regulator [YclK]

[Bacillus subtilis]

306684 Seq. No.

Seq. ID uC-zmflb73145b05b1

Method BLASTX NCBI GI g728800 BLAST score 370 E value 2.0e-35 Match length 149 % identity 50

ACETOIN UTILIZATION ACUB PROTEIN >gi_481846_pir_S39644 acuB protein - Bacillus subtilis >gi_348051 (L17309) NCBI Description

acetoin utilization protein [Bacillus subtilis] >gi 2293317

(AF008220) acetoin catabolism protein AcuB [Bacillus subtilis] >gi_2635454_emb_CAB14948_ (Z99119) acetoin

dehydrogenase [Bacillus subtilis]

Seq. No. 306685

Seq. ID uC-zmflb73145b08b1

Method BLASTX NCBI GI g2293150 BLAST score 338 E value 1.0e-31 Match length 101 % identity 58

NCBI Description (AF008220) YtfD [Bacillus subtilis]

>gi_2635562_emb_CAB15056_ (Z99119) similar to N-acylamino

acid racemase [Bacillus subtilis]

Seq. No. 306686

Seq. ID uC-zmflb73145b09b1

Method BLASTX NCBI GI q2635806 BLAST score 238 E value 9.0e-20 Match length 168 % identity

NCBI Description (Z99120) similar to two-component sensor histidine kinase

[YvqC] [Bacillus subtilis] >gi_2832820_emb_CAA11744_

(AJ223978) YvqE protein [Bacillus subtilis]

Seq. No. 306687



```
Seq. ID
                  uC-zmflb73145b12b1
Method
                  BLASTX
NCBI GI
                  g2181975
                  179
BLAST score
E value
                  7.0e-13
Match length
                  119
% identity
                  35
                 (Z96072) arsA [Mycobacterium tuberculosis]
NCBI Description
                  306688
Seq. No.
Seq. ID
                  uC-zmflb73145c03b1
Method
                  BLASTX
NCBI GI
                  g2851477
BLAST score
                  193
E value
                  2.0e-14
Match length
                  65
% identity
NCBI Description
                  ARGINYL-TRNA SYNTHETASE (ARGININE--TRNA LIGASE) (ARGRS)
                  >gi 2224756 emb CAB09703 (Z97024) arginyl tRNA synthetase
                  [Bacillus subtilis] >gi_2636270_emb_CAB15761_ (Z99123)
                  arginyl-tRNA synthetase [Bacillus subtilis]
Seq. No.
                  306689
Seq. ID
                  uC-zmflb73145c05b1
Method
                  BLASTX
NCBI GI
                  g3257835
BLAST score
                  387
E value
                  3.0e-37
Match length
                  168
% identity
                  47
NCBI Description
                  (AP000006) 329aa long hypothetical dipeptide transport
                  ATP-binding protein dppD [Pyrococcus horikoshii]
Seq. No.
                  306690
Seq. ID
                  uC-zmflb73145c07b1
Method
                  BLASTX
NCBI GI
                  g732341
BLAST score
                  317
                  3.0e-34
E value
Match length
                  167
% identity
                  48
NCBI Description
                  THIAMIN-PHOSPHATE PYROPHOSPHORYLASE (TMP PYROPHOSPHORYLASE)
                  (TMP-PPASE) (THIAMIN-PHOSPHATE SYNTHASE)
                  >gi 629033 pir S39681 hypothetical protein - Bacillus
                  subtilis >gi 413950 emb CAA51582 (X73124) ipa-26d
                  [Bacillus subtilis] >gi 2636364 emb CAB15855 (Z99123)
                  thiamine-phosphate pyrophosphorylase [Bacillus subtilis]
Seq. No.
                  306691
Seq. ID
                  uC-zmflb73145d02b1
Method
                  BLASTN
NCBI GI
                  g1770523
BLAST score
                  36
```

E value 6.0e-11 Match length 40 97 % identity

NCBI Description H.sapiens U32 small nucleolar RNA gene



Seq. No. 306692

Seq. ID uC-zmflb73145d04b1

Method BLASTN NCBI GI g143513 BLAST score 79 E value 3.0e-36 Match length 251 % identity 89

B.cereus SASP-2 gene encoding a small acid-soluble spore NCBI Description

protein, complete cds

Seq. No. 306693

Seq. ID uC-zmflb73145d07b1

Method BLASTX NCBI GI g728799 BLAST score 363 E value 2.0e-34 Match length 85 % identity 73

ACETOIN UTILIZATION ACUA PROTEIN >gi_481847_pir__S39645 NCBI Description

acuA protein - Bacillus subtilis >gi_348052 (L17309)

acetoin utilization protein [Bacillus subtilis] >gi 2293318

(AF008220) acetoin catabolism protein AcuA [Bacillus subtilis] >gi_2635453_emb_CAB14947_ (Z99119) acetoin

dehydrogenase [Bacillus subtilis]

Seq. No. 306694

Seq. ID uC-zmflb73145e03b1

Method BLASTX NCBI GI g3123297 BLAST score 718 E value 5.0e-76 Match length 177 % identity 76

EXCINUCLEASE ABC SUBUNIT B (DINA PROTEIN) >gi 2618841 NCBI Description

(AF017113) excinuclease ABC subunit B [Bacillus subtilis] >gi_2636043_emb_CAB15534.1_ (Z99122) excinuclease ABC

(subunit B) [Bacillus subtilis]

Seq. No. 306695

Seq. ID uC-zmflb73145e05b1

Method BLASTX NCBI GI g2634032 BLAST score 753 E value 4.0e-80 Match length 172 % identity 84

NCBI Description (Z99112) nusA [Bacillus subtilis]

306696 Seq. No.

Seq. ID uC-zmflb73145e07b1

Method BLASTX NCBI GI g1075694 BLAST score 248 E value 4.0e-21 Match length 139



% identity 36

NCBI Description pheromone cAD1 binding protein precursor - Enterococcus

faecalis plasmid pAD1 >gi_388269 (L19532) traC [Plasmid

pAD1]

Seq. No. 306697

Seq. ID uC-zmflb73145e08b1

Method BLASTX
NCBI GI g131638
BLAST score 376
E value 3.0e-36
Match length 94
% identity 87

NCBI Description PHOSPHORIBOSYLAMINOIMIDAZOLECARBOXAMIDE FORMYLTRANSFERASE

(AICAR TRANSFORMYLASE) / IMP CYCLOHYDROLASE (INOSI**N**ICASE)

(IMP SYNTHETASE) (ATIC) >gi_66485_pir__DTBSPH purH

bifunctional enzyme - Bacillus subtilis >gi_143373 (J02732)

phosphoribosyl aminoimidazole carboxy formyl

formyltransferase/inosine monophosphate cyclohydrolase (PUR-H(J)) [Bacillus subtilis] >gi_2632966_emb_CAB12472_(Z99107) phosphoribosylaminoimidazole carboxy formyl

formyltransferase [Bacillus subtilis]

Seq. No. 306698

Seq. ID uC-zmflb73145e09b1

Method BLASTN
NCBI GI g4584087
BLAST score 163
E value 2.0e-86
Match length 229
% identity 93

NCBI Description Bacillus cereus bc297a, alkD genes and partial glyS gene

Seq. No. 306699

Seq. ID uC-zmflb73145e12b1

Method BLASTX
NCBI GI g2632436
BLAST score 154
E value 6.0e-10
Match length 63
% identity 43

NCBI Description (Z99104) similar to hypothetical proteins [Bacillus

subtilis]

Seq. No. 306700

Seq. ID uC-zmflb73145f02b1

Method BLASTX
NCBI GI g3334227
BLAST score 247
E value 5.0e-21
Match length 126
% identity 45

NCBI Description 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)

>gi 555806 (U11864) 4-hydroxyphenylpyruvate acid

dioxygenase [Streptomyces avermitilis]

Seq. No. 306701



129

87

Match length

% identity

```
uC-zmflb73145f04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q586801
BLAST score
                  346
E value
                  2.0e-32
Match length
                  117
% identity
                  61
                  HYPOTHETICAL 18.8 KD PROTEIN IN ECSC-PBPF INTERGENIC REGION
NCBI Description
                  >gi 538931 pir B40614 hypothetical protein X (pbpF 5'
                  region) - Bacillus subtilis >gi 304160 (L10630) product
                  unknown [Bacillus subtilis] >gi 2226228 emb CAA74516_
                  (Y14083) Hypothetical protein [Bacillus subtilis]
                  >gi 2633346 emb CAB12850 (Z99109) alternate gene name:
                  yixC; similar to hypothetical proteins from B. subtilis
                  [Bacillus subtilis]
Seq. No.
                  306702
Seq. ID
                  uC-zmflb73145f11b1
Method
                  BLASTX
NCBI GI
                  g2634164
BLAST score
                  489
                  4.0e-49
E value
Match length
                  204
                  46
% identity
NCBI Description (Z99113) yndJ [Bacillus subtilis]
                  306703
Seq. No.
Seq. ID
                  uC-zmflb73145g01b1
Method
                  BLASTX
NCBI GI
                  g2633966
BLAST score
                  197
                  5.0e-15
E value
Match length
                  143
                  31
% identity
                  (Z99112) chromosome segregation SMC protein homolg
NCBI Description
                   [Bacillus subtilis]
Seq. No.
                  306704
Seq. ID
                  uC-zmflb73145q07b1
                  BLASTX
Method
                  q1763712
NCBI GI
BLAST score
                  248
E value
                   6.0e-21
Match length
                  103
% identity
                  (Z83337) member of the SNF2 helicase family [Bacillus
NCBI Description
                  subtilis]
Seq. No.
                   306705
                   uC-zmflb73145g09b1
Seq. ID
Method
                  BLASTX
                   g729328
NCBI GI
BLAST score
                   562
E value
                  1.0e~57
```

NCBI Description GLUCOSE 1-DEHYDROGENASE >gi_98132_pir__A33528 glucose



1-dehydrogenase (EC 1.1.1.47) - Bacillus megaterium >gi_142975 (J04805) glucose dehydrogenase (EC 1.1.1.47) [Bacillus megaterium]

Seq. No. 306706

Seq. ID uC-zmflb73145g12b1

Method BLASTX
NCBI GI g2459737
BLAST score 158
E value 2.0e-10
Match length 116
% identity 35

NCBI Description (U95375) oxidoreductase [Haloferax volcanii]

Seq. No. 306707

Seq. ID uC-zmflb73145h01b1

Method BLASTX
NCBI GI g1881371
BLAST score 180
E value 4.0e-13
Match length 126
% identity 35

NCBI Description (AB001488) PROBABLE TRANSPORT PROTEIN, SIMILAR PRODUCT IN

MYCOBACTERIUM LEPRAE. [Bacillus subtilis]

>gi_2632865_emb_CAB12372_ (Z99106) similar to transporter
[Bacillus subtilis] >gi 2632878 emb CAB12384 (Z99107)

similar to transporter [Bacillus subtilis]

Seq. No. 306708

Seq. ID uC-zmflb73145h05b1

Method BLASTX
NCBI GI g2633552
BLAST score 331
E value 1.0e-30
Match length 93
% identity 68

NCBI Description (Z99110) alternate gene name: yidA; similar to 3-oxoacyl-

acyl-carrier protein reductase [Bacillus subtilis]

Seq. No. 306709

Seq. ID uC-zmflb73145h07b1

Method BLASTX
NCBI GI g2266421
BLAST score 242
E value 1.0e-32
Match length 121
% identity 60

NCBI Description (Y13917) yngK [Bacillus subtilis] >gi 2634211 emb CAB13711

(Z99113) alternate gene name: yotA; similar to hypothetical

proteins [Bacillus subtilis]

Seq. No. 306710

Seq. ID uC-zmflb73145h08b1

Method BLASTX
NCBI GI g131611
BLAST score 628
E value 2.0e-65

43514



Match length % identity 66

NCBI Description

PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (GARS) (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE

SYNTHETASE) >gi 68645 pir AJBSAG

phosphoribosylamine--glycine ligase (EC 6.3.4.13) -Bacillus subtilis >gi_143374 (J02732) phosphoribosyl glycinamide synthetase (PUR-D; gtg start codon) [Bacillus subtilis] >gi_2465561 (AF011544) phosphoribosylglycinamide

synthetase; GAR synthetase [Bacillus subtilis]

>gi_2632967_emb_CAB12473_ (Z99107) phosphoribosylglycinamide synthetase [Bacillus subtilis]

Seq. No. 306711

uC-zmflb73146a11a2 Seq. ID

Method BLASTX NCBI GI g1223579 BLAST score 211 E value 6.0e-17 Match length 69 % identity

NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]

Seq. No. 306712

Seq. ID uC-zmflb73146a11b1

Method BLASTX NCBI GI g1223579 BLAST score 303 E value 5.0e-30 Match length 130 % identity 60

NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]

Seq. No. 306713

Seq. ID uC-zmflb73146b07b1

Method BLASTX NCBI GI q3080391 BLAST score 414 E value 2.0e-40 Match length 97 % identity

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 306714

Seq. ID uC-zmflb73146b10b1

Method BLASTX NCBI GI q2894534 BLAST score 420 E value 6.0e-49 Match length 160 % identity 66

NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 306715

Seq. ID uC-zmflb73146b11b1

Method BLASTX NCBI GI q3319344



BLAST score 2.0e-11 E value Match length 140 % identity 40

NCBI Description (AF077407) contains similarity to UDP-glucoronosyl and UDP-glucosyl transferases (Pfam: UDPGT.hmm, score: 85.94)

[Arabidopsis thaliana]

Seq. No. 306716

Seq. ID uC-zmflb73146f06b1

Method BLASTX NCBI GI q4006827 BLAST score 176 E value 2.0e-13 Match length 62 % identity 58

(AC005970) subtilisin-like protease [Arabidopsis thaliana] NCBI Description

Seq. No.

306717

Seq. ID uC-zmflb73146h04a2 Method BLASTX

NCBI GI a3738302 BLAST score 230 E value 5.0e-19 Match length 73 % identity 67

NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana]

>gi_4249398 (AC006072) putative tubby protein [Arabidopsis

thaliana]

Seq. No. 306718

Seq. ID uC-zmflb73146h09a2

Method BLASTX NCBI GI q2911040 BLAST score 201 E value 3.0e-16 Match length 53 % identity 68

NCBI Description (AL021961) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 306719

Seq. ID uC-zmflb73147a09b1

Method BLASTX NCBI GI g4263777 BLAST score 412 E value 3.0e-40 Match length 162 % identity 50

NCBI Description (AC006068) putative serine carboxypeptidase II [Arabidopsis

thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative

serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No. 306720

uC-zmflb73147h08b1 Seq. ID

Method BLASTX NCBI GI g82696

Match length

% identity

45

96



```
BLAST score
E value
                   1.0e-30
Match length
                   83
% identity
                   81
NCBI Description
                  glycine-rich protein - maize >gi 22293 emb CAA43431
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                   306721
Seq. ID
                  uC-zmflb73148b09a1
Method
                  BLASTN
NCBI GI
                  g4240538
BLAST score
                  74
E value
                  5.0e-34
Match length
                  118
% identity
                  91
NCBI Description
                  Zea mays knotted class 1 homeodomain protein liqueless3
                   (1g3) mRNA, complete cds
Seq. No.
                  306722
Seq. ID
                  uC-zmflb73148c05a1
Method
                  BLASTN
NCBI GI
                  g722327
BLAST score
                  118
                  6.0e-60
E value
Match length
                  182
% identity
                  91
NCBI Description
                  Zea mays clone Zm-Rab2-B GTP binding protein (rab2) mRNA,
                  complete cds
Seq. No.
                  306723
Seq. ID
                  uC-zmflb73148g01b1
Method
                  BLASTX
                  g3646324
NCBI GI
BLAST score
                  158
E value
                  2.0e-10
Match length
                  48
% identity
                  69
NCBI Description
                  (AJ000761) MADS-box protein [Malus domestica]
Seq. No.
                  306724
Seq. ID
                  uC-zmflb73148h01b1
Method
                  BLASTX
NCBI GI
                  q2984709
BLAST score
                  474
E value
                  2.0e-47
Match length
                  90
% identity
                  99
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  306725
Seq. ID
                  uC-zmflb73149c07a1
Method
                  BLASTX
NCBI GI
                  q1084479
BLAST score
                  212
E value
                  6.0e-17
```





H+-transporting ATP synthase (EC 3.6.1.34) delta chain -NCBI Description maize (fragment) >gi 311237 emb CAA46804 (X66005) H(+)-transporting ATP synthase [Zea mays] Seq. No. 306726 Seq. ID uC-zmflb73149c11b1 Method BLASTX NCBI GI q2660675 BLAST score 342 E value 5.0e-32 Match length 156 50 % identity

(AC002342) similar to DNA-damage-inducible protein P NCBI Description [Arabidopsis thaliana]

Seq. No. 306727 uC-zmflb73149e04b1 Seq. ID Method BLASTX NCBI GI q2181180 BLAST score 284 3.0e-25 E value Match length 144 % identity 42

NCBI Description (Z84377) xylosidase [Aspergillus niger]

306728 Seq. No. Seq. ID uC-zmflb73149f07b1 BLASTN Method g3821780 NCBI GI BLAST score 36 E value 9.0e-11 Match length 47 % identity 66

NCBI Description Xenopus laevis cDNA clone 27A6-1

306729 Seq. No. Seq. ID uC-zmflb73149g10b1 Method BLASTX NCBI GI

g2257743 BLAST score 450 E value 9.0e-45 Match length 154 % identity 53

(U62020) lysine-sensitive aspartate kinase [Arabidopsis NCBI Description

thaliana]

306730 Seq. No.

Seq. ID uC-zmflb73149h01b1

BLASTX Method NCBI GI q3928084 BLAST score 346 E value 1.0e-32 Match length 154 50 % identity

(AC005770) retrotransposon-like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 306731 Seq. ID uC-zmflb73149h02b1 Method BLASTX NCBI GI q2501231 BLAST score 320 E value 1.0e-29 Match length 115 % identity 55 HYPOTHETICAL 38.1 KD PROTEIN >gi_99505_pir__\$24930 NCBI Description hypothetical protein - pink corydalis >gi 18258_emb_CAA45139_ (X63595) protein of unknown function [Corydalis sempervirens] >gi 444333 prf 1906382A pCSC71 protein [Corydalis sempervirens] Seq. No. 306732

Seq. No. 306/32 Seq. ID uC-zmflb73149h08b1 Method BLASTN

Method BLASTN
NCBI GI g312180
BLAST score 57
E value 3.0e-23
Match length 117
% identity 87

NCBI Description Z.mays GapC4 gene

Seq. No. 306733
Seq. ID uC-zmflb73150c06a1
Method BLASTX
NCBI GI g1730796
BLAST score 143
E value 3.0e-09
Match length 50
% identity 58

NCBI Description HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC

REGION >gi_2132760_pir__S60964 probable membrane protein

YNL163c - yeast (Saccharomyces cerevisiae)

>gi_1050790_emb_CAA63276_ (X92517) N1718 [Saccharomyces
cerevisiae] >gi_1302132_emb_CAA96050_ (Z71439) ORF YNL163c

[Saccharomyces cerevisiae]

Seq. No. 306734

Seq. ID uC-zmflb73150e02b1

Method BLASTX
NCBI GI g82696
BLAST score 237
E value 4.0e-20
Match length 71
% identity 75

NCBI Description glycine-rich protein - maize >gi 22293 emb CAA43431

(X61121) glycine-rich protein [Zea mays]

Seq. No. 306735

Seq. ID uC-zmflb73150e03b1

Method BLASTX
NCBI GI g82696
BLAST score 266
E value 2.0e-23
Match length 79

43519



% identity NCBI Description glycine-rich protein - maize >gi 22293 emb CAA43431 (X61121) glycine-rich protein [Zea mays] 306736 Seq. No. uC-zmflb73150f02b1 Seq. ID Method BLASTX g2668742

NCBI GI BLAST score 262 5.0e-23 E value 91 Match length 63 % identity

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 306737

uC-zmflb73150f03b1 Seq. ID

Method BLASTX NCBI GI q1170937 BLAST score 181 E value 9.0e-14 Match length 50 % identity 72

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

306738 Seq. No.

Seq. ID uC-zmflb73150f12b1

Method BLASTX NCBI GI q134598 BLAST score 419 E value 4.0e-41 Match length 95 % identity 83

NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)

Seq. No. 306739

Seq. ID uC-zmflb73150g11b1

Method BLASTX g4586021 NCBI GI BLAST score 204 5.0e-16 E value Match length 70 % identity 59

NCBI Description (AC007170) putative cytoplasmic aconitate hydratase

[Arabidopsis thaliana]

Seq. No. 306740

Seq. ID uC-zmflb73150h03b1

Method BLASTX NCBI GI q1174745 BLAST score 200 E value 1.0e-15 Match length 71 % identity 56

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)



>gi_1363523_pir__S53761 triose-phosphate isomerase (EC
5.3.1.1) precursor, chloroplast - rye
>gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase
[Secale cereale] >gi_1095494_prf__2109226B triosephosphate
isomerase [Secale cereale]

Seq. No. 306741

Seq. ID uC-zmflb73150h06b1

Method BLASTN
NCBI GI g22217
BLAST score 193
E value 1.0e-104
Match length 201
% identity 99

NCBI Description Z.mays c2 gene for chalcone synthase

Seq. No. 306742

Seq. ID uC-zmflb73151a08b1

Method BLASTN
NCBI GI g168436
BLAST score 103
E value 1.0e-50
Match length 123
% identity 96

NCBI Description Zea mays catalase (Cat3) gene, complete cds

Seq. No. 306743

Seq. ID uC-zmflb73151a10a2

Method BLASTN
NCBI GI g2623247
BLAST score 42
E value 3.0e-14
Match length 78
% identity 88

NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds

Seq. No. 306744

Seq. ID uC-zmflb73151c01b1

Method BLASTX
NCBI GI g135411
BLAST score 515
E value 8.0e-54
Match length 108
% identity 93

NCBI Description TUBULIN ALPHA-2 CHAIN >gi 82732 pir S15772 tubulin alpha-2

chain - maize >gi 22148 emb CAA33733 (X15704)

alpha2-tubulin [Zea mays]

Seq. No. 306745

Seq. ID uC-zmflb73151e06b1

Method BLASTN
NCBI GI g2924732
BLAST score 34
E value 2.0e-09
Match length 74
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



MUA2, complete sequence [Arabidopsis thaliana]

Seq. No. 306746 Seq. ID uC-zmflb73151e12b1 Method BLASTX NCBI GI q4454051 BLAST score 462 E value 3.0e-46 Match length 140 % identity 56 NCBI Description (AL035394) putative polygalacturonase [Arabidopsis thaliana] Seq. No. 306747 Seq. ID uC-zmflb73151f09b1 Method BLASTX NCBI GI q2062175 BLAST score 374 7.0e-36 E value Match length 122 % identity 61 NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana] 306748 Seq. No. uC-zmf1b73151g04a2 Seq. ID Method BLASTX NCBI GI q3176683 BLAST score 145 E value 4.0e-09 Match length 45 % identity NCBI Description (AC003671) F1707.12 [Arabidopsis thaliana] Seq. No. 306749 Seq. ID uC-zmflb73152d05b1 Method BLASTX NCBI GI g2462749 BLAST score 481 E value 2.0e-48 Match length 158 % identity 58 NCBI Description (AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana] Seq. No. 306750 uC-zmflb73152e03a1Seq. ID Method BLASTX NCBI GI g129707 BLAST score 161 E value 4.0e-11 Match length 69 % identity 61 NCBI Description PROTOCHLOROPHYLLIDE REDUCTASE (PCR) (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE) >gi 100550 pir S08406 protochlorophyllide reductase (EC

43522

1.3.1.33) - oat (fragment) >gi_829253_emb_CAA34913_ (X17067) protochlorophyllide reductase (314 AA) [Avena



sativa]

```
Seq. No.
                   306751
Seq. ID
                   uC-zmflb73152e05b1
Method
                   BLASTX
                   g2827086
NCBI GI
BLAST score
                   157
E value
                   9.0e-15
Match length
                   81
% identity
                   63
NCBI Description
                   (AF022778) DNA recombination are repair protein [Homo
                   sapiens] >gi_3328152 (AF073362) endo/exonuclease Mre11
                   [Homo sapiens]
Seq. No.
                   306752
Seq. ID
                   uC-zmflb73152g06b1
Method
                   BLASTX
NCBI GI
                   g2911068
BLAST score
                   384
E value
                   4.0e-37
                   73
Match length
% identity
                   88
                  (AL021960) G10-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   306753
                   uC-zmflb73153a01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g542175
BLAST score
                   148
E value
                   2.0e-09
Match length
                   93
                   39
% identity
                  endoxyloglucan transferase - wheat >gi 469511 dbj BAA03924
NCBI Description
                   (D16457) endo-xyloglucan transferase [Triticum aestivum]
Seq. No.
                   306754
                   uC-zmflb73153a02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076777
BLAST score
                   306
E value
                   3.0e-28
Match length
                   69
                   88
% identity
                  protein H2A - wheat >gi 536890 dbj BAA07277 (D38088)
NCBI Description
                   protein H2A [Triticum aestivum]
Seq. No.
                   306755
Seq. ID
                   uC-zmflb73153b01b1
Method
                   BLASTX
NCBI GI
                   g3885335
BLAST score
                   159
                   7.0e-11
E value
Match length
                   95
% identity
                   42
NCBI Description
                   (AC005623) ethylene-insensitive3-like protein [Arabidopsis
```

thaliana]



```
      Seq. No.
      306756

      Seq. ID
      uC-zmflb73153h09b1

      Method
      BLASTX

      NCBI GI
      g1800219

      BLAST score
      514

      E value
      1.0e-52
```

Match length 103 % identity 97

NCBI Description (U56731) phytochrome C [Sorghum bicolor]

Seq. No. 306757

Seq. ID uC-zmflb73154a05b2

Method BLASTN
NCBI GI g22223
BLAST score 210
E value 1.0e-115
Match length 267
% identity 98

NCBI Description Maize cab-1 gene for chlorophyll a/b-binding protein

Seq. No. 306758

Seq. ID uC-zmflb73154e01b2

Method BLASTX
NCBI GI g3810596
BLAST score 217
E value 5.0e-23
Match length 129
% identity 47

NCBI Description (AC005398) reverse-transcriptase-like protein [Arabidopsis

thaliana]

Seq. No. 306759

Seq. ID uC-zmflb73154e12b2

Method BLASTX
NCBI GI g3912919
BLAST score 566
E value 2.0e-58
Match length 139
% identity 78

NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No. 306760

Seq. ID uC-zmflb73154g03b2

Method BLASTX
NCBI GI 94204315
BLAST score 163
E value 3.0e-11
Match length 116
% identity 31

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No. 306761

Seq. ID uC-zmflb73155a02a1

Method BLASTN
NCBI GI g899607
BLAST score 117
E value 3.0e-59

Match length % identity 89 NCBI Description Zea mays polyubiquitin (MubC5) mRNA, complete cds Seq. No. 306762 Seq. ID uC-zmflb73155a05b2 Method BLASTX NCBI GI g3242403 BLAST score 191 E value 2.0e-14 Match length 110 % identity 37 NCBI Description (D83178) endonuclease [Hordeum vulgare] Seq. No. 306763 Seq. ID uC-zmflb73155b10a1 Method BLASTX NCBI GI g3851333 208

Method BLASTX
NCBI GI g3851333
BLAST score 208
E value 2.0e-16
Match length 40
% identity 90

NCBI Description (Y09302) putative MADS-domain transcription factor [Zea

nays]

Seq. No. 306764

Seq. ID uC-zmflb73155b12b2

Method BLASTX
NCBI GI g2244990
BLAST score 498
E value 2.0e-50
Match length 106
% identity 89

NCBI Description (Z97340) similarity to LIM homeobox protein -

Caenorhabditis [Arabidopsis thaliana]

Seq. No. 306765

Seq. ID uC-zmflb73155c12b2

Method BLASTX
NCBI GI g3549667
BLAST score 253
E value 9.0e-22
Match length 82
% identity 59

NCBI Description (AL031394) Arabidopsis dynamin-like protein ADL2

[Arabidopsis thaliana]

Seq. No. 306766

Seq. ID uC-zmflb73155d12a1

Method BLASTX
NCBI GI 94220523
BLAST score 231
E value 2.0e-19
Match length 73
% identity 68

NCBI Description (AL035356) putative alliin lyase [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                   uC-zmflb73155g10b2
Method
                   BLASTN
NCBI GI
                   g558364
BLAST score
                   62
E value
                   3.0e-26
Match length
                   128
% identity
NCBI Description Z.mays mRNA for ADP-glucose pyrophosphorylase
Seq. No.
                   306768
Seq. ID
                   uC-zmflb73156d06b1
Method
                   BLASTX
NCBI GI
                   q1335862
BLAST score
                   207
E value
                   9.0e-17
Match length
                   72
% identity
                   62
NCBI Description
                  (U42608) clathrin heavy chain [Glycine max]
Seq. No.
                   306769
Seq. ID
                   uC-zmflb73156d10b1
Method
                   BLASTX
NCBI GI
                   g3608495
BLAST score
                   176
E value
                   1.0e-13
Match length
                   69
% identity
                   65
NCBI Description
                   (AF089738) plastid division protein FtsZ [Arabidopsis
                   thaliana] >gi_4510351 gb AAD21440.1 (AC006921) plastid
                   division protein FtsZ [Arabidopsis thaliana]
Seq. No.
                   306770
Seq. ID
                   uC-zmflb73156d12b1
Method
                  BLASTX
NCBI GI
                   g4581164
BLAST score
                   471
E value
                   3.0e-47
Match length
                  159
% identity
                   56
NCBI Description
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
Seq. No.
                  306771
Seq. ID
                  uC-zmflb73156f04b1
Method
                  BLASTX
NCBI GI
                  q1890577
BLAST score
                  150
E value
                  9.0e-10
Match length
                  69
% identity
                  51
                  (X93175) xyloglucan endotransglycosylase (XET) [Hordeum
NCBI Description
```

vulgare]

Seq. No. 306772

Seq. ID uC-zmflb73156h09b1

Method BLASTX NCBI GI g1076670



BLAST score 162 E value 3.0e-11 Match length 101 % identity 45

NCBI Description NADH dehydrogenase (EC 1.6.99.3) - potato

>gi_668985_emb_CAA59062_ (X84319) NADH dehydrogenase

[Solanum tuberosum]

Seq. No. 306773

Seq. ID uC-zmflb73157a09a1

Method BLASTN
NCBI GI g3420038
BLAST score 112
E value 4.0e-56
Match length 187
% identity 48

NCBI Description Zea mays gypsy/Ty3-type retrotransposon Tekay, complete

sequence

Seq. No. 306774

Seq. ID uC-zmflb73157b04b2

Method BLASTX
NCBI GI g4006827
BLAST score 234
E value 5.0e-20
Match length 69
% identity 70

NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 306775

Seq. ID uC-zmflb73157b05a1

Method BLASTN
NCBI GI g602605
BLAST score 74
E value 4.0e-34
Match length 97
% identity 94

NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No. 306776

Seq. ID uC-zmflb73157c09b2

Method BLASTX
NCBI GI g3913018
BLAST score 565
E value 2.0e-58
Match length 120
% identity 93

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

(ALDP) >gi_218155 dbj BAA02730 (D13513) chloroplastic

aldolase [Oryza sativa]

Seq. No. 306777

Seq. ID uC-zmflb73157g08b2

Method BLASTX
NCBI GI g4559377
BLAST score 570
E value 7.0e-59



```
Match length
% identity
                   69
NCBI Description
                   (AC006526) putative photomorphogenesis repressor protein
                  COP1 [Arabidopsis thaliana]
Seq. No.
                   306778
                  uC-zmflb73157h07b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2145358
BLAST score
                  144
                   6.0e-09
E value
Match length
                  30
                  87
% identity
NCBI Description
                  (Y10922) HD-Zip protein [Arabidopsis thaliana]
                  306779
Seq. No.
                  uC-zmflb73158a08b2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  232
                  1.0e-128
E value
Match length
                  343
% identity
                  92
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                  complete sequence
Seq. No.
                  306780
                  uC-zmflb73159a10b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3043415
BLAST score
                  336
                  9.0e-32
E value
Match length
                  68
% identity
                  94
NCBI Description
                  (Y17053) At-hsc70-3 [Arabidopsis thaliana]
                  306781
Seq. No.
Seq. ID
                  uC-zmflb73159b12a2
Method
                  BLASTN
NCBI GI
                  g22221
BLAST score
                  54
E value
                  2.0e-21
Match length
                  78
                  92
% identity
NCBI Description Z.mays ZSF4C3 gene for zein
Seq. No.
                  306782
```

uC-zmflb73160c06b2 Seq. ID

57

Method BLASTX NCBI GI g3236240 BLAST score 186 E value 5.0e-20 Match length 106

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 306783

% identity

43528

Match length

% identity

94

62



```
uC-zmflb73160d03b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4185311
BLAST score
                  245
E value
                  8.0e-39
Match length
                  113
% identity
                  77
NCBI Description (AF090446) polyprotein [Zea mays]
                  306784
Seq. No.
                  uC-zmflb73160f01b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3779033
BLAST score
                  336
E value
                  2.0e-31
Match length
                  121
% identity
                  50
NCBI Description (AC005171) cycloartenol synthase [Arabidopsis thaliana]
Seq. No.
                  306785
Seq. ID
                  uC-zmflb73160f03a1
Method
                  BLASTN
NCBI GI
                 · g22155
BLAST score
                  113
E value
                  7.0e-57
Match length
                  157
% identity
                  92
NCBI Description Z.mays mRNA for alpha-tubulin
                  306786
Seq. No.
Seq. ID
                  uC-zmflb73160g08a1
Method
                  BLASTN
NCBI GI
                  q1103627
BLAST score
                  96
E value
                  1.0e-46
Match length
                  164
% identity
                  90
NCBI Description Z.mays Fer1 gene
                  306787
Seq. No.
Seq. ID
                  uC-zmflb73161c02b2
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  415
E value
                  9.0e-45
Match length
                  121
% identity
                  75
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  306788
Seq. ID
                  uC-zmflb73161e10b2
Method
                  BLASTX -
NCBI GI
                  g2224605
BLAST score
                  342
E value
                  4.0e-32
```



NCBI Description (AB002330) KIAA0332 [Homo sapiens]

Seq. No. 306789

Seq. ID uC-zmflb73161f04a1

Method BLASTX
NCBI GI g4103987
BLAST score 146
E value 2.0e-09
Match length 39
% identity 74

NCBI Description (AF030516) 5,10-methylenetetrahydrofolate

dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase

[Pisum sativum]

Seq. No. 306790

Seq. ID uC-zmflb73161g04a1

Method BLASTX
NCBI GI g1172861
BLAST score 247
E value 2.0e-21
Match length 65
% identity 74

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR

(RUBISCO LARGE SUBUNIT) >gi_1363613_pir__S58560

ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain

- maize chloroplast >gi_18036_emb_CAA78027_ (Z11973)

Ribulose bisphosphate carboxylase [Zea mays]

>gi_902230_emb_CAA60294_ (X86563) rubisco large subunit

[Zea mays]

Seq. No. 306791

Seq. ID uC-zmflb73162b03b2

Method BLASTX
NCBI GI g1519253
BLAST score 174
E value 1.0e-12
Match length 39
% identity 90

NCBI Description (U65958) GF14-d protein [Oryza sativa]

Seq. No. 306792

Seq. ID uC-zmflb73162c03b2

Method BLASTX
NCBI GI g283051
BLAST score 600
E value 2.0e-62
Match length 114
% identity 96

NCBI Description RNA-directed DNA polymerase (EC 2.7.7.49) - maize

transposon (fragment)

Seq. No. 306793

Seq. ID uC-zmflb73162f07b2

Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 1.0e-11



```
Match length
% identity
                   67
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   306794
Seq. ID
                   uC-zmflb73162f12b2
Method
                   BLASTX
NCBI GI
                   q1703199
BLAST score
                   191
E value
                   1.0e-14
Match length
                   69
% identity
                   46
NCBI Description PROTEIN KINASE AFC1 >gi_601787 (U16176) protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   306795
Seq. ID
                   uC-zmflb73162q05b2
Method
                   BLASTX
NCBI GI
                   g531389
BLAST score
                   279
E value
                   5.0e-25
Match length
                   101
% identity
                   51
NCBI Description
                  (U12626) copia-like retrotransposon Hopscotch polyprotein
                   [Zea mays]
Seq. No.
Seq. ID
                   306796
                   uC-zmflb73162q10b2
Method
                  BLASTN
NCBI GI
                   q507770
BLAST score
                   34
E value
                   1.0e-09
Match length
                   144
% identity
                   88
NCBI Description
                  Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete
Seq. No.
                   306797
Seq. ID
                  uC-zmflb73162h04b2
Method
                  BLASTX
NCBI GI
                  g127580
BLAST score
                   381
E value
                   6.0e-37
Match length
                  94
% identity
                  62
NCBI Description
                  MYB-RELATED PROTEIN ZM1 >gi_82729_pir__S04898 transforming
```

protein (myb) homolog (clone Zm1) - maize

>gi_227032_prf__1613412C myb-related gene Zm1 [Zea mays]

para):

Seq. No. 306798

Seq. ID uC-zmflb73163a04b2

Method BLASTX NCBI GI q4388717 BLAST score 270 E value 5.0e-24 Match length 90 % identity 60



NCBI Description (AC006413) putative nuclear phosphoprotein (contains multiple TPR repeats prosite:QDOC50005) [Arabidopsis

thaliana]

Seq. No. 306799

Seq. ID uC-zmflb73163a09b2

Method BLASTX
NCBI GI g132724
BLAST score 194
E value 6.0e-15
Match length 49
% identity 73

NCBI Description 50S RIBOSOMAL PROTEIN L18 >gi 71259 pir R5BS8F ribosomal

protein L18 - Bacillus stearothermophilus

Seq. No. 306800

Seq. ID uC-zmflb73163c03b2

Method BLASTN
NCBI GI g551482
BLAST score 295
E value 1.0e-165
Match length 472
% identity 96

NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA,

complete cds

Seq. No. 306801

Seq. ID uC-zmflb73163e08b2

Method BLASTX
NCBI GI g4102600
BLAST score 511
E value 3.0e-57
Match length 142
% identity 76

NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]

Seq. No. 306802

Seq. ID uC-zmflb73163g05b2 Method BLASTX

NCBI GI g4218122 BLAST score 282 E value 5.0e-25 Match length 163 % identity 45

NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 306803

Seq. ID uC-zmflb73163g08b2

Method BLASTX
NCBI GI g4585976
BLAST score 394
E value 3.0e-38
Match length 132
% identity 58

NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No. 306804



Seq. ID uC-zmflb73164a10b2 Method BLASTX NCBI GI g2623307 BLAST score 182 5.0e-14 E value Match length 62 % identity 56 NCBI Description (AC002409) putative ubiquitin protease [Arabidopsis thaliana] Seq. No. 306805 Seq. ID uC-zmflb73164d01a1 Method BLASTN NCBI GI q1421729 BLAST score 36 E value 6.0e-11 Match length 145 % identity 80 NCBI Description Zea mays T cytoplasm male sterility restorer factor 2 (rf2) mRNA, complete cds Seq. No. 306806 Seq. ID uC-zmflb73164d08a1 Method BLASTN NCBI GI g168436 BLAST score 142 E value 2.0e-74 Match length 178 % identity 95 MCBI Description Zea mays catalase (Cat3) gene, complete cds Seq. No. 306807 Seq. ID uC-zmflb73165h03b2 Method BLASTX NCBI GI g3334133 BLAST score 261 5.0e-23 E value Match length 78 % identity 64 NCBI Description CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi_1432145 (U61231) cytochrome P450 [Arabidopsis thaliana] Seq. No. 306808 Seq. ID uC-zmflb73166b01b2 BLASTX Method g473874 307 4.0e-42 142 39 NCBI Description (U08285) a membrane-associated salt-inducible protein [Nicotiana tabacum]

NCBI GI BLAST score E value Match length % identity

Seq. No. 306809

Seq. ID uC-zmflb73166e05b2

Method BLASTN NCBI GI g4185305



BLAST score 138 E value 2.0e-71 Match length 416 % identity 88

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag

protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 306810

Seq. ID uC-zmflb73167b11b2

Method BLASTX
NCBI GI g478753
BLAST score 207
E value 7.0e-17
Match length 41
% identity 90

NCBI Description tubulin alpha-4 chain - maize (fragment)

Seq. No. 306811

Seq. ID uC-zmflb73167d02b2

Method BLASTX
NCBI GI g3402677
BLAST score 195
E value 6.0e-15
Match length 127
% identity 42

NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 306812

Seq. ID uC-zmflb73167d05b2

Method BLASTX
NCBI GI g1209756
BLAST score 397
E value 1.0e-38
Match length 108
% identity 65

NCBI Description (U43629) integral membrane protein [Beta vulgaris]

Seq. No. 306813

Seq. ID uC-zmflb73167e12b2

Method BLASTN
NCBI GI g2463566
BLAST score 42
E value 3.0e-14
Match length 125
% identity 83

NCBI Description Zea mays mRNA for squalene synthase, complete cds

Seq. No. 306814

Seq. ID uC-zmflb73167f04b2

Method BLASTX
NCBI GI g3264596
BLAST score 290
E value 3.0e-26
Match length 83
% identity 73





```
(AF057183) putative tonoplast aquaporin [Zea mays]
NCBI Description
                    306815
 Seq. No.
 Seq. ID
                    uC-zmflb73168b10a1
 Method
                    BLASTN
 NCBI GI
                    q1167857
 BLAST score
                    35
 E value
                    3.0e-10
 Match length
                   79
 % identity
                    86
 NCBI Description S.cereale cv. Petkus "Halo" encoding cpn60
 Seq. No.
                    306816
 Seq. ID
                    uC-zmflb73168c06a1
 Method
                    BLASTN
 NCBI GI
                    g3776004
 BLAST score
                    41
 E value
                    9.0e-14
 Match length
                    89
 % identity
                    87
 NCBI Description Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH15
 Seq. No.
                    306817
 Seq. ID
                    uC-zmflb73169d03b2
 Method
                    BLASTX
 NCBI GI
                    g728905
 BLAST score
                    385
 E value
                    3.0e-37
 Match length
                    120
 % identity
                    58
                   PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC
 NCBI Description
                    RETICULUM CA2+-ATPASE) >gi 1078206 pir S51995 probable
                    ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae)
                    >gi 171114 (L01795) ATPase [Saccharomyces cerevisiae]
                    >gi 595560 (U12980) Drs2p: Membrane spanning
                    Ca-ATPase(P-type), member of the cation transport(E1-E2)
                    ATPase [Saccharomyces cerevisiae]
 Seq. No.
                    306818
 Seq. ID
                    uC-zmflb73169d10b2
 Method
                    BLASTX
 NCBI GI
                    g3036795
 BLAST score
                    158
 E value
                    9.0e-11
 Match length
                    49
 % identity
                    63
 NCBI Description
                   (AL022373) putative protein [Arabidopsis thaliana]
                    >gi_3805857_emb_CAA21477_ (AL031986) putative protein
                    [Arabidopsis thaliana]
 Seq. No.
                    306819
 Seq. ID
                    uC-zmflb73169g02b2
```

BLASTX

Method NCBI GI g2117619 BLAST score 525 E value 1.0e-53 Match length 146



% identity 68

NCBI Description peroxidase (EC 1.11.1.7) 4 precursor - wheat

>gi_732976_emb_CAA59487_ (X85230) peroxidase [Triticum

aestivum]

Seq. No. 306820

Seq. ID uC-zmflb73169h03b2

Method BLASTN
NCBI GI g22163
BLAST score 55
E value 9.0e-23
Match length 99
% identity 89

NCBI Description Z.mays MANT2 mRNA for adenine nucleotide translocator

(ADP/ATP translocase)

Seq. No. 306821

Seq. ID uC-zmflb73170b02b2

Method BLASTX
NCBI GI g2792214
BLAST score 191
E value 8.0e-15
Match length 81
% identity 52

NCBI Description (AF032685) NBS-LRR type resistance protein [Hordeum

vulgare]

Seq. No. 306822

Seq. ID uC-zmflb73170b05a1

Method BLASTX
NCBI GI g4103627
BLAST score 163
E value 1.0e-11
Match length 47

% identity 68

NCBI Description (AF026480) lipase [Dianthus caryophyllus]

Seq. No. 306823

Seq. ID uC-zmflb73170b05b2

Method BLASTX
NCBI GI g2832660
BLAST score 147
E value 6.0e-10
Match length 49
% identity 53

NCBI Description (AL021710) lipase-like protein [Arabidopsis thaliana]

Seq. No. 306824

Seq. ID uC-zmflb73170d12b2

Method BLASTN
NCBI GI g563234
BLAST score 33
E value 4.0e-09
Match length 73
% identity 86

NCBI Description Zea mays xyloglucan endo-transglycosylase homolog gene,

complete cds

```
Seq. No.
                   306825
Seq. ID
                   uC-zmflb73170e12b2
Method
                   BLASTX
NCBI GI
                   g3075390
BLAST score
                   171
E value
                   2.0e-12
Match length
                   41
% identity
                   80
NCBI Description
                  (AC004484) protein kinase ARSK1 [Arabidopsis thaliana]
Seq. No.
                   306826
Seq. ID
                   uC-zmflb73171c04b1
Method
                   BLASTX
NCBI GI
                   q1332579
BLAST score
                   225
E value
                   6.0e-19
Match length
                   69
% identity
NCBI Description
                  (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                   306827
Seq. ID
                   uC-zmflb73171d10b1
Method
                   BLASTN
NCBI GI
                   q1181672
BLAST score
                   50
E value
                   2.0e-19
Match length
                   138
% identity
                   84
NCBI Description
                  Sorghum bicolor heat shock protein 70 cognate (hsc70) mRNA,
                   partial cds
Seq. No.
                   306828
Seq. ID
                   uC-zmflb73171f01b1
Method
                   BLASTX
NCBI GI
                   g135411
BLAST score
                   580
E value
                   4.0e-60
Match length
                   110
% identity
                   97
                   TUBULIN ALPHA-2 CHAIN >gi_82732_pir__S15772 tubulin alpha-2
NCBI Description
                   chain - maize >gi_22148 emb CAA33733 (X15704)
                   alpha2-tubulin [Zea mays]
Seq. No.
                   306829
Seq. ID
                   uC-zmflb73172g02b2
Method
                   BLASTX
NCBI GI
                   q1181673
BLAST score
                   193
E value
                  8.0e-17
Match length
                  57
% identity
                  88
```

NCBI Description (U41652) heat shock protein cognate 70 [Sorghum bicolor]

Seq. No. 306830

Seq. ID uC-zmflb73172g10b2

Method BLASTN



```
NCBI GI
                  q602605
BLAST score
                  60.
E value
                  1.0e-25
Match length
                  132
% identity
                  86
NCBI Description
                  Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
Seq. No.
                  306831
Seq. ID
                  uC-zmflb73173a06b1
Method
                  BLASTX
NCBI GI
                  g115771
BLAST score
                  339
E value
                  3.0e-32
Match length
                  81
                  80
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi 22224 emb_CAA32900_ (X14794) chlorophyll a/b-binding
                  preprotein (AA 1 - 262) [Zea mays]
Seq. No.
                  306832
Seq. ID
                  uC-zmflb73173a11b1
Method
                  BLASTX
NCBI GI
                  g2967837
BLAST score
                  202
E value
                  1.0e-15
Match length
                  116
% identity
                  41
NCBI Description
                  (AF052641) cyst nematode resistance gene candidate
                  [Triticum aestivum]
Seq. No.
                  306833
Seq. ID
                  uC-zmflb73173c03b1
Method
                  BLASTX
NCBI GI
                  g3695392
BLAST score
                  154
E value
                  5.0e-13
Match length
                  80
% identity
                  45
NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]
Seq. No.
                  306834
Seq. ID
                  uC-zmflb73173e08b1
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  34
E value
                  2.0e-09
Match length
                  34
% identity
                  100
```

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 306835

Seq. ID uC-zmflb73173q05b1

Method BLASTN NCBI GI g1800216

BLAST score 36

```
E value
                  9.0e-11
Match length
                  40
% identity
                  97
NCBI Description Sorghum bicolor phytochrome B (PHYB) gene, partial cds
                  306836
Seq. No.
                  uC-zmflb73173h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4519671
BLAST score
                  227
E value
                  1.0e-29
Match length
                  107
% identity
                  67
NCBI Description
                  (AB017693) transfactor [Nicotiana tabacum]
                  306837
Seq. No.
                  uC-zmflb73174b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3702323
BLAST score
                  144 -
E value
                  3.0e-15
Match length
                  100
% identity
                  47
NCBI Description
                  (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                  306838
                  uC-zmflb73174c09b1
                  BLASTN
```

Seq. ID uC-zmflk
Method BLASTN
NCBI GI g22163
BLAST score 82
E value 1.0e-38
Match length 86
% identity 99

NCBI Description Z.mays MANT2 mRNA for adenine nucleotide translocator

(ADP/ATP translocase)

Seq. No. 306839

Seq. ID uC-zmflb73174f03b1

Method BLASTX
NCBI GI g3915826
BLAST score 156
E value 2.0e-10
Match length 114
% identity 33

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 306840

Seq. ID uC-zmflb73174g06b1

Method BLASTX
NCBI GI g2668742
BLAST score 239
E value 2.0e-20
Match length 75
% identity 68

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 306841



```
uC-zmflb73174h09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4049403
BLAST score
                  203
E value
                  6.0e-16
Match length
                  43
                  79
% identity
NCBI Description
                  (AJ131708) gamma response I protein [Arabidopsis thaliana]
Seq. No.
                  306842
                  uC-zmflb73174h09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4049403
BLAST score
                  188
E value
                  6.0e-14
Match length
                  99
% identity
NCBI Description
                  (AJ131708) gamma response I protein [Arabidopsis thaliana]
Seq. No.
                  306843
Seq. ID
                  uC-zmflb73174h12b1
Method
                  BLASTX
NCBI GI
                  g2702277
BLAST score
                  378
E value
                  3.0e-36
Match length
                  114
% identity
NCBI Description
                  (AC003033) putative cyclin g-associated kinase [Arabidopsis
                  thaliana] >gi 2914689 (AC003974) putative cyclin
                  g-associated kinase [Arabidopsis thaliana]
Seq. No.
                  306844
Seq. ID
                  uC-zmflb73175a10b1
Method
                  BLASTX
NCBI GI
                  g464840
BLAST score
                  228
E value
                  5.0e-19
Match length
                  52
% identity
                  81
NCBI Description
                  TUBULIN ALPHA-1 CHAIN >gi 421781 pir S32666 tubulin
                  alpha-1 chain - fern (Anemia phyllitidis)
                  >gi_296494 emb CAA48927 (X69183) alpha tubulin [Anemia
                  phyllitidis]
Seq. No.
                  306845
Seq. ID
                  uC-zmflb73175b05b1
                  BLASTX
Method
NCBI GI
                  g1483150
BLAST score
                  285
E value
                  2.0e-25
Match length
                  87
% identity
                  66
NCBI Description
                  (D84417) monodehydroascorbate reductase [Arabidopsis
                  thaliana]
```

306846

uC-zmflb73175c05b1

Seq. No.

Seq. ID

```
Method
NCBI GI
                   q3551245
BLAST score
                   272
E value
                   5.0e-24
Match length
                   71
% identity
                   70
NCBI Description
                  (AB012702) P40-like protein [Daucus carota]
Seq. No.
                   306847
Seq. ID
                   uC-zmf1b73175c11b1
Method
                   BLASTX
NCBI GI
                   g4104929
BLAST score
                   460
E value
                   5.0e-46
Match length
                   134
% identity
                   66
NCBI Description
                  (AF042195) auxin response factor 7 [Arabidopsis thaliana]
Seq. No.
                   306848
Seq. ID
                   uC-zmflb73175e03b1
Method
                   BLASTX
NCBI GI
                   g2944233
BLAST score
                   217
E value
                   2.0e-17
Match length
                   104
% identity
                   49
NCBI Description
                  (AF030409) sodium-hydrogen exchanger 6 [Homo sapiens]
Seq. No.
                   306849
Seq. ID
                   uC-zmflb73175q05b1
Method
                   BLASTX
NCBI GI
                   g4220479
BLAST score
                   522
E value
                   2.0e-53
Match length
                   134
% identity
                   86
NCBI Description
                  (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                   306850
Seq. ID
                  uC-zmflb73176f10b2 ·
Method
                  BLASTX
NCBI GI
                  g3063465
BLAST score
                  240
E value
                  1.0e-20
Match length
                  60
% identity
                  78
NCBI Description
                  (AC003981) F22013.27 [Arabidopsis thaliana]
Seq. No.
                  306851
Seq. ID
                  uC-zmflb73176h06b2
```

Method BLASTX

NCBI GI g2654868 BLAST score 268 E value 2.0e-23 Match length 137 % identity 47

NCBI Description (AF015301) RbohAp108 [Arabidopsis thaliana]

```
Seq. No.
                   306852
Seq. ID
                   uC-zmflb73177c01b1
Method
                   BLASTX
NCBI GI
                   q1170937
BLAST score
                   238
E value
                   4.0e-20
Match length
                   66
% identity
                   71
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
Seq. No.
                   306853
Seq. ID
                   uC-zmflb73177d04b1
Method
                  BLASTX
NCBI GI
                   g3341694
BLAST score
                   210
E value
                   9.0e-17
Match length
                  88
% identity
                   45
NCBI Description
                  (AC003672) PREG-like protein [Arabidopsis thaliana]
Seq. No.
                  306854
Seq. ID
                  uC-zmflb73177e01b1
Method
                  BLASTX
NCBI GI
                  q1053057
BLAST score
                  183
E value
                  3.0e-15
Match length
                  76
% identity
                  61
NCBI Description
                  (U38422) histone H3 [Triticum aestivum]
Seq. No.
                  306855
Seq. ID
                  uC-zmflb73177e12b1
Method
                  BLASTN
NCBI GI
                  q168396
BLAST score
                  51
E value
                  1.0e-19
Match length
                  71
% identity
                  93
                  Zea mays auxin-binding protein (abpl) gene, exons 1-5 and
NCBI Description
                  complete cds
Seq. No.
                  306856
```

Seq. ID uC-zmflb73177f02b1

Method BLASTX NCBI GI g2052094 BLAST score 571 E value 7.0e-59 Match length 165 % identity 69

NCBI Description (Z49147) phenylalanine ammonia-lyase [Hordeum vulgare]

Seq. No. 306857

Seq. ID uC-zmflb73177g09b1



```
Method
NCBI GI
                   q4455322
BLAST score
                   187
E value
                   3.0e-15
Match length
                  107
                  48
% identity
NCBI Description
                  (AL035525) putative protein kinase [Arabidopsis thaliana]
                  306858
Seq. No.
Seq. ID
                  uC-zmflb73177h03b1
Method
                  BLASTX
NCBI GI
                  q82696
BLAST score
                  165
E value
                  1.0e-11
Match length
                  57
% identity
                  58
NCBI Description
                  glycine-rich protein - maize >gi 22293 emb CAA43431
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                  306859
Seq. ID
                  uC-zmflb73177h10b1
Method
                  BLASTX
NCBI GI
                  g129881
BLAST score
                  677
E value
                  2.0e-71
Match length
                  161
% identity
                  81
NCBI Description
                  PYROPHOSPHATE -- FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi 482294 pir A36094
                  pyrophosphate--fructose-6-phosphate 1-phosphotransferase
                   (EC 2.7.1.90) alpha chain - potato (cv. Kennebec)
                  >gi 169538 (M55190) pyrophosphate-fructose 6-phosphate
                  1-phosphotransferase alpha-subunit [Solanum tuberosum]
Seq. No.
                  306860
Seq. ID
                  uC-zmflb73178a01b1
Method
                  BLASTX
NCBI GI
                  g399853
BLAST score
                  300
E value
                  3.0e-27
Match length
                  87
% identity
                  72
NCBI Description
                  HISTONE H2B.1 >gi 283041_pir S28048 histone H2B - maize
                  >gi_22323_emb_CAA40564 (X57312) H2B histone [Zea mays]
Seq. No.
                  306861
Seq. ID
                  uC-zmflb73178a11b1
Method
                  BLASTN
NCBI GI
                  q1661161
BLAST score
                  33
E value
                  4.0e-09
Match length
                  45
% identity
                  93
NCBI Description
                  Oryza sativa water stress inducible protein (KCDL917) mRNA,
```

complete cds

Seq. No.

Seq. ID



```
Seq. No.
                  306862
                  uC-zmflb73178b09b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168508
BLAST score
                  63
                  1.0e-26
E value
Match length
                  118
% identity
                  87
NCBI Description Maize oleosin KD18 (KD18; L2) gene, complete cds
Seq. No.
                  306863
Seq. ID
                  uC-zmflb73178d09b1
Method
                  BLASTX
NCBI GI
                  g2244965
BLAST score
                  395
E value
                  1.0e-50
Match length
                  141
% identity
                  72
NCBI Description
                  (Z97340) unnamed protein product [Arabidopsis thaliana]
Seq. No.
                  306864
Seq. ID
                  uC-zmflb73178f03b1
Method
                  BLASTX
NCBI GI
                  g135411
BLAST score
                  612
E value
                  8.0e-64
Match length
                  113
% identity
                  100
NCBI Description
                  TUBULIN ALPHA-2 CHAIN >gi 82732 pir S15772 tubulin alpha-2
                  chain - maize >gi 22148 emb CAA33733 (X15704)
                  alpha2-tubulin [Zea mays]
Seq. No.
                  306865
Seq. ID
                  uC-zmflb73178g08b1
Method
                  BLASTX
NCBI GI
                  g282994
BLAST score
                  294
E value
                  7.0e-27
Match length
                  89
% identity
                  65
NCBI Description
                  Sip1 protein - barley >gi 167100 (M77475) seed imbibition
                  protein [Hordeum vulgare]
Seq. No.
                  306866
Seq. ID
                  uC-zmflb73178g12b1
Method
                  BLASTN
NCBI GI
                  g2921303
BLAST score
                  148
E value
                  1.0e-77
Match length
                  259
% identity
                  90
NCBI Description
                  Zea mays herbicide safener binding protein (SBP1) mRNA,
```

43544

complete cds

uC-zmflb73178h03b1



```
Method.
                  g549770
NCBI GI
BLAST score
                  151
E value
                   5.0e-19
                   99
Match length
                   56
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
                  protein L3 - rice >gi 303853 dbj BAA02155 (D12630)
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                   306868
Seq. ID
                  uC-zmflb73179a03a2
Method
                  BLASTX
NCBI GI
                  q4099833
                   567
BLAST score
E value
                   2.0e-58
Match length
                  132
                  78
% identity
NCBI Description
                  (U90265) bifunctional nuclease [Zinnia elegans]
Seq. No.
                   306869
                  uC-zmflb73179a11a2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q480669
BLAST score
                   223
                   3.0e-18
E value
Match length
                   68
% identity
                   71
NCBI Description
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Jerusalem
                  artichoke (fragment) >gi_1359894_emb_CAA81210_ (Z26251)
                  NADPH-ferrihemoprotein reductase [Helianthus tuberosus]
Seq. No.
                   306870
Seq. ID
                  uC-zmflb73179a11b1
Method
                  BLASTX
NCBI GI
                   q4220538
BLAST score
                   444
E value
                   5.0e-44
Match length
                   145
% identity
                   63
NCBI Description
                   (AL035356) NADPH-ferrihemoprotein reductase ATR1
                   [Arabidopsis thaliana]
Seq. No.
                   306871
Seq. ID
                   uC-zmflb73179b02a2
Method
                   BLASTX
NCBI GI
                   g3820531
BLAST score
                   162
E value
                   1.0e-11
Match length
                  58
% identity
                   53
NCBI Description
                   (AF072736) beta-glucosidase [Pinus contorta]
```

 Seq. No.
 306872

 Seq. ID
 uC-zmf.

Seq. ID uC-zmflb73179b06a2

Method BLASTN NCBI GI g1061305



BLAST score 116
E value 6.0e-59
Match length 139
% identity 96

NCBI Description Z.mays Dof2 mRNA

Seq. No. 306873

Seq. ID uC-zmflb73179b06b1

Method BLASTN
NCBI GI g1061305
BLAST score 72
E value 2.0e-32
Match length 136
% identity 88

NCBI Description Z.mays Dof2 mRNA

Seq. No. 306874

Seq. ID uC-zmflb73179c06b1

Method BLASTN
NCBI GI g551482
BLAST score 55
E value 3.0e-22
Match length 87
% identity 91

NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA,

complete cds

Seq. No. 306875

Seq. ID uC-zmflb73179g10b1

Method BLASTX
NCBI GI g2117355
BLAST score 233
E value 2.0e-22
Match length 119
% identity 52

NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) alpha-II

chain precursor - potato >gi_587562_emb_CAA56520_ (X80236)

and the same of th

mitochondrial processing peptidase [Solanum tuberosum]

Seq. No. 306876

Seq. ID uC-zmflb73179h05a2

Method BLASTX
NCBI GI g1169198
BLAST score 206
E value 3.0e-16
Match length 71
% identity 58

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR

>gi_479738_pir__S35270 hypothetical protein - Arabidopsis

thaliana >gi_166926 (L11367) [Arabidopsis thaliana

unidentified mRNA sequence, complete cds.], gene product

[Arabidopsis thaliana]

Seq. No. 306877

Seq. ID uC-zmflb73180b02b1

Method BLASTX NCBI GI g100440

E value

Match length

1.0e-47



```
∰BLAST score
E value
                      1.0e-11
   Match length
                      31
    % identity
                      94
    NCBI Description
                      heat shock protein 70 (clone D7) - potato (fragment)
                      >gi 100441 pir S21363 heat shock protein 70 (clone D3) -
                      potato (fragment) >gi_21477_emb_CAA78036_ (Z11984) 70-kD
                      heat shock protein [Solanum tuberosum]
   Seq. No.
                      306878
   Seq. ID
                      uC-zmflb73180c08b1
   Method
                      BLASTX
   NCBI GI
                      g4262149
   BLAST score
                      365
   E value
                      6.0e-35
   Match length
                      102
    % identity
                      65
   NCBI Description
                      (AC005275) putative xyloglucan endotransglycosylase
                      [Arabidopsis thaliana]
   Seq. No.
                      306879
   Seq. ID
                      uC-zmflb73180c11a1
   Method
                      BLASTX
   NCBI GI
                      g2924247
   BLAST score
                      337
   E value
                      1.0e-31
   Match length
                      78
    % identity
                      82
   NCBI Description
                      (Y07782) expansin [Oryza sativa]
   Seq. No.
                      306880
                      uC-zmflb73180d07a1
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      g2950395
   BLAST score
                      160
                      4.0e-11
   E value
   Match length
                      36
    % identity
                      78
   NCBI Description
                      (AJ224847) oxidoreductase [Zea mays]
   Seq. No.
                      306881
   Seq. ID
                      uC-zmflb73180e02b1
   Method
                      BLASTX
                      g3281853
   NCBI GI
   BLAST score
                      196
   E value
                      4.0e-15
   Match length
                      61
   % identity
                      64
   NCBI Description
                      (AL031004) putative protein [Arabidopsis thaliana]
   Seq. No.
                      306882
   Seq. ID
                      uC-zmflb73180e07b1
   Method
                      BLASTN
   NCBI GI
                      q3341647
   BLAST score
                      98
```



% identity 91 NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase

Seq. No. 306883

Seq. ID uC-zmflb73180f04b1

Method BLASTX
NCBI GI g1054843
BLAST score 503
E value 5.0e-51
Match length 148
% identity 59

NCBI Description (X92847) D12 oleate desaturase [Solanum commersonii]

Seq. No. 306884

Seq. ID uC-zmflb73180f11a1

Method BLASTX
NCBI GI g2980805
BLAST score 208
E value 2.0e-16
Match length 51
% identity 82

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 306885

Seq. ID uC-zmflb73180g02b1

Method BLASTX
NCBI GI g3182903
BLAST score 219
E value 4.0e-18
Match length 80
% identity 61

NCBI Description ACTIN, CYTOPLASMIC (BBCA1) >gi 1552218_dbj_BAA13444.1_

(D87738) cytoplasmic actin BbCA1 [Branchiostoma belcheri]

Seq. No. 306886

Seq. ID uC-zmflb73180g09b1

Method BLASTX
NCBI GI g3540178
BLAST score 545
E value 5.0e-56
Match length 140
% identity 81

NCBI Description (AC004122) calcium-transporting ATPase [Arabidopsis

thaliana]

Seq. No. 306887

Seq. ID uC-zmflb73180h03a1

Method BLASTN NCBI GI g4416300 BLAST score 67

E value 2.0e-29 Match length 161

% identity 87

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 306888



```
uC-zmflb73180h04a1
Seq. ID
Method
                   BLASTX 🤏
NCBI GI
                   q629592
BLAST score
                   190
                   2.0e-14
E value
Match length
                   56
% identity
                   61
NCBI Description hypothetical protein - rape
Seq. No.
                   306889
Seq. ID
                   uC-zmflb73180h07b1
Method
                  BLASTX
NCBI GI
                   g4581119
BLAST score
                   244
E value
                   5.0e-21
Match length
                   86
% identity
                   58
NCBI Description
                  (AC005825) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   306890
Seq. ID
                  uC-zmflb73181e02b2
Method
                  BLASTX
NCBI GI
                   g2129740
BLAST score
                   285
E value
                  7.0e-26
Match length
                   64
% identity
                  81
NCBI Description
                  small nuclear ribonucleoprotein - Arabidopsis thaliana
                  >gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis
                   thaliana >gi_1255711 (M93439) small nuclear
                   ribonucleoprotein [Arabidopsis thaliana] >gi_1354469
                   (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]
Seq. No.
                   306891
Seq. ID
                  uC-zmflb73181e12b2
Method
                  BLASTN
NCBI GI
                  g459267
BLAST score
                  40
E value
                  1.0e-13
Match length
                  64
% identity
                  91
NCBI Description
                  Z.mays gene for HMG protein
Seq. No.
                  306892
Seq. ID
                  uC-zmflb73181f12b1
Method
                  BLASTX
NCBI GI
                  g397396
BLAST score
                  217
E value
                  9.0e-18
Match length
                  54
% identity
NCBI Description
                  (X66077) DNA-binding protein [Zea mays]
Seq. No.
                  306893
Seq. ID
                  uC-zmflb73181h09b1
Method
```

43549

BLASTX

g129916

NCBI GI

NCBI Description



```
BLAST score
E value
                            1.0e-29
         Match length
                            84
                            79
          % identity
          NCBI Description
                            PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY
                            phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                            >gi_21835_emb_CAA33302 (X15232) phosphoglycerate kinase
                            (AA 1 - 401) [Triticum aestivum]
          Seq. No.
                            306894
          Seq. ID
                            uC-zmflb73182a02a1
         Method
                            BLASTN
          NCBI GI
                            g397395
                            121
          BLAST score
         E value
                            8.0e-62
         Match length
                            133
          % identity
                            98
         NCBI Description Z.mays MNB1b mRNA for DNA-binding protein
         Seq. No.
                            306895
         Seq. ID
                            uC-zmflb73182b07a1
         Method
                            BLASTX
         NCBI GI
                            g130582
         BLAST score
                            200
         E value
                            2.0e-15
         Match length
                            123
          % identity
                            34
                            RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94
         NCBI Description
                            [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
                            >gi_100342_pir__S04273 hypothetical protein - common
                            tobacco >gi 20045 emb CAA32025 (X13777) ORF [Nicotiana
                            tabacum]
         Seq. No.
                            306896
         Seq. ID
                            uC-zmflb73182b10b1
         Method
                            BLASTX
         NCBI GI
                            q585204
         BLAST score
                            483
         E value
                            1.0e-48
         Match length
                            117
         % identity
                            GLUTAMINE SYNTHETASE ROOT ISOZYME 4 (GLUTAMATE--AMMONIA
         NCBI Description
                            LIGASE) (GS107) >gi_481809_pir__S39480 glutamate--ammonia
                            ligase (EC 6.3.1.2) 1-4, cytosolic - maize
                            >gi_434330_emb_CAA46722 (X65929) glutamine synthetase [Zea
                            mays]
         Seq. No.
                            306897
         Seq. ID
                            uC-zmflb73182c07a1
         Method
                           BLASTN
         NCBI GI
                            q4416300
         BLAST score
                            267
         E value
                            1.0e-148
         Match length
                            367
         % identity
                            93
```

. 25 -

region, complete sequence

Zea mays chromosome 4 22 kDa zein-associated intercluster



```
Seq. No.
                  306898
Seq. ID
                  uC-zmflb73182d04a1
Method
                  BLASTN
NCBI GI
                  g871493
BLAST score
                  42
                  2.0e-14
E value
Match length
                  50
% identity
                  96
NCBI Description O.sativa ZB8 gene
                  306899
Seq. No.
Seq. ID
                  uC-zmflb73182e04b1
Method
                  BLASTX
NCBI GI
                  g2465923
BLAST score
                  242
E value
                  2.0e-20
Match length
                  141
% identity
                  39
NCBI Description
                   (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                  306900
Seq. ID
                  uC-zmflb73182f01b1
Method
                  BLASTX
NCBI GI
                  g2244975
BLAST score
                  181
E value
                  2.0e-13
Match length
                  64
                  59
% identity
NCBI Description
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  306901
Seq. ID
                  uC-zmflb73182g09b1
Method
                  BLASTN
NCBI GI
                  g2245648
BLAST score
                  128
E value
                  1.0e-65
Match length
                  148
% identity
                  97
NCBI Description
                  Zea mays discolored-1 (mutant allele dsc1-Ref::Mul) gene,
                  partial sequence
Seq. No.
                  306902
Seq. ID
                  uC-zmflb73183g03b1
Method
                  BLASTX
                  g113497
NCBI GI
BLAST score
                  273
E value
                  5.0e-24
Match length
                  76
% identity
                  62
NCBI Description
                  ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)
                  (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE)
                  >gi_99880_pir__S07472 alpha-galactosidase (EC 3.2.1.22)
```

precursor - guar >gi 18292 emb CAA32772 (X14619)

alpha-galactosidase preproprotein [Cyamopsis tetragonoloba]

```
Seq. No.
                   306903
                  uC-zmflb73183h04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4056489
BLAST score
                   146
E value
                   4.0e-09
Match length
                   80
% identity
                   54
NCBI Description
                   (AC005896) putative white protein [Arabidopsis thaliana]
Seq. No.
                   306904
Seq. ID
                   uC-zmflb73184b03b1
Method
                   BLASTX
NCBI GI
                   q2582971
BLAST score
                   221
E value
                   7.0e-35
Match length
                   150
% identity
                   55
NCBI Description
                  (D83711) TKRP125 [Nicotiana tabacum]
Seq. No.
                   306905
Seq. ID
                  uC-zmflb73184d09b1
Method
                  BLASTX
NCBI GI
                  g2760317
BLAST score
                  158
E value
                   8.0e-22
Match length
                  129
% identity
                   47
NCBI Description
                  (AC002130) F1N21.1 [Arabidopsis thaliana]
Seq. No.
                   306906
Seq. ID
                  uC-zmflb73184d12a1
Method
                  BLASTX
NCBI GI
                  g3041738
BLAST score
                  194
E value
                  8.0e-15
Match length
                  54
% identity
                   67
NCBI Description
                  T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
                   (HIV-1 NEF INTERACTING PROTEIN) >gi_2559010 (AF026292)
                  chaperonin containing t-complex polypeptide 1, eta subunit;
                  CCT-eta [Homo sapiens]
Seq. No.
                  306907
Seq. ID
                  uC-zmflb73184g07a1
Method
                  BLASTX
NCBI GI
                  g3128173
BLAST score
                  304
E value
                  4.0e-28
Match length
                  108
% identity
NCBI Description
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  306908
```

Seq. ID uC-zmflb73184h09b1

Method BLASTX NCBI GI g2984709

```
BLAST score
                  522
E value 🐕
                  3.0e-53
Match length
                  131
                  79
% identity
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  306909
Seq. No.
Seq. ID
                  uC-zmflb73185c03b1
Method
                  BLASTX
NCBI GI
                  g3873823
BLAST score
                  180
E value
                  4.0e-13
Match length
                  91
% identity
                  43
NCBI Description
                  (Z73422) predicted using Genefinder [Caenorhabditis
                  elegans]
                  306910
Seq. No.
Seq. ID
                  uC-zmflb73185c11b1
Method
                  BLASTN
NCBI GI
                  g169818
BLAST score
                  44
                  9.0e-16
E value
Match length
                  100
% identity
                  86
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                  306911
Seq. ID
                  uC-zmflb73185g12a1
Method
                  BLASTN
NCBI GI
                  q498774
BLAST score
                  155
E value
                  7.0e-82
Match length
                  262
% identity
                  90
NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein
Seq. No.
                  306912
Seq. ID
                  uC-zmflb73186a05b1
Method
                  BLASTX
NCBI GI
                  g548770
BLAST score
                  613
E value
                  6.0e-64
Match length
                  146
% identity
                  83
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal
                  protein L3 - rice >gi_303853 dbj BAA02155 (D12630)
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                  306913
Seq. ID
                  uC-zmflb73186f01b1
Method
                  BLASTX
```

NCBI GI q2288985 BLAST score 151 E value 9.0e-10 Match length 64 % identity 50

E value

Match length

% identity

1.0e-15

64





```
NCBI Description
                       (AC002335) hypothetical protein [Arabidopsis thaliana]
                       306914
     Seq. No.
                       uC-zmflb73186f02b1
     Seq. ID
    Method
                       BLASTX
    NCBI GI
                       q548770
    BLAST score
                       292
    E value
                       9.0e-27
    Match length
                       71
                       79
     % identity
                       60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal
    NCBI Description
                       protein L3 - rice >gi 303853 dbj BAA02155 (D12630)
                       ribosomal protein L3 [Oryza sativa]
     Seq. No.
                       306915
     Seq. ID
                       uC-zmflb73186f05b1
    Method
                       BLASTX
    NCBI GI
                       q3367591
    BLAST score
                       188
    E value
                       5.0e-14
    Match length
                       78
     % identity
                       51
    NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
    Seq. No.
                       306916
    Seq. ID
                       uC-zmflb73186f11b1
    Method
                       BLASTX
    NCBI GI
                       g3061308
    BLAST score
                       177
    E value
                       3.0e-13
    Match length
                       75
                       49
     % identity
    NCBI Description (AB006074) topoisomerase III [Mus musculus]
    Seq. No.
                       306917
                       uC-zmflb73186h01b1
     Seq. ID
    Method
                       BLASTX
    NCBI GI
                       g3024018
    BLAST score
                       247
    E value
                       1.0e-21
    Match length
                       59
     % identity
                       80
    NCBI Description
                       INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
                       >gi_1546919_emb_CAA69225_ (Y07920) translation initiation
                       factor 5A [Zea mays] >gi 2668738 (AF034943) translation
                       initiation factor 5A [Zea mays]
    Seq. No.
                       306918
    Seq. ID
                       uC-zmflb73186h07b1
    Method
                       BLASTX
    NCBI GI
                       g3789948
    BLAST score
                       141
```

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NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]



```
Seq. No.
                   306919
                                                                          - 12
Seq. ID
                  uC-zmflb73187c04b1
Method
                  BLASTX
NCBI GI
                   g3850821
BLAST score
                   442
                   9.0e-44
E value
Match length
                  173
% identity
                  54
NCBI Description
                  (Y18350) U2 snRNP auxiliary factor, large subunit
                   [Nicotiana plumbaginifolia]
                  306920
Seq. No.
                  uC-zmflb73187d01b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2984708
BLAST score
                  36
                  3.0e-11
E value
Match length
                   44
                   95
% identity
NCBI Description
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
                  306921
Seq. No.
Seq. ID
                  uC-zmflb73187d09b1
Method
                  BLASTX
NCBI GI
                  g1076820
BLAST score
                  161
                  2.0e-11
E value
Match length
                  35
                  83
% identity
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize
Seq. No.
                  306922
                  uC-zmflb73187e05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122753
BLAST score
                  239
E value
                  3.0e-20
Match length
                  71
% identity
                  65
NCBI Description
                  60S RIBOSOMAL PROTEIN L44 >gi 2244789 emb CAB10211.1
                   (Z97336) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                  306923
                  uC-zmflb73187e11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961375
BLAST score
                  140
                  9.0e-09
E value
Match length
                  50
% identity
                  50
NCBI Description
                  (AL022141) NAM like protein [Arabidopsis thaliana]
Seq. No.
                  306924
```

- , C -

uC-zmflb73188b05b1 Seq. ID

Method BLASTX NCBI GI g2982431

% identity

```
BLAST score
   E value
                      7.0e-47
   Match length
                      167
    % identity
                      5
                      (AL022224) leucine rich repeat-like protein [Arabidopsis
   NCBI Description
                      thaliana]
   Seq. No.
                      306925
                      uC-zmflb73188b09b1
   Seq. ID
                      {\tt BLASTX}
   Method
   NCBI GI
                      g2832625
   BLAST score
                      321
                      1.0e-29
   E value
   Match length
                      101
    % identity
                      59
   NCBI Description
                      (AL021711) putative protein [Arabidopsis thaliana]
                      306926
   Seq. No.
                      uC-zmflb73188c11b1
   Seq. ID
   Method
                      BLASTN
   NCBI GI
                      g602252
   BLAST score
                      74
                      1.0e-33
   E value
   Match length
                      158
    % identity
                      87
   NCBI Description Zea mays enolase (eno2) mRNA, complete cds
                      306927
   Seq. No.
                      uC-zmflb73188d05b1
   Seq. ID
   Method
                      BLASTX
                      g3600035
   NCBI GI
   BLAST score
                      146
   E value
                      1.0e-09
   Match length
                      48
    % identity
                      58
   NCBI Description
                      (AF080119) contains similarity to GTP-binding proteins
                      [Arabidopsis thaliana]
   Seq. No.
                      306928
   Seq. ID
                      uC-zmflb73188d09b1
   Method
                      BLASTX
   NCBI GI
                      g2914700
   BLAST score
                      229
   E value
                      2.0e-19
   Match length
                      58
                      78
   % identity
   NCBI Description
                      (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
                      thaliana]
   Seq. No.
                      306929
   Seq. ID
                      uC-zmflb73188e04a1
   Method
                      BLASTN
   NCBI GI
                      q1458135
   BLAST score
                      35
   E value
                      3.0e-10
   Match length
                      59
```



NCBI Description Mus musculus histone H3.1-D (H3-D) and histone H4-D (H4-D) genes, complete cds

Seq. No. 306930

Seq. ID uC-zmflb73188e11b1

Method BLASTX
NCBI GI g137460
BLAST score 255
E value 4.0e-22
Match length 76
% identity 70

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi_67952_pir__PXPZV9 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 69K chain - carrot >gi_167560 (J03769)

vacular H+-ATPase [Daucus carota]

Seq. No. 306931

Seq. ID uC-zmflb73188f03b1

Method BLASTN
NCBI GI g550435
BLAST score 82
E value 1.0e-38
Match length 106
% identity 94

NCBI Description Z.mays CYP71C1 mRNA for cytochrome P-450

Seq. No. 306932

Seq. ID uC-zmflb73188h03b1

Method BLASTX
NCBI GI g3747048
BLAST score 197
E value 8.0e-16
Match length 48
% identity 81

NCBI Description (AF093539) methionine synthase [Zea mays]

Seq. No. 306933

Seq. ID uC-zmflb73188h12b1

Method BLASTX
NCBI GI g300265
BLAST score 165
E value 5.0e-12
Match length 36
% identity 94

NCBI Description HSP68=68 kda heat-stress DnaK homolog [Lycopersicon

peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]

Seq. No. 306934

Seq. ID uC-zmflb73189c06b1

Method BLASTX
NCBI GI g3242789
BLAST score 224
E value 8.0e-19
Match length 64
% identity 64

NCBI Description (AF055357) respiratory burst oxidase protein D [Arabidopsis

thaliana]



Seq. No. 306935

Seq. ID uC-zmflb73189g03b1

Method BLASTX
NCBI GI g3193324
BLAST score 175
E value 1.0e-12
Match length 107
% identity 38

NCBI Description (AF069299) contains similarity to WD domains, G-beta

repeats (Pfam: G-beta.hmm, score: 22.80 and 35.84)

[Arabidopsis thaliana]

ΨŽ.

Seq. No. 306936

Seq. ID uC-zmflb73190d08b1

Method BLASTX
NCBI GI g3258570
BLAST score 154
E value 4.0e-10
Match length 127
% identity 37

NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]

Seq. No. 306937

Seq. ID uC-zmflb73190f07b1

Method BLASTX
NCBI GI g1771158
BLAST score 197
E value 4.0e-15
Match length 149
% identity 30

NCBI Description (Y07861) MFP1 protein [Lycopersicon esculentum]

Seq. No. 306938

Seq. ID uC-zmflb73191b02b1

Method BLASTN
NCBI GI g21449
BLAST score 75
E value 4.0e-34
Match length 79
% identity 99

NCBI Description S.tuberosum DNA for U6 small nuclear RNA promoter region

Seq. No. 306939

Seq. ID uC-zmflb73191b12b1

Method BLASTX
NCBI GI g1181673
BLAST score 618
E value 2.0e-64
Match length 122
% identity 98

NCBI Description (U41652) heat shock protein cognate 70 [Sorghum bicolor]

Seq. No. 306940

Seq. ID uC-zmflb73191c02b1

Method BLASTX NCBI GI g2554835



BLAST score 274-E value 3.0e-24 Match length 89 % identity 64

NCBI Description Chain I, Acetohydroxy Acid Isomeroreductase Complexed With

Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate) >gi 2554836 pdb 1YVE J Chain J,

Acetohydroxy Acid Isomeroreductase Complexed With Nadph,

τ,

Magnesium And Inhibitor Ipoha (N-Hydroxy-N-

Isopropyloxamate) >gi_2554837_pdb_1YVE_K Chain K,

Acetohydroxy Acid Isomeroreductase Complexed With Nadph,

Magnesium And Inhibitor Ipoha (N-Hydroxy-N-

Isopropyloxamate) >gi_2554838_pdb_1YVE_L Chain L,

Acetohydroxy Acid Isomeroreductase Complexed With Nadph,

Magnesium And Inhibitor Ipoha (N-Hydroxy-N-

Isopropyloxamate)

Seq. No. 306941

Seq. ID uC-zmflb73191h11b1

Method BLASTX
NCBI GI g3075390
BLAST score 202
E value 2.0e-31
Match length 89
% identity 82

NCBI Description (AC004484) protein kinase ARSK1 [Arabidopsis thaliana]

Seq. No. 306942

Seq. ID uC-zmflb73192c03a1

Method BLASTN
NCBI GI g2935572
BLAST score 43
E value 5.0e-15
Match length 131
% identity 84

NCBI Description Oryza sativa strain Indica IR58 KNOX class homeodomain

protein (Oskn2) mRNA, complete cds

Seq. No. 306943

Seq. ID uC-zmflb73192d06b1

Method BLASTX
NCBI GI g2317910
BLAST score 200
E value 5.0e-22
Match length 101
% identity 51

NCBI Description (U89959) CER1 protein [Arabidopsis thaliana]

Seq. No. 306944

Seq. ID uC-zmflb73192e09a1

Method BLASTN
NCBI GI g1698669
BLAST score 112
E value 3.0e-56
Match length 220
% identity 88

NCBI Description Zea mays S-like RNase (kin1) mRNA, complete cds

Seq. No. 306945
Seq. ID uC-zmflb73192f09b1
Method BLASTX

NCBI GI g4006831 BLAST score 163 E value 7.0e-19 Match length 137 % identity 33

NCBI Description (AC005970) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 306946

Seq. ID uC-zmflb73192g10b1

Method BLASTX
NCBI GI g4455338
BLAST score 344
E value 3.0e-33
Match length 117
% identity 62

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 306947

Seq. ID uC-zmflb73193a01b1

Method BLASTX
NCBI GI g113621
BLAST score 361
E value 1.0e-57
Match length 138
% identity 85

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624 prf 1307278A

1. The second

cytoplasmic aldolase [Zea mays]

Seq. No. 306948

Seq. ID uC-zmflb73193a05a1

Method BLASTN
NCBI GI 9498772
BLAST score 219
E value 1.0e-120
Match length 289
% identity 95

NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein

Seq. No. 306949

Seq. ID uC-zmflb73193b04b1

Method BLASTN
NCBI GI 9483443
BLAST score 65
E value 5.0e-28
Match length 65
% identity 100

NCBI Description Z.mays IBP2 mRNA for initiator-binding protein



```
Seq. No.
                   306950
                  uC\text{-}zmf1b73193b09b1\\
Seq. ID
Method
                  BLASTX
                   g1181331
NCBI GI
BLAST score
                   193
                   3.0e-17
E value
                   91
Match length
                   56
% identity
NCBI Description (X77569) calnexin [Zea mays]
                   306951
Seq. No.
                   uC-zmflb73193e10a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2213871
BLAST score
                   158
                   8.0e-11
E value
                   61
Match length
% identity
                   66
                  (AF003126) poly(A)-binding protein [Mesembryanthemum
NCBI Description
                   crystallinum]
                   306952
Seq. No.
                   uC\text{-}zmf1b73193f10a1\\
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168462
BLAST score
                   43
                   8.0e-15
E value
Match length
                   66
                   93
% identity
                  Zea mays defective suppressor-mutator from the
NCBI Description
                   brittle-1-mutable allele
                   306953
Seq. No.
                   uC-zmflb73193g04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g122022
BLAST score
                   346
E value
                   1.0e-32
Match length
                   74
                   95
% identity
NCBI Description
                   HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat
                   >gi 21801 emb CAA42530 (X59873) histone H2B [Triticum
                   aestivum]
                   306954
Seq. No.
Seq. ID
                   uC-zmflb73193h10b1
Method
                   BLASTX
NCBI GI
                   g1086149
BLAST score
                   704
E value
                   1.0e-74
Match length
                   151
% identity
                   89
NCBI Description psaA protein - Sorghum chloroplast
```

306955

Seq. No.

Seq. ID uC-zmflb73194c05b2

Method BLASTX

E value

Match length

4.0e-35



```
*.X.
NCBI GI
                   g2586083
BLAST score
                   234
                   3.0e-19
E value
                   176
Match length
% identity
                   (U72725) receptor kinase-like protein [Oryza
NCBI Description
                   longistaminata]
                   306956
Seq. No.
                   uC-zmf1b73194c12b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455331
BLAST score
                   245
                   1.0e-20
E value
Match length
                   97
% identity
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]
                   306957
Seq. No.
Seq. ID
                   uC-zmflb73194e09b2
Method
                   BLASTX
NCBI GI
                   g2191187
BLAST score
                   167
                   2.0e-11
E value
                   70
Match length
                   47
% identity
                   (AF007271) contains similarity to a DNAJ-like domain
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   306958
Seq. ID
                   uC-zmflb73194f09b2
Method
                   BLASTX
NCBI GI
                   q2384758
BLAST score
                   695
E value
                   2.0e-73
Match length
                   136
% identity
                   96
                   (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
NCBI Description
                   sativa]
Seq. No.
                   306959
                   uC-zmflb73194f12b2
Seq. ID
Method
                   BLASTN
                   q949979
NCBI GI
BLAST score
                   52
                   4.0e-20
E value
                   85
Match length
                   92
 % identity
NCBI Description Z.mays Glossy2 locus DNA
                   306960
Seq. No.
                   uC-zmflb73194g04b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4539662
BLAST score
                   260
```



% identity

(AF061282) polyprotein [Sorghum bicolor] NCBI Description

Seq. No.

306961

Seq. ID

uC-zmflb73194h03b2

Method NCBI GI BLASTX

BLAST score

g2493650

E value Match length 2.0e-20 148

% identity

45

242

NCBI Description

RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD

CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)

>gi 1167858 emb CAA93139 (Z68903) chaperonin [Secale

cereale]

Seq. No.

306962

Seq. ID

uC-zmflb73194h05b2

Method NCBI GI BLASTX

BLAST score

g2979544 228

E value Match length 1.0e-18

% identity

111 50

NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No.

306963

Seq. ID

uC-zmflb73194h08b2

Method

BLASTN

NCBI GI

g4388782

BLAST score

143

E value

1.0e-74

Match length

219

% identity

91

NCBI Description

Zea mays 40S ribosomal protein S27 homolog mRNA, complete

Seq. No.

306964

Seq. ID

uC-zmflb73194h11b2

Method NCBI GI BLASTN g3955064

BLAST score

42

E value

4.0e-14

Match length

82

% identity

88

NCBI Description Zea mays PHYT I gene for acidic phytase

Seq. No.

306965

Seq. ID

uC-zmflb73195c03b1

Method NCBI GI BLASTX q2829897

BLAST score

184

E value Match length 2.0e-13

% identity

63 57

NCBI Description

(AC002311) Unknown protein [Arabidopsis thaliana]

NCBI Description

306971

Seq. No.



```
Seq. No.
                    306966
  Seq. ID
                    uC-zmflb73195f10b1
  Method
                    BLASTX
                    g4455351
  NCBI GI
  BLAST score
                    195
  E value
                    6.0e-15
  Match length
                    55
  % identity
                    58
                    (AL035524) putative protein [Arabidopsis thaliana]
  NCBI Description
                    306967
  Seq. No.
                    uC-zmflb73195g12b1
  Seq. ID
  Method
                    BLASTX
                    g2129753
  NCBI GI
  BLAST score
                    348
  E value
                    1.0e-32
  Match length
                    139
                    56
  % identity
                    threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
  NCBI Description
                    thaliana (fragment) >gi 1448917 (L41666) threonine synthase
                     [Arabidopsis thaliana]
                    306968
  Seq. No.
  Seq. ID
                    uC-zmflb73195h08b1
  Method
                    BLASTX
  NCBI GI
                    g1345132
                     472
  BLAST score
  E value
                    3.0e-47
  Match length
                    164
  % identity
                     (U47029) ERECTA [Arabidopsis thaliana]
  NCBI Description
                    >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase
                     [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
                    protein kinase, ERECTA [Arabidopsis thaliana]
                     306969
  Seq. No.
  Seq. ID
                    uC-zmflb73196a07b1
  Method
                    BLASTX
                     g1199467
  NCBI GI
  BLAST score
                     257
  E value
                     3.0e-22
  Match length
                     112
  % identity
                     42
  NCBI Description
                     (D64155) possible aldehyde decarbonylase [Arabidopsis
                     thaliana]
  Seq. No.
                     306970
  Seq. ID
                    uC-zmflb73196b01b1
  Method
                    BLASTX
  NCBI GI
                     q2668742
  BLAST score
                     429
                     3.0e-42
  E value
  Match length
                     86
  % identity
                     97
```

(AF034945) glycine-rich RNA binding protein [Zea mays]



```
uC-zmflb73196b03b1
Seq. ID
                                                                        - 74
Method
                   BLASTX
NCBI GI
                   g4406784
BLAST score
                   259
E value
                   2.0e-22
Match length
                   146
 % identity
                   38
                   (AC006532) putative oligopeptide transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   306972
 Seq. No.
                   uC-zmflb73196h10b1
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g125065
BLAST score
                   251
 E value
                   2.0e-21
Match length
                   121
 % identity
                   50
 NCBI Description
                   60 KD JASMONATE-INDUCED PROTEIN >gi 419795 pir S25092
                   jasmonate-induced protein - barley >gi 19011 emb CAA47017
                   (X66376) jasmonate-induced protein [Hordeum vulgare]
                   306973
 Seq. No.
 Seq. ID
                   uC-zmflb73197b01b1
Method
                   BLASTX
 NCBI GI
                   g4263787
 BLAST score
                   165
 E value
                   3.0e-11
Match length
                   44
 % identity
                   73
 NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]
                   306974
 Seq. No.
                   uC-zmflb73197c08b1
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g551482
 BLAST score
                   239
 E value
                   1.0e-132
Match length
                   431
 % identity
                   94
 NCBI Description
                   Zea mays ABA- and ripening-inducible-like protein mRNA,
                   complete cds
                   306975
 Seq. No.
                   uC-zmflb73197e11b1
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   g2980781
 BLAST score
                   174
                   1.0e-12
E value
Match length
                   58
 % identity
                   57
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
```

306976 Seq. No.

Seq. ID uC-zmflb73197f08b1

Method BLASTX NCBI GI g1706958



```
BLAST score
                  8.0e-24
E value
Match length
                  146
% identity
                  32
NCBI Description
                  (U58284) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  306977
Seq. ID
                  uC-zmflb73198a12b1
Method
                  BLASTX
NCBI GI
                  g2493147
BLAST score
                  182
E value
                  1.0e-13
Match length
                  50
% identity
                  74
NCBI Description
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >qi 857574
                   (U27098) H+-ATPase [Oryza sativa]
Seq. No.
                  306978
Seq. ID
                  uC-zmflb73198d07b1
Method
                  BLASTX
NCBI GI
                  g2924247
BLAST score
                  211
E value
                  4.0e-25
Match length
                  67
% identity
                  90
NCBI Description (Y07782) expansin [Oryza sativa]
                  306979
Seq. No.
Seq. ID
                  uC-zmflb73198d12b1
Method
                  BLASTX
NCBI GI
                  g2191178
BLAST score
                  163
E value
                  4.0e-11
Match length
                  108
% identity
                  37
NCBI Description
                  (AF007270) contains similarity to MIPP proteins
                   [Arabidopsis thaliana]
Seq. No.
                  306980
                  uC-zmflb73198g03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538978
BLAST score
                  209
E value
                  1.0e-16
Match length
                  71
% identity
                  56
NCBI Description
                  (AL049487) hypothetical protein [Arabidopsis thaliana]
                  306981
Seq. No.
                  uC-zmflb73198h09b1
Seq. ID
Method
                  BLASTN
```

NCBI GI g4512215 BLAST score 89 E value 2.0e-42 Match length 118 92 % identity

NCBI Description Zea mays ZmRR1 mRNA for response regulator, complete cds



```
Seq. No.
                    306982
                    uC-zmflb73199a07b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g532623
 BLAST score
                    251
 E value
                    1.0e-21
 Match length
                    87
                    64
 % identity
 NCBI Description
                   (L35913) lipase [Zea mays]
                    306983
 Seq. No.
 Seq. ID
                    uC-zmflb73199b05b1
 Method
                    BLASTX
 NCBI GI
                    q1083942
 BLAST score
                    149
 E value
                    7.0e-10
 Match length
                    69
                    43
 % identity
                    rubber particle cytochrome P450 - guayule
 NCBI Description
                    >gi 791093 emb CAA55025 (X78166) rubber particle protein
                    [Parthenium argentatum]
                    306984
 Seq. No.
 Seq. ID
                    uC-zmflb73199d05b1
                    BLASTN
 Method
 NCBI GI
                    g2773153
 BLAST score
                    41
                    9.0e-14
 E value
 Match length
                    81
 % identity
 NCBI Description
                    Oryza sativa abscisic acid- and stress-inducible protein
                    (Asr1) mRNA, complete cds
 Seq. No.
                    306985
 Seq. ID
                    uC-zmflb73199e11b1
 Method
                    BLASTX
 NCBI GI
                    g4519671
 BLAST score
                    147
 E value
                    6.0e-10
 Match length
                    111
 % identity
                    41
 NCBI Description
                    (AB017693) transfactor [Nicotiana tabacum]
                    306986
 Seq. No.
                    uC-zmflb73199h09b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1632822
 BLAST score
                    306
 E value
                    3.0e-33
 Match length
                    77
                    94
 % identity
                    (Y08962) transmembrane protein [Oryza sativa] >gi_1667594
 NCBI Description
                    (U77297) transmembrane protein [Oryza sativa]
```

Seq. No. 306987

Seq. ID uC-zmflb73200a06b1

```
BLASTX
Method
                   g135411
NCBI GI
                   477
BLAST score
                   5.0e-48
E value
                   99
Match length
                   95
% identity
                   TUBULIN ALPHA-2 CHAIN >gi_82732_pir__S15772 tubulin alpha-2
NCBI Description
                   chain - maize >gi 22148 emb_CAA33733_ (X15704)
                   alpha2-tubulin [Zea mays]
                   306988
Seq. No.
                   uC-zmflb73200a10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g115771
BLAST score
                   484
                   1.0e-48
E value
                   109
Match length
                   83
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll a/b-binding protein precursor - maize
                   >gi 22224 emb CAA32900_ (X14794) chlorophyll a/b-binding
                   preprotein (AA 1 - 262) [Zea mays]
                   306989
Seq. No.
                   uC-zmflb73200b01b1
Seq. ID
                   BLASTN
Method
                   g1296954
NCBI GI
                   35
BLAST score
                   4.0e-10
E value
                   51
Match length
                   92
% identity
NCBI Description O.sativa mRNA for novel protein, osr40c1
                   306990
Seq. No.
                   uC-zmflb73200b06b1
Seq. ID
                   BLASTX
Method
                   g2625154
NCBI GI
                   177
BLAST score
                   4.0e-13
E value
                   75
Match length
                   56
% identity
                   (AF032877) alpha-tubulin [Chloromonas sp. ANT3]
NCBI Description
                   306991
Seq. No.
                   uC-zmflb73200c01b1
Seq. ID
                   BLASTX
Method
                   g4128133
NCBI GI
                   154
BLAST score
                    6.0e-18
E value
Match length
                    74
```

% identity 64

(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens] NCBI Description

306992 Seq. No.

Seq. ID uC-zmflb73200c09b1

Method BLASTN



NCBI GI g396148 BLAST score 132 E value 7.0e-68 Match length 220 % identity 91

NCBI Description Z.mays CHI gene

Seq. No. 306993

Seq. ID uC-zmflb73200d06a1

Method BLASTX
NCBI GI g3980412
BLAST score 154
E value 3.0e-10
Match length 75
% identity 52

NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 306994

Seq. ID uC-zmflb73200d07b1

Method BLASTX
NCBI GI g4099148
BLAST score 310
E value 3.0e-28
Match length 71
% identity 83

NCBI Description (U84268) YLP [Hordeum vulgare]

Seq. No. 306995

Seq. ID uC-zmflb73200f02b1

Method BLASTX
NCBI GI g2119278
BLAST score 268
E value 9.0e-49
Match length 114
% identity 80

NCBI Description tubulin beta-1 chain - rice

Seq. No. 306996

Seq. ID uC-zmflb73200f09b1

Method BLASTX
NCBI GI g135411
BLAST score 523
E value 3.0e-53
Match length 113
% identity 88

NCBI Description TUBULIN ALPHA-2 CHAIN >gi_82732_pir__S15772 tubulin alpha-2

chain - maize >gi 22148 emb CAA33733 (X15704)

بيوفي ريون

alpha2-tubulin [Zea mays]

Seq. No. 306997

Seq. ID uC-zmflb73200h02a1

Method BLASTN
NCBI GI g22245
BLAST score 176
E value 2.0e-94
Match length 248
% identity 93



NCBI Description Zea mays DNA for cin4 element (showing homology to reverse transcriptase)

Seq. No. 306998

Seq. ID uC-zmflb73200h02b1

Method BLASTN
NCBI GI g3452296
BLAST score 62
E value 2.0e-26
Match length 117
% identity 90

NCBI Description Zea mays retrotransposon Ji-4 3' LTR, partial sequence

Seq. No. 306999

Seq. ID uC-zmflb73200h09b1

Method BLASTX
NCBI GI g2076623
BLAST score 251
E value 2.0e-21
Match length 77
% identity 62

NCBI Description (Z95151) PtrB [Mycobacterium leprae]

Seq. No. 307000

Seq. ID uC-zmflb73201c03b1

Method BLASTX
NCBI GI g1703200
BLAST score 220
E value 4.0e-23
Match length 127
% identity 72

NCBI Description PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase

[Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353)

protein kinase [Arabidopsis thaliana]

>gi 4220516 emb CAA22989 (AL035356) protein kinase (AFC2)

[Arabidopsis thaliana]

Seq. No. 307001

Seq. ID uC-zmflb73201e08b1

Method BLASTX
NCBI GI g2160161
BLAST score 211
E value 1.0e-16
Match length 154
% identity 11

NCBI Description (AC000132) F21M12.7 gene product [Arabidopsis thaliana]

Seq. No. 307002

Seq. ID uC-zmflb73201f07b1

Method BLASTX
NCBI GI g2062167
BLAST score 310
E value 2.0e-28
Match length 122
% identity 49

NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis

thaliana]



```
307003
Seq. No.
Seq. ID
                  uC-zmflb73201g07b1
Method
                  BLASTX
NCBI GI
                  g1498597
BLAST score
                  160
                  4.0e-11
E value
                  53
Match length
% identity
                  (U66105) phospholipid transfer protein [Zea mays]
NCBI Description
                  307004
Seq. No.
                  uC-zmflb73201h09b1
Seq. ID
                  BLASTX
Method
                  g2887333
NCBI GI
BLAST score
                  149
E value
                  1.0e-09
                  63
Match length
% identity
                  44
NCBI Description (AL021817) lysophospholipase [Schizosaccharomyces pombe]
                  307005
Seq. No.
                  uC-zmflb73202a10b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2832242
                  94
BLAST score
                  2.0e-45
E value
Match length
                  172
                  89
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  307006
Seq. ID
                  uC-zmflb73202d05b1
Method
                  BLASTX
NCBI GI
                   g2791834
BLAST score
                   272
E value
                   3.0e-24
Match length
                   63
% identity
                   87
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
NCBI Description
                   307007
Seq. No.
Seq. ID
                   uC-zmflb73202e11b1
                   BLASTN
Method
                   g602605
NCBI GI
BLAST score
                   122
                   2.0e-62
E value
Match length
                   178
% identity
                   65
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
                   307008
Seq. No.
Seq. ID
                   uC-zmflb73203c12a1
```

Method BLASTX
NCRI GI G3128231

NCBI GI g3128231 BLAST score 213 E value 4.0e-17 138



130 Match length % identity 16 (AC004077) hypothetical protein [Arabidopsis thaliana] NCBI Description >qi 3337370 (AC004481) hypothetical protein [Arabidopsis thaliana] 307009 Seq. No. uC-zmflb73203e05a1 Seq. ID BLASTN Method NCBI GI g563234 BLAST score 111 9.0e-56 E value 195 Match length % identity 89 NCBI Description Zea mays xyloglucan endo-transglycosylase homolog gene, complete cds 307010 Seq. No. uC-zmflb73204a03b1Seq. ID BLASTX Method NCBI GI g168404 BLAST score 162 E value 2.0e-17 Match length 50 % identity 79 NCBI Description (J01238) actin [Zea mays] Seq. No. 307011 Seq. ID uC-zmflb73204b02b1 BLASTX Method NCBI GI g2921304 BLAST score 301 8.0e-28 E value Match length 66 92 % identity NCBI Description (AF033496) herbicide safener binding protein [Zea mays] 307012 Seq. No. uC-zmflb73204b06b1 Seq. ID Method BLASTX NCBI GI g1167955 BLAST score 215 3.0e-17 E value Match length 107 % identity 46 (U43497) putative 32.7 kDa jasmonate-induced protein NCBI Description [Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein [Hordeum vulgare] Seq. No. 307013 uC-zmflb73204b07b1 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g3249085
BLAST score 282
E value 3.0e-25
Match length 101
% identity 57

NCBI Description





```
NCBI Description
                  (AC004473) T13D8.31 [Arabidopsis thaliana]
Seq. No.
                  307014
Seq. ID
                  uC-zmflb73204d04a1
Method
                  BLASTX
NCBI GI
                  q629844
BLAST score
                  254
E value
                  6.0e-22
Match length
                  66
% identity
                  79
NCBI Description
                  heat shock protein hsp70-5 - maize (fragment)
                  >gi 498775 emb CAA55184 (X78415) heat shock protein 70 kDa
                  [Zea mays]
Seq. No.
                  307015
Seq. ID
                  uC-zmflb73204d09b1
Method
                  BLASTX
NCBI GI
                  g3935157
BLAST score
                  184
                  3.0e-14
E value
Match length
                  42
% identity
                  79
NCBI Description
                  (AC005106) T25N20.21 [Arabidopsis thaliana]
Seq. No.
                  307016
Seq. ID
                  uC-zmflb73204g06b1
Method
                  BLASTN
NCBI GI
                  g4584684
BLAST score
                  72
                  4.0e-32
E value
Match length
                  207
                  84
% identity
NCBI Description
                  Hordeum vulgare high light-induced mRNA for putative lectin
                  (18kDa)
Seq. No.
                  307017
Seq. ID
                  uC-zmflb73205a07b2
Method
                  BLASTX
NCBI GI
                  g3860272
BLAST score
                  293
E value
                  2.0e-26
Match length
                  62
% identity
                  90
NCBI Description
                  (AC005824) putative suppressor protein [Arabidopsis
                  thaliana] >gi_4314399 gb AAD15609 (AC006232) putative skd1
                  protein [Arabidopsis thaliana]
Seq. No.
                  307018
Seq. ID
                  uC-zmflb73205a08b2
Method
                  BLASTX
NCBI GI
                  g4455278
BLAST score
                  209
E value
                  1.0e-16
Match length
                  124
% identity
                  40
```

(AL035527) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
Seq. ID
                  uC-zmflb73205d04b2
Method
                  BLASTN
NCBI GI
                  q644492
BLAST score
                  74
E value
                  6.0e-34
Match length
                  110
% identity
                  92
NCBI Description Corn elongation factor lalpha gene, complete cds
Seq. No.
                  307020
Seq. ID
                  uC-zmflb73205d11b2
Method
                  BLASTX
NCBI GI
                  g2829910
BLAST score
                  220
E value
                  5.0e-18
Match length
                  106
% identity
                  23
NCBI Description (AC002291) Unknown protein, contains regulator of
                  chromosome condensation motifs [Arabidopsis thaliana]
Seq. No.
                  307021
Seq. ID
                  uC-zmflb73205g03b2
Method
                  BLASTX
NCBI GI
                  g642134
                  393
BLAST score
E value
                  2.0e-38
Match length
                  87
% identity
                  80
                  (D45355) protein kinase [Arabidopsis thaliana]
NCBI Description
                  >gi_3063704_emb_CAA18595.1 (AL022537) protein kinase AME3
                  [Arabidopsis thaliana]
Seq. No.
                  307022
Seq. ID
                  uC-zmflb73205h12b2
Method
                  BLASTX
NCBI GI
                  q1076746
BLAST score
                  491
```

E value 9.0e-50 Match length 99 % identity 94

NCBI Description heat shock protein 70 - rice (fragment)

>gi_763160_emb_CAA47948 (X67711) heat shock protein 70

[Oryza sativa]

Seq. No. 307023

Seq. ID uC-zmflb73206b10b1

Method BLASTX NCBI GI q2980779 BLAST score 204 E value 6.0e-16 Match length 106 % identity

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

307024 Seq. No.

Seq. ID uC-zmflb73206f11b1

BLAST score

E value

121

1.0e-61



```
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  35
E value
                   4.0e-10
Match length
                  35
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  307025
Seq. No.
Seq. ID
                  uC-zmflb73206g05b1
Method
                  BLASTX
NCBI GI
                  g2832685
BLAST score
                  550
E value
                  2.0e-56
Match length
                  135
% identity
                  80
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
Seq. No.
                  307026
Seq. ID
                  uC-zmflb73206g12b1
Method
                  BLASTX
NCBI GI
                  q2191187
BLAST score
                  147
E value
                  4.0e-09
Match length
                  47
% identity
                  62
NCBI Description
                  (AF007271) contains similarity to a DNAJ-like domain
                   [Arabidopsis thaliana]
                  307027
Seq. No.
Seq. ID
                  uC-zmflb73207a02b1
Method
                  BLASTN
NCBI GI
                  q435941
BLAST score
                  58
                  5.0e-24
E value
Match length
                  90
                  91
% identity
NCBI Description Oryza sativa Nipponbare bZIP DNA-binding factor (osZIP-1a)
                  mRNA, complete cds
                  307028
Seq. No.
Seq. ID
                  uC-zmflb73207a05b1
Method
                  BLASTX
NCBI GI
                  q961450
BLAST score
                  161
E value
                  6.0e-11
Match length
                  97
% identity
                  33
NCBI Description
                  (D63879) KIAA0156 gene product is related to Xenopus
                  nucleolin. [Homo sapiens]
Seq. No.
                  307029
Seq. ID
                  uC-zmflb73207b06b1
Method
                  BLASTN
NCBI GI
                  g602605
```

Seq. ID

NCBI GI BLAST score

E value

Method

```
Match length
                   173
% identity
                   60
NCBI Description
                  Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
                  307030
Seq. No.
                  uC-zmflb73207b09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q135104
BLAST score
                  233
                  2.0e-19
E value
Match length
                  57
% identity
                  67
NCBI Description
                  MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE (CONTAINS:
                  GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE), AND
                  PROLYL-TRNA SYNTHETASE (PROLINE--TRNA LIGASE))
                  >gi_68554_pir SYHUQT glutamyl-prolyl-tRNA synthetase -
                  human >gi 31958 emb CAA38224 (X54326) glutaminyl-tRNA
                  synthetase [Homo sapiens]
Seq. No.
                  307031
Seq. ID
                  uC-zmflb73207c07b1
Method
                  BLASTX
NCBI GI
                  g4587584
BLAST score
                  512
E value
                  4.0e-52
Match length
                  123
% identity
                  81
NCBI Description
                  (AC007232) unknown protein [Arabidopsis thaliana]
Seq. No.
                  307032
Seq. ID
                  uC-zmflb73207e07b1
Method
                  BLASTX
NCBI GI
                  g4325370
BLAST score
                  454
E value
                  8.0e-47
Match length
                  115
% identity
                  74
NCBI Description
                   (AF128396) similar to human phosphotyrosyl phosphatase
                  activator PTPA (GB:X73478) [Arabidopsis thaliana]
Seq. No.
                  307033
Seq. ID
                  uC-zmflb73207e08b1
Method
                  BLASTX
NCBI GI
                  q2160156
BLAST score
                  263
                  6.0e-23
E value
                  95
Match length
% identity
                  54
NCBI Description
                  (AC000132) Strong similarity to S. pombe leucyl-tRNA
                  synthetase (gb_Z73100). [Arabidopsis thaliana]
Seq. No.
                  307034
```

43576

uC-zmflb73207e09b1

BLASTX g3088920

1.0e-14



```
Match length
                    73
% identity
                   59
 NCBI Description
                    (AF059363) alcohol dehydrogenase D [Gossypium nelsonii]
                   >gi 3088922 (AF059364) alcohol dehydrogenase D [Gossypium
                   nelsonii]
 Seq. No.
                   307035
 Seq. ID
                   uC-zmflb73207f01a1
 Method
                   BLASTX
 NCBI GI
                   g1345502
 BLAST score
                   289
 E value
                   2.0e-35
 Match length
                   155
 % identity
                   46
 NCBI Description
                   (X57297) TNP2 [Antirrhinum majus]
                   307036
 Seq. No.
 Seq. ID
                   uC-zmflb73207f07b1
 Method
                   BLASTX
 NCBI GI
                   q4038594
 BLAST score
                   374
 E value
                   5.0e-36
 Match length
                   113
 % identity
                   63
 NCBI Description
                    (AJ222798) tDET1 protein [Lycopersicon esculentum]
                   >gi_4454332 emb CAA11914 (AJ224356) tDET1 protein
                    [Lycopersicon esculentum]
 Seq. No.
                   307037
                   uC-zmflb73207f09b1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q4325370
 BLAST score
                   374
                   5.0e-36
 E value
                   95
 Match length
 % identity
                   72
 NCBI Description
                   (AF128396) similar to human phosphotyrosyl phosphatase
                   activator PTPA (GB:X73478) [Arabidopsis thaliana]
 Seq. No.
                   307038
 Seq. ID
                   uC-zmflb73207g01b1
 Method
                   BLASTX
 NCBI GI
                   g2982259
 BLAST score
                   396
 E value
                   1.0e-38
 Match length
                   84
 % identity
 NCBI Description
                   (AF051212) probable 60s ribosomal protein L13a [Picea
```

Seq. No. 307039

uC-zmflb73207h06b1 Seq. ID

mariana]

Method BLASTX g3892055 NCBI GI BLAST score 366 E value 4.0e-35 Match length 85

```
% identity
                   (AC002330) putative transport protein [Arabidopsis
NCBI Description
                  thaliana]
                   307040
Seq. No.
                  uC-zmflb73207h09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2982259
BLAST score
                  152
                  1.0e-11
E value
Match length
                  51
                   60
% identity
                   (AF051212) probable 60s ribosomal protein L13a [Picea
NCBI Description
                  mariana]
                   307041
Seq. No.
                  uC-zmflb73208a12b1
Seq. ID
                  BLASTX
Method
                  g1928991
NCBI GI
BLAST score
                   214
E value
                   2.0e-17
Match length
                   89
% identity
                   56
                   (U92815) heat shock protein 70 precursor [Citrullus
NCBI Description
                  lanatus]
                   307042
                  uC-zmflb73208b10b1
                  BLASTX
                   g4105131
```

Seq. No. Seq. ID Method

NCBI GI BLAST score 255 2.0e-22 E value Match length 79 % identity 67

(AF043539) ClpC protease [Spinacia oleracea] NCBI Description

307043 Seq. No. uC-zmflb73208c09b1 Seq. ID

BLASTX Method

NCBI GI g3047104 BLAST score 460 E value 4.0e-46 Match length 115 % identity 72

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

307044 Seq. No.

uC-zmflb73208g09b1 Seq. ID

Method BLASTX NCBI GI g3660465 BLAST score 391 E value 6.0e-38 Match length 136 % identity 57

NCBI Description (AJ001753) Inositol 1,3,4-Trisphosphate 5/6 kinase

[Arabidopsis thaliana]

```
307045
Seq. No.
                  uC-zmflb73210a11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173027
BLAST score
                  324
                  5.0e-30
E value
Match length
                  91
% identity
                  70
                  60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
NCBI Description
                  protein L31 [Nicotiana glutinosa]
Seq. No.
                  307046
Seq. ID
                  uC-zmflb73210b04b1
Method
                  BLASTX
NCBI GI
                  q4586021
BLAST score
                  201
                  1.0e-15
E value
Match length
                  43
% identity
                   (AC007170) putative cytoplasmic aconitate hydratase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  307047
Seq. ID
                  uC-zmflb73210b05b1
Method
                  BLASTX
NCBI GI
                  q1944504
BLAST score
                  204
E value
                  3.0e-16
Match length
                  57
% identity
                  75
                  (D64036) protein cdc2 kinase [Oryza sativa]
NCBI Description
                   307048
Seq. No.
                  uC-zmflb73210b10a1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g2653557
BLAST score
                  60
                   4.0e-25
E value
Match length
                  136
% identity
                   86
                  Zea mays mRNA for ferredoxin-sulfite reductase precursor,
NCBI Description
                   complete cds
                   307049
Seq. No.
                  uC-zmflb73210c08a1
Seq. ID
                  BLASTN
Method
```

Method BLASTN
NCBI GI g2331300
BLAST score 106
E value 1.0e-52
Match length 206
% identity 87

NCBI Description Zea mays ribosomal protein S4 type I (rps4) mRNA, complete

cds

Seq. No.

307050

Seq. ID

uC-zmf1b73210c09b1

Method

BLASTX

```
g2911072
NCBI GI
BLAST score
                   222
                   2.0e-25
E value
                   101
Match length
% identity
                   63
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   307051
Seq. No.
                  uC\text{-}zmf1b73210d05a1\\
Seq. ID
                   BLASTN
Method
                   g498772
NCBI GI
                   131
BLAST score
                   2.0e-67
E value
                   329
Match length
% identity
                   86
NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
                   307052
Seq. No.
                   uC-zmflb73210f11a1
Seq. ID
Method
                   BLASTX
                   g4469015
NCBI GI
                   359
BLAST score
                   4.0e-34
E value
                   107
Match length
                   70
% identity
                   (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                   307053
Seq. No.
                   uC-zmflb73212a03a1
Seq. ID
                   BLASTN
Method
                   g1213276
NCBI GI
BLAST score
                   88
                   6.0e-42
E value
                   123
Match length
                   93
% identity
NCBI Description Z.mays ZEMa gene
                   307054
Seq. No.
                   uC-zmflb73212f12a1
Seq. ID
                   BLASTX
Method
                   g4263527
NCBI GI
                   197
BLAST score
                   3.0e-15
E value
                   76
Match length
                   51
% identity
                   (AC004044) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   307055
Seq. No.
                   uC-zmflb73213a07a1
Seq. ID
```

Method BLASTX
NCBI GI g3859944
BLAST score 150
E value 1.0e-09
Match length 64
% identity 55

NCBI Description (AF084570) FKBP12 interacting protein [Arabidopsis

thaliana]



```
307056
Seq. No.
Seq. ID
                  uC-zmflb73213a07b1
Method
                  BLASTX
NCBI GI
                  g3859944
BLAST score
                  234
                  1.0e-19
E value
                  98
Match length
% identity
                  (AF084570) FKBP12 interacting protein [Arabidopsis
NCBI Description
                  thaliana]
                  307057
Seq. No.
Seq. ID
                  uC-zmflb73213b01b1
                  BLASTN
Method
NCBI GI
                  g312180
BLAST score
                  33
E value
                  4.0e-09
                  124
Match length
% identity
                  83
NCBI Description Z.mays GapC4 gene
                  307058
                                                                , ;~;.
Seq. No.
                  uC-zmflb73213d11a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2735016
BLAST score
                  61
E value
                   8.0e-26
Match length
                  212
                   86
% identity
                  Zea mays KI domain interacting kinase 1 (KIK1) mRNA,
NCBI Description
                  complete cds
                   307059
Seq. No.
Seq. ID
                   uC-zmflb73213d11b1
Method
                   BLASTX
NCBI GI
                   g2735017
BLAST score
                   657
E value
                   3.0e-69
Match length
                   124
% identity
                   99
                  (U82481) KI domain interacting kinase 1 [Zea mays]
NCBI Description
                   307060
Seq. No.
                   uC-zmflb73213f09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1172633
BLAST score
                   219
                   8.0e-18
E value
Match length
                   55
```

78 % identity

NCBI Description PROLIFERA PROTEIN >gi 675491 (L39954) contains MCM2/3/5 family signature; PROSITE; PS00847; disruption leads to

early lethal phenotype; similar to MCM2/3/5 family, most

similar to YBR1441 [Arabidopsis thaliana]

Seq. No. 307061

BLAST score

E value

42

3.0e-14



```
uC-zmflb73214c10b1
Seq. ID
                  BLASTX
Method
                  g3914005
NCBI GI
                  180
BLAST score
                  6.0e-19
E value
                  106
Match length
                  58
% identity
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586
                  (U85494) LON1 protease [Zea mays]
                  307062
Seq. No.
                  uC-zmflb73214d10b1
Seq. ID
                  BLASTX
Method
                  g2224915
NCBI GI
BLAST score
                  468
E value
                  8.0e-47
                  140
Match length
% identity
                   63
NCBI Description (U95968) beta-expansin [Oryza sativa]
Seq. No.
                  307063
                  uC-zmflb73214d12b1
Seq. ID
                  BLASTX
Method
                   g4580395
NCBI GI
BLAST score
                   597
E value
                   6.0e-62
Match length
                   173
% identity
                   71
NCBI Description (AC007171) putative kinesin-related protein [Arabidopsis
                   thaliana]
                   307064
Seq. No.
                   uC-zmflb73214e03b1
Seq. ID
                   BLASTN
Method
                   g940880
NCBI GI
                   35
BLAST score
                   4.0e-10
E value
                   71
Match length
                   89
% identity
NCBI Description Z.mays zag2 gene
                   307065
Seq. No.
                   uC-zmflb73214g10b1
Seq. ID
                   BLASTX
Method
                   g4371293
NCBI GI
                   149
BLAST score
                   6.0e-10
E value
                   92
Match length
% identity
                   39
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   307066
                   uC-zmflb73214h10b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g312180
```

ė.

```
Match length
                  87
% identity
NCBI Description Z.mays GapC4 gene
Seq. No.
                  307067
                  uC-zmflb73215b02a2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  9.0e-11
Match length
                  36
                  100
% identity
```

NCBI Description Xenopus laevis cDNA clone 27A6-1

307068

307069

uC-zmflb73215b04a2 Seq. ID Method BLASTN NCBI GI g2642212 BLAST score 36 5.0e-11 E value Match length 56 % identity 91

Seq. No.

Seq. No.

NCBI Description Zea mays nitrate-induced NOI protein gene, complete cds

Seq. No. Seq. ID uC-zmflb73215f06a2 Method BLASTN NCBI GI q22487 BLAST score 34 E value 1.0e-09 Match length 38 % identity 97

NCBI Description Maize gene for sucrose synthase

uC-zmflb73216b06b2 Seq. ID BLASTX Method g3789952 NCBI GI BLAST score 359 3.0e-34 E value Match length 98 % identity 74

(AF094775) chlorophyll a/b-binding protein presursor [Oryza NCBI Description

sativa]

307070

307071 Seq. No.

uC-zmflb73216d05b2Seq. ID

BLASTX Method g4539003 NCBI GI BLAST score 210 E value 7.0e-17 Match length 63 % identity 63

(AL049481) putative protein [Arabidopsis thaliana] NCBI Description

307072 Seq. No.

uC-zmflb73216h11b2 Seq. ID



```
Method
                   BLASTN
                   g3449316
NCBI GI
BLAST score
                   41
                   1.0e-13
E value
                   69
Match length
                   90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K9D7, complete sequence [Arabidopsis thaliana]
                   307073
Seq. No.
                   uC-zmflb73217d03b2
Seq. ID
                   BLASTX
Method
                   g584866
NCBI GI
                   241
BLAST score
E value
                   1.0e-20
Match length
                   68
% identity
                   68
                   CYTOCHROME P450 77A1 (CYPLXXVIIA1) (P-450EG6)
NCBI Description
                   >gi_542074_pir__S40267 cytochrome P450 - eggplant
                   >gi 438243 emb CAA50647 (X71656) P450 hydroxylase [Solanum
                   melongena]
                   307074
Seq. No.
                   uC-zmflb73217e02b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3249105
BLAST score
                   329
                   6.0e-31
E value
Match length
                   84
                   73
% identity
                   (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                   (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
                   307075
Seq. No.
                   uC-zmflb73217f01b2
Seq. ID
                   BLASTX
Method
                   g2290772
NCBI GI
                   162
BLAST score
                   9.0e-13
E value
Match length
                   93
% identity
                   (AF002164) AP-3 delta-adaptin subunit [Drosophila
NCBI Description
                   melanogaster]
                   307076
Seq. No.
                   uC-zmflb73217g06b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4567249
BLAST score
                   265
                   2.0e-23
E value
Match length
                   59
% identity
                   81
                   (AC007070) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 307077

Seq. ID uC-zmflb73218a01b2

Method BLASTX

```
g2632252
NCBI GI
BLAST score
                   179
E value
                   1.0e-21
Match length
                   60
```

% identity (Y12464) serine/threonine kinase [Sorghum bicolor] NCBI Description

307078 Seq. No.

uC-zmflb73218a05b2 Seq. ID

87

Method BLASTX NCBI GI g2252843 BLAST score 152 E value 2.0e-10 Match length 41 % identity

(AF013293) No definition line found [Arabidopsis thaliana] NCBI Description

Seq. No. 307079

uC-zmflb73218f02b2 Seq. ID

Method BLASTX NCBI GI q1170937 BLAST score 475 E value 9.0e-48 116 Match length 85 % identity

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 307080

Seq. ID uC-zmflb73218f09b2

Method BLASTX NCBI GI q1483177 BLAST score 190 E value 2.0e-14 Match length 53 % identity 60

(D86598) antifreeze-like protein (af70) [Picea abies] NCBI Description

Seq. No. 307081

uC-zmflb73219b01b2 Seq. ID

Method BLASTX q4455176 NCBI GI BLAST score 353 2.0e-33 E value Match length 144 52 % identity

NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]

307082 Seq. No.

uC-zmflb73219b02b2 Seq. ID

Method BLASTX NCBI GI g136063 BLAST score 194 E value 4.0e-15 Match length 36

111

307084

```
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi 68426 pir_ISZMT triose-phosphate isomerase (EC
                  5.3.1.1) - maize >gi 168647 (L00371) triosephosphate
                  isomerase 1 [Zea mays] >gi 217974 dbj BAA00009 (D00012)
                  triosephosphate isomerase [Zea mays]
Seq. No.
                  307083
Seq. ID
                  uC-zmflb73219e07b2
Method
                  BLASTX
NCBI GI
                  g1707364
BLAST score
                  180
                  3.0e-28
E value
```

% identity NCBI Description (X94626) AATP2 [Arabidopsis thaliana]

Seq. ID uC-zmflb73219f06b2 Method BLASTX NCBI GI q3688808 BLAST score 211 E value 8.0e-17 Match length 127 % identity

Match length

Seq. No.

NCBI Description (AF084104) AcsA [Bacillus firmus]

Seq. No. 307085 Seq. ID uC-zmflb73219f11b2 Method BLASTX NCBI GI g170644 BLAST score 170 4.0e-12 E value 62

Match length % identity 58

Seq. No.

(M92931) 5'-phosphoribosyl-4-(N-succinocarboxamide)-5-ami NCBI Description noimidazole synthetase [Vigna aconitifolia]

Seq. ID uC-zmflb73219h12b2 BLASTN Method NCBI GI q3319339 34

BLAST score 2.0e-09 E value Match length 46 93 % identity

NCBI Description Arabidopsis thaliana BAC F9D12

307086

307087 Seq. No.

Seq. ID uC-zmflb73220b02b2

Method BLASTX g2190547 NCBI GI BLAST score 200 E value 2.0e-15 Match length 53 % identity 68

(AC001229) ESTs NCBI Description





gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb_AA404382 come from this gene. [Arabidopsis thaliana]

Seq. No. 307088

Seq. ID uC-zmflb73220e09b2

Method BLASTX
NCBI GI 93402683
BLAST score 142
E value 2.0e-09
Match length 85
% identity 36

NCBI Description (AC004697) patatin-like protein [Arabidopsis thaliana]

Seq. No. 307089

Seq. ID uC-zmflb73220f11b2

Method BLASTX
NCBI GI g2979557
BLAST score 256
E value 4.0e-22
Match length 133
% identity 47

NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

>gi 3386625 (AC004665) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 307090

Seq. ID uC-zmflb73220g05b2

Method BLASTX
NCBI GI g3063449
BLAST score 156
E value 2.0e-10
Match length 66
% identity 52

NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana]

Seq. No. 307091

Seq. ID uC-zmflb73220g07b2

Method BLASTX
NCBI GI g899608
BLAST score 390
E value 6.0e-38
Match length 87
% identity 19

NCBI Description (U29158) polyubiquitin [Zea mays]

Seq. No. 307092

Seq. ID uC-zmflb73220h09b2

Method BLASTX
NCBI GI g3135543
BLAST score 353
E value 8.0e-34
Match length 86
% identity 84

NCBI Description (AF062393) aquaporin [Oryza sativa]

Seq. No. 307093

Seq. ID uC-zmflb73221a02b1



```
Method
NCBI GI
                  q3122673
BLAST score
                  168
E value
                  3.0e-12
Match length
                  54
% identity
                  67
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447_
NCBI Description
                  (Z97341) ribosomal protein [Arabidopsis thaliana]
                  307094
Seq. No.
Seq. ID
                  uC-zmflb73221c06b1
                  BLASTN
Method
                  g498772
NCBI GI
BLAST score
                  55
                  4.0e-22
E value
Match length
                  83
% identity
NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
                  307095
Seq. No.
Seq. ID
                  uC-zmflb73221d03a2
Method
                  BLASTN
NCBI GI
                  g3319775
BLAST score
                  84
                  2.0e-39
E value
                  160
Match length
% identity
                  87
NCBI Description Zea mays mRNA for cytosolic seryl-tRNA synthetase
                  307096
Seq. No.
                  uC-zmf1b73221d07a2
Seq. ID
                  BLASTX
Method
                  g3152582
NCBI GI
BLAST score
                  145
                  3.0e-09
E value
Match length
                   43
% identity
                  58
                  (AC002986) YUP8H12R.20 [Arabidopsis thaliana]
NCBI Description
                  307097
Seq. No.
                  uC-zmflb73221h10a2
Seq. ID
                  BLASTN
Method
                  g2995254
NCBI GI
BLAST score
                   60
                   4.0e-25
E value
Match length
                  110
% identity
                   88
NCBI Description Hordeum vulgare mRNA for hypothetical protein
                   307098
Seq. No.
                   uC-zmflb73222b04b1
Seq. ID
                                                               ٠.
```

BLASTN Method g1495250 NCBI GI BLAST score 40 5.0e-13 E value Match length 80 % identity 88



NCBI Description A.thaliana mRNA for heat-shock protein

Seq. No. 307099
Seq. ID uC-zmflb73222c08a1
Method BLASTX
NCBI GI g3236261

NCB1 G1 g323626
BLAST score 290
E value 5.0e-26
Match length 84
% identity 57

NCBI Description (AC004684) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 307100

Seq. ID uC-zmflb73222d01b1

Method BLASTX
NCBI GI g4006833
BLAST score 161
E value 9.0e-11
Match length 87
% identity 40

NCBI Description (AC005970) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 307101

Seq. ID uC-zmflb73222f12b1

Method BLASTX
NCBI GI g1350548
BLAST score 193
E value 4.0e-16
Match length 70
% identity 59

NCBI Description (L47609) heat shock-like protein [Picea glauca]

Seq. No. 307102

Seq. ID uC-zmflb73222h01b1

Method BLASTX
NCBI GI g3212863
BLAST score 479
E value 2.0e-48
Match length 121
% identity 78

NCBI Description (AC004005) putative translation initiation factor

[Arabidopsis thaliana]

Seq. No. 307103

Seq. ID uC-zmflb73222h02b1

Method BLASTN
NCBI GI g1042267
BLAST score 111
E value 2.0e-55
Match length 118
% identity 99

NCBI Description {Mul element insertion site, clone 19} [maize, Transposon,

119 nt]

Seq. No. 307104

```
uC-zmflb73222h09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3413704
BLAST score
                  221
E value
                  7.0e-18
                  117
Match length
% identity
                  42
                  (AC004747) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  307105
                  uC-zmflb73222h11b1
Seq. ID
Method
                  BLASTX
                  g1173218
NCBI GI
BLAST score
                  195
E value
                  3.0e-15
Match length
                  73
% identity
                  62
                  40S RIBOSOMAL PROTEIN S15A >qi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  307106
Seq. No.
                  uC-zmflb73223a01b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3882018
BLAST score
                  266
                  3.0e-23
E value
Match length
                  111
% identity
                  48
                  (Y18377) cytokinin oxidase [Zea mays]
NCBI Description
Seq. No.
                  307107
                  uC-zmflb73223f07b2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g602605
BLAST score
                  36
                  1.0e-10
E value
Match length
                  100
% identity
                  84
NCBI Description Zea mays tandem genes for alphal-tubulin and alpha2-tubulin
                  307108
Seq. No.
                  uC-zmflb73223g05b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231684
BLAST score
                  398
E value
                  1.0e-38
Match length
                  153
                  53
% identity
NCBI Description
                  PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE)
                  >gi_282982_pir__S25081 phosphoenolpyruvate carboxylase (EC
                  4.1.1.31) - Flaveria pringlei >gi_18458_emb_CAA45505_
```

(X64144) phosphoenolpyruvate carboxylase [Flaveria

pringlei]

Seq. No.

307109

Seq. ID

uC-zmflb73223g06b2

```
Method BLASTX
NCBI GI g3786010
BLAST score 176
E value 1.0e-12
Match length 42
% identity 81
NCBI Description (AC005499) putative serine/threonine protein kinase
```

[Arabidopsis thaliana]

 Seq. No.
 307110

 Seq. ID
 uC-zmflb73223g10b2

 Method
 BLASTX

 NCBI GI
 g2244771

 BLAST score
 201

 E value
 1.0e-15

 Match longth
 94

Match length 94 % identity 45

NCBI Description (Z97335) kinesin homolog [Arabidopsis thaliana]

Seq. No. 307111

Seq. ID uC-zmflb73223h04b2

Method BLASTX
NCBI GI g1402910
BLAST score 249
E value 3.0e-21
Match length 81
% identity 59

NCBI Description (X98316) peroxidase [Arabidopsis thaliana]

>gi_1429223_emb_CAA67550_ (X99096) peroxidase [Arabidopsis

.....

42

thaliana]

Seq. No. 307112

Seq. ID uC-zmflb73224a05b1

Method BLASTN
NCBI GI g1651897
BLAST score 510
E value 0.0e+00
Match length 558
% identity 98

NCBI Description Synechocystis sp. PCC6803 complete genome, 3/27,

271600-402289

Seq. No. 307113

Seq. ID uC-zmflb73224a06b1

Method BLASTN
NCBI GI g1652225
BLAST score 264
E value 1.0e-147
Match length 412
% identity 91

NCBI Description Synechocystis sp. PCC6803 complete genome, 6/27,

630555-781448

Seq. No. 307114

Seq. ID uC-zmflb73224a07b1

Method BLASTN NCBI GI g1653083



```
BLAST score
E value
                  0.0e + 00
Match length
                  416
                  100
% identity
                  Synechocystis sp. PCC6803 complete genome, 13/27,
NCBI Description
                  1576593-1719643
Seq. No.
                  307115
                  uC-zmflb73224a09b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1653477
BLAST score
                  213
E value
                  1.0e-116
Match length
                  217
                  100
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 16/27,
                  1991550-2137258
                  307116
Seq. No.
Seq. ID
                  uC-zmflb73224a12b1
Method
                  BLASTN
NCBI GI
                  g1651768
BLAST score
                  245
E value
                  1.0e-135
Match length
                  261
                  98
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 2/27,
                  133860-271599
Seq. No.
                  307117
                  uC-zmflb73224b02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1651664
BLAST score
                  517
E value
                  7.0e-53
Match length
                  104
                  98
% identity
NCBI Description
                  (D90899) iron(III) dicitrate transport system permease
                  protein FecE [Synechocystis sp.]
Seq. No.
                  307118
Seq. ID
                  uC-zmflb73224b04b1
Method
                  BLASTN
NCBI GI
                  g1001396
BLAST score
                  67
E value
                  4.0e-29
Match length
                  67
                  100
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 18/27,
                  2267260-2392728
Seq. No.
                  307119
```

Seq. ID uC-zmflb73224b05b2

Method BLASTX NCBI GI g3913426 BLAST score 182 E value 7.0e-16

1900 P



Match length 62 % identity 52

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi 1532048 emb CAA69074_ (Y07766)

S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No. 307120

Seq. ID uC-zmflb73224b08b1

Method BLASTN
NCBI GI g1652225
BLAST score 257
E value 1.0e-143
Match length 269
% identity 99

NCBI Description Synechocystis sp. PCC6803 complete genome, 6/27,

630555-781448

Seq. No. 307121

Seq. ID uC-zmflb73224b12b1

Method BLASTX
NCBI GI g1346061
BLAST score 383
E value 6.0e-37
Match length 76
% identity 96

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 1 (GAPDH 1)

(GAP-1) >gi_1084175_pir__S54150 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Synechocystis sp. (PCC 6803)

>gi 785044 emb CAA60134 (X86375) glyceraldehyde

3-phosphate dehydrogenase (phosphorylating) [Synechocystis

sp.]

Seq. No. 307122

Seq. ID uC-zmflb73224c03b1

Method BLASTX
NCBI GI g1144565
BLAST score 292
E value 9.0e-27
Match length 67
% identity 91

NCBI Description (U35144) Mg-Protoporhyrin IX [Synechocystis sp.]

Seq. No. 307123

Seq. ID uC-zmflb73224c06b1

Method BLASTN
NCBI GI g1652725
BLAST score 165
E value 9.0e-88
Match length 342
% identity 87

NCBI Description Synechocystis sp. PCC6803 complete genome, 10/27,

1188886-1311234

Seq. No. 307124

Seq. ID uC-zmf1b73224c09b1

Method BLASTN NCBI GI g1652956



BLAST score 410 E value 0.0e+00 Match length 418 % identity 100 NCBI Description Synecho

NCBI Description Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592

Seq. No. 307125

Seq. ID uC-zmf1b73224c11b2

Method BLASTN
NCBI GI g167027
BLAST score 39
E value 1.0e-12
Match length 59
% identity 92

NCBI Description Hordeum vulgare cold-regulated mRNA, partial cds

Seq. No. 307126

Seq. ID uC-zmflb73224d05b1

Method BLASTX
NCBI GI g1651850
BLAST score 380
E value 1.0e-36
Match length 76
% identity 89

NCBI Description (D90900) NADH-glutamate synthase small subunit

[Synechocystis sp.]

Seq. No. 307127

Seq. ID uC-zmflb73224d06b1

Method BLASTX
NCBI GI g1651801
BLAST score 472
E value 2.0e-66
Match length 154
% identity 86

NCBI Description (D90900) potential FMN-protein [Synechocystis sp.]

Seq. No. 307128

Seq. ID uC-zmflb73224d06b2

Method BLASTX
NCBI GI g2511531
BLAST score 728
E value 3.0e-77
Match length 138
% identity 99

NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]

>gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1

[Eleusine indica]

Seq. No. 307129

Seq. ID uC-zmflb73224d07b1

Method BLASTX
NCBI GI g3986110
BLAST score 314
E value 6.0e-29
Match length 123

% identity (AB012716) heat shock protein 70 cognate [Salix gilgiana] NCBI Description 307130 Seq. No. uC-zmflb73224d08b1 Seq. ID BLASTN Method g2062705 NCBI GI BLAST score 37 3.0e-11 E value Match length 37 100 % identity Human butyrophilin (BTF5) mRNA, complete cds NCBI Description 307131 Seq. No. Seq. ID uC-zmflb73224d09a1 Method BLASTX NCBI GI q4234846 BLAST score 148 1.0e-09 E value Match length 84 % identity 43 (AF082130) gag-pol polyprotein [Zea mays] NCBI Description 307132 Seq. No. uC-zmflb73224e01b1 Seq. ID BLASTN g1653477 348 0.0e+00368 99 Synechocystis sp. PCC6803 complete genome, 16/27, NCBI Description

Method NCBI GI BLAST score E value Match length % identity

1991550-2137258

307133 Seq. No.

uC-zmflb73224e04b1 Seq. ID

BLASTX Method NCBI GI g1001455 BLAST score 367 E value 2.0e-56 Match length 134 88 % identity

(D63999) hypothetical protein [Synechocystis sp.] NCBI Description

307134 Seq. No.

uC-zmflb73224e05b1Seq. ID

Method BLASTX g1001593 NCBI GI BLAST score 229 8.0e-19 E value Match length 77 % identity 65

(D64000) glucose inhibited division protein A NCBI Description

[Synechocystis sp.]

Seq. No. 307135

Seq. ID uC-zmflb73224e06b1

E value

Match length

1.0e-36

86



```
Method
                   BLASTX
NCBI GI
                   g1652322
BLAST score
                   366
                   3.0e-38
E value
Match length
                   139
% identity
                   68
NCBI Description
                  (D90904) penicillin-binding protein 1B [Synechocystis sp.]
Seq. No.
Seq. ID
                   uC-zmflb73224e12b1
Method
                   BLASTN
NCBI GI
                   q1001701
BLAST score
                   283
E value
                   1.0e-158
Match length
                   303
                   99
% identity
                  Synechocystis sp. PCC6803 complete genome, 23/27,
NCBI Description
                   2868767-3002965
Seq. No.
                   307137
Seq. ID
                   uC-zmflb73224f05b1
Method
                   BLASTN
NCBI GI
                   g1651768
BLAST score
                   555
                   0.0e + 00
E value
                   574
Match length
                   99
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 2/27,
                   133860-271599
Seq. No.
                   307138
Seq. ID
                   uC-zmflb73224f08b1
Method
                   BLASTX
NCBI GI
                   q1001201
BLAST score
                   167
E value
                   8.0e-12
Match length
                   102
% identity
                   42
NCBI Description
                  (D64003) hypothetical protein [Synechocystis sp.]
Seq. No.
                   307139
Seq. ID
                   uC-zmflb73224q02b1
Method
                  BLASTX
NCBI GI
                   g1651836
BLAST score
                   498
E value
                   1.0e-50
Match length
                   109
% identity
                   86
NCBI Description
                  (D90900) hypothetical protein [Synechocystis sp.]
Seq. No.
                   307140
Seq. ID
                  uC-zmflb73224q02b2
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                   380
```



% identity NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays] 307141 Seq. No. uC-zmf1b73224g03b1 Seq. ID Method BLASTX NCBI GI g1653181 BLAST score 586 E value 8.0e-61 Match length 132 % identity 87 NCBI Description (D90911) hydrogenase subunit [Synechocystis sp.] >gi_1771717 emb CAA66209 (X97610) hydrogenase subunit [Synechocystis sp.] 307142 Seq. No. Seq. ID uC-zmflb73224g04b2 Method BLASTX NCBI GI q115786 BLAST score 240 E value 2.0e-20 Match length 74 % identity 66 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 82680_pir__A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays] Seq. No. 307143 Seq. ID uC-zmflb73224q06b1 Method BLASTX NCBI GI g1652876 BLAST score 726 E value 4.0e-77 Match length 164 % identity 88 NCBI Description (D90909) hypothetical protein [Synechocystis sp.] Seq. No. 307144 Seq. ID uC-zmflb73224g06b2 Method BLASTX NCBI GI g1946371 BLAST score 289 E value 6.0e-26 Match length 104 % identity 51 NCBI Description (U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana] Seq. No. 307145 Seq. ID uC-zmflb73224g07b1 Method BLASTX

Method BLASTX
NCBI GI g1652259
BLAST score 524
E value 2.0e-53
Match length 106
% identity 96





```
(D90904) hypothetical protein [Synechocystis sp.]
NCBI Description
                                                                             ~2-
Seq. No.
                  307146
                  uC\text{-}zmf1b73224g09b2\\
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3128228
BLAST score
                  476
E value
                  5.0e-48
                  105
Match length
                  85
% identity
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                  thaliana] >gi 3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
Seq. No.
                  307147
                  uC-zmflb73224g10b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244771
BLAST score
                  251
E value
                  3.0e-21
Match length
                  113
% identity
                  46
                  (Z97335) kinesin homolog [Arabidopsis thaliana]
NCBI Description
                  307148
Seq. No.
                  uC-zmflb73224h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1652337
BLAST score
                  614
E value
                  3.0e-64
Match length
                  119
% identity
                  98
NCBI Description
                  (D90904) hypothetical protein [Synechocystis sp.]
Seq. No.
                  307149
Seq. ID
                  uC-zmflb73224h09b1
Method
                  BLASTX
NCBI GI
                  g1001545
BLAST score
                  525
E value
                  2.0e-53
Match length
                  139
% identity
                  75
                  (D64000) oligopeptide transport system permease protein
NCBI Description
                   [Synechocystis sp.]
                  307150
Seq. No.
Seq. ID
                  uC-zmflb73225b06b1
Method
                  BLASTN
NCBI GI
                  q22292
BLAST score
                  59
E value
                  9.0e-25
Match length
                  107
```

Seq. No. 307151

% identity

Seq. ID uC-zmflb73225b12b1

89

NCBI Description Z.mays mRNA for glycine-rich protein

```
BLASTX
Method
                  q2499708
NCBI GI
BLAST score
                  278
               1.0e-24
E value
                  59
Match length
                  95
% identity
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi 1020409_dbj_BAA11135_ (D73410) phospholipase D [Zea
                  307152
Seq. No.
                  uC-zmflb73225c04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587584
BLAST score
                  460
                 5.0e-46
E value
                  124
Match length
                  73
% identity
```

(AC007232) unknown protein [Arabidopsis thaliana] NCBI Description

307153 Seq. No. uC-zmf1b73225e02b1Seq. ID Method BLASTX NCBI GI g3860277 BLAST score 519

6.0e-53 E value Match length 137 74 % identity

(ACO05824) putative ribosomal protein L10 [Arabidopsis NCBI Description thaliana] >gi 4314394 gb AAD15604 (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

307154 Seq. No.

Seq. ID uC-zmflb73225e11b1

Method BLASTX g4417288 NCBI GI 305 BLAST score 4.0e-32 E value Match length 134 % identity 53

(AC007019) unknown protein [Arabidopsis thaliana] NCBI Description

307155 Seq. No.

uC-zmflb73226a02b1 Seq. ID

BLASTN Method q1498596 NCBI GI 51 BLAST score E value 9.0e-20 255 Match length % identity

NCBI Description Zea mays phospholipid transfer protein mRNA, complete cds

Seq. No. 307156

Seq. ID uC-zmflb73226a12b1

Method BLASTX NCBI GI g2914703



```
BLAST score 279
E value 8.0e-25
Match length 95
% identity 56
```

NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

Seq. No. 307157

Seq. ID uC-zmflb73226c03a1

Method BLASTN
NCBI GI g2921303
BLAST score 161
E value 2.0e-85
Match length 313
% identity 88

NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA,

complete cds

Seq. No. 307158

Seq. ID uC-zmflb73226e05b1

Method BLASTN
NCBI GI g1313908
BLAST score 57
E value 3.0e-23
Match length 65
% identity 97

NCBI Description Zea mays mRNA for CDPK-related protein kinase, complete

cds, clone ZmCRK3

Seq. No. 307159

Seq. ID uC-zmflb73226e11a1

Method BLASTX
NCBI GI g1839597
BLAST score 154
E value 1.0e-10
Match length 33
% identity 88

NCBI Description (S82324) calcium/calmodulin-dependent protein kinase

homolog CaM kinase homolog MCK1 [Zea mays=maize, cv. Merit,

7.

root caps, Peptide, 625 aa] [Zea mays]

Seq. No. 307160

Seq. ID uC-zmflb73226f09b1

Method BLASTN
NCBI GI g22484
BLAST score 67
E value 2.0e-29
Match length 127
% identity 89

NCBI Description Z.mays RNA for superoxide dismutase Sod4A

Seq. No. 307161

Seq. ID - uC-zmflb73226h04b1

Method BLASTX
NCBI GI g3264596
BLAST score 191
E value 3.0e-18
Match length 80



```
% identity ...
                  (AF057183) putative tonoplast aquaporin [Zea mays]
NCBI Description
Seq. No.
                   307162
                   uC-zmflb73226h05b1
Seq. ID
                   BLASTX
Method
                   q3335355
NCBI GI
BLAST score
                   534
E value
                   6.0e-57
                   144
Match length
% identity
                   22
                   (AC004512) Match to polyubiquitin DNA gb_L05401 from A.
NCBI Description
                   thaliana. Contains insertion of mitochondrial NADH
                   dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene
                   with an expressed insert. EST gb_AA586248 comes from this
                   region. [Arabi
                   307163.
Seq. No.
                   uC-zmflb73226h10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g951172
BLAST score
                   280
                   4.0e-25
E value
Match length
                   81
                   65
% identity
NCBI Description
                  (U31521) MADS box protein [Zea mays]
                  .>gi 1001934 emb CAA56504 (X80206) ZAG2 [Zea mays]
Seq. No.
                   307164
                   uC-zmflb73226h11b1
Seq. ID
                   BLASTX
Method
                   g3152591
NCBI GI
BLAST score
                   178
E value
                   1.0e-13
Match length
                   64
                   47
% identity
NCBI Description (AC002986) Similar to hypothetical protein gb Z97336 from
                   A. thaliana. This gene is probably cut off. [Arabidopsis
                   thaliana]
Seq. No.
                   307165
                   uC-zmflb73228b09a1
Seq. ID
Method
                   BLASTN
                                                                   ~ .* E
                   q300078
NCBI GI
BLAST score
                   284
                   1.0e-159
E value
                   288
Match length
% identity
                   100
NCBI Description
                   HSP18=18 kda heat shock protein
                   {microsporogenesis-specific} [Zea mays, Oh43, clone
```

cMHSP18-1, mRNA, 790 nt]

Seq. No. 307166

uC-zmf1b73228e11a1Seq. ID

Method BLASTX NCBI GI g1531758 BLAST score 209

E value 1.0e-16
Match length 61
% identity 64

NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)

unknown protein [Arabidopsis thaliana]

Seq. No. 307167

Seq. ID uC-zmflb73229a01b2

Method BLASTX
NCBI GI g2781433
BLAST score 275
E value 6.0e-25
Match length 57
% identity 89

NCBI Description (AF030052) RSW1-like cellulose synthase catalytic subunit

[Oryza sativa subsp. japonica]

Seq. No. 307168

Seq. ID uC-zmflb73229c12b2

Method BLASTN
NCBI GI g1532072
BLAST score 83
E value 7.0e-39
Match length 111
% identity 96

NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 307169

Seq. ID uC-zmflb73229h01b2

Method BLASTN
NCBI GI g1906603
BLAST score 35
E value 2.0e-10
Match length 35
% identity 100

NCBI Description Zea mays ACCase gene, intron containing colonist1 and

colonist2 retrotransposons and reverse transcriptase

pseudogene, complete sequence

Seq. No. 307170

Seq. ID uC-zmflb73229h02b2

Method BLASTX
NCBI GI g3047083
BLAST score 232
E value 1.0e-19
Match length 54
% identity 80

NCBI Description (AF058914) similar to FLAP endonuclease-1 (SW:P39748)

[Arabidopsis thaliana]

Seq. No. 307171

Seq. ID uC-zmflb73229h05b2

Method BLASTX
NCBI GI g4522004
BLAST score 156
E value 6.0e-11
Match length 48

Seq. No.



```
% identity
                  (AC007069) putative histidine kinase, sensory transduction
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  307172
                  uC-zmflb73230a03b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1495366
BLAST score
                  356
                   9.0e-34
E value
Match length
                   150
                   49
% identity
                  (Z69370) nitrite transporter [Cucumis sativus]
NCBI Description
                   307173
Seq. No.
Seq. ID
                   uC-zmflb73230a12b2
                   BLASTX
Method
NCBI GI
                   q4204315
BLAST score
                   187
                   6.0e-14
E value
                   107
Match length
% identity
                  (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   307174
Seq. No.
Seq. ID
                   uC-zmflb73230b05b2
Method
                   BLASTX
NCBI GI
                   g135411
BLAST score
                   668
E value
                   2.0e-70
Match length
                   124
% identity
                   TUBULIN ALPHA-2 CHAIN >gi 82732_pir__S15772 tubulin alpha-2
NCBI Description
                   chain - maize >gi_22148_emb_CAA33733_ (X15704)
                   alpha2-tubulin [Zea mays]
                   307175
Seq. No.
                   uC-zmflb73230c10b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3668088
                   240
BLAST score
E value
                   3.0e-20
Match length
                   132
% identity
                   38
                  (AC004667) G9a-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   307176
                   uC-zmflb73230e07b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455334
BLAST score
                   188
E value
                   3.0e-14
                   119
Match length
% identity
                   38
                  (AL035525) myosin-like protein [Arabidopsis thaliana]
NCBI Description
```



```
uC-zmflb73230h06b2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  35
                  4.0e-10
E value
Match length
                  35
                  100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  307178
Seq. No.
                  uC-zmflb73232a04b1
Seq. ID
Method
                  BLASTN
                  g1008878
NCBI GI
BLAST score
                  287
E value
                  1.0e-160
Match length
                  338
% identity
                  97
NCBI Description Zea mays RS1 mRNA, complete cds
                  307179
Seq. No.
Seq. ID
                  uC-zmflb73232a07b1
                  BLASTX
Method
NCBI GI
                  g2723471
BLAST score
                  289
E value
                  5.0e-34
Match length
                  106
% identity
                  68
NCBI Description
                  (D87819) sucrose transporter [Oryza sativa]
                  307180
Seq. No.
Seq. ID
                  uC-zmflb73232a12b1
Method
                  BLASTX
                  q3924605
NCBI GI
BLAST score
                  228
E value
                  4.0e-19
Match length
                  100
% identity
                  50
NCBI Description
                  (AF069442) putative inhibitor of apoptosis [Arabidopsis
                  thaliana]
Seq. No.
                  307181
                  uC-zmflb73232b04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g854644
BLAST score
                  414
E value
                  0.0e+00
Match length
                  463
% identity
                  98
NCBI Description Z.mays ZMM1 gene
Seq. No.
                  307182
Seq. ID
                  uC-zmflb73232b07b1
```

Method BLASTN NCBI GI q3821780 BLAST score 35 E value 4.0e-10 Match length 35



```
% identity
 NCBI Description Xenopus laevis cDNA clone 27A6-1
 Seq. No.
                   307183
 Seq. ID
                   uC-zmflb73232c08b1
 Method
                   BLASTX
 NCBI GI
                   g2809387
 BLAST score
                   152
 E value
                   7.0e-10
 Match length
                   35
 % identity
                   77
 NCBI Description
                   (AF024635) NADPH cytochrome P450 reductase [Petroselinum
                   crispum]
 Seq. No.
                   307184
 Seq. ID
                   uC-zmflb73232d01b1
 Method
                   BLASTX
 NCBI GI
                   g4455240
 BLAST score
                   455
 E value
                   2.0e-45
 Match length
                   146
 % identity
                   60
                   (AL035523) putative protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   307185
                   uC-zmflb73232d03b1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2129655
 BLAST score
                   328
 E value
                   9.0e-31
 Match length
                   88
 % identity
                   66
 NCBI Description
                   OBP32pep protein - Arabidopsis thaliana (fragment)
                   >gi_1022799 (U37698) OBP32pep [Arabidopsis thaliana]
 Seq. No.
                   307186
                   uC-zmflb73232h03b1
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g3821780
BLAST score
                   36
                   8.0e-11
E value
Match length
                   48
                   67
 % identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
 Seq. No.
                   307187
 Seq. ID
                   uC-zmflb73232h04b1
```

Method BLASTX NCBI GI g3953466 BLAST score 620 E value 1.0e-64 Match length 152 % identity 77

NCBI Description (AC002328) F20N2.11 [Arabidopsis thaliana]

Seq. No. 307188

Seq. ID uC-zmflb73232h09b1



```
Method
                  BLASTX
NCBI GI
                  q3868758
BLAST score
                  249
E value
                  3.0e-21
                  107
Match length
                  49
% identity
NCBI Description
```

(D89802) elongation factor 1B gamma [Oryza sativa]

307189 Seq. No. uC-zmflb73233a01b1 Seq. ID Method BLASTN g2655290 NCBI GI BLAST score 55 E value 4.0e-22

Match length 150 85 % identity

Oryza sativa germin-like protein 4 (GER4) mRNA, complete NCBI Description

307190 Seq. No.

uC-zmflb73233d01a1 Seq. ID

BLASTN Method NCBI GI g747914 BLAST score 80 E value 4.0e-37 Match length 234 % identity 90

Z.mays CaM1 mRNA for calmodulin NCBI Description

307191 Seq. No.

uC-zmflb73233d06b1 Seq. ID

BLASTX Method NCBI GI g452593 BLAST score 329 E value 1.0e-30 138 Match length % identity 50

NCBI Description (D21814) ORF [Lilium longiflorum]

307192 Seq. No.

uC-zmflb73233d11a1 Seq. ID

Method BLASTX g3176686 NCBI GI BLAST score 245 E value 7.0e-21Match length 78 56 % identity

NCBI Description (AC003671) Similar to high affinity potassium transporter,

HAK1 protein gb_U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

307193 Seq. No.

Seq. ID uC-zmflb73233g06b1

Method BLASTN NCBI GI g2773153 BLAST score 42 E value 3.0e-14



```
Match length
                    85
 % identity
                    Oryza sativa abscisic acid- and stress-inducible protein
 NCBI Description
                    (Asr1) mRNA, complete cds
                    307194
 Seq. No.
                    uC-zmflb73233g12b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4091080
 BLAST score
                    186
                    9.0e-14
 E value
 Match length
                    45
                    78
 % identity
 NCBI Description
                    (AF045571) nucleic acid binding protein [Oryza sativa]
                    307195
 Seq. No.
                    uC-zmflb73233h03b1
 Seq. ID
                    BLASTN
 Method
                    q340933
 NCBI GI
 BLAST score
                    64
                    2.0e-27
 E value
Match length
                    117
                    89
 % identity
 NCBI Description Zea mays 10-kDa zein gene, complete cds
                    307196
 Seq. No.
                    uC-zmflb73233h04b1
 Seq. ID
                    BLASTX
 Method
                    g1125032
 NCBI GI
                    182
 BLAST score
 E value
                    9.0e-14
                    78
 Match length
  % identity
                    47
                   (D32166) cellulase precursor [Populus alba]
 NCBI Description
                    307197
  Seq. No.
                    uC-zmflb73234b04b2
  Seq. ID;
  Method
                    BLASTX
  NCBI GI
                    g2225997
  BLAST score
                    423
  E value
                    7.0e-42
 Match length
                    93
                    87
  % identity
  NCBI Description
                    (Y09699) putative inward rectifying potassium channel
                    [Solanum tuberosum]
                    307198
  Seq. No.
                    uC-zmflb73234b10b2
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q4388820
  BLAST score
                    330
                    1.0e-30
  E value
  Match length
                    69
                    81
  % identity
  NCBI Description
                    (AC006528) putative myb DNA-binding protein [Arabidopsis
```

```
307199
Seq. No.
                   uC\text{-}zmflb73234e07b2\\
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3319776
BLAST score
                   425
                   5.0e-42
E value
                   107
Match length
                   85
% identity
                   (AJ007665) seryl-tRNA synthetase [Zea mays]
NCBI Description
                   307200
Seq. No.
                   uC-zmf1b73234f04b2
Seq. ID
                   BLASTX
Method
                   q3645899
NCBI GI
BLAST score
                   410
E value
                   3.0e-40
Match length
                   111
% identity
                   68
                   (U68408) 5' end not determined experimentally [Zea mays]
NCBI Description
Seq. No.
                   307201
                   uC-zmflb73234h12b2
Seq. ID
Method
                   BLASTX
                   g4455338
NCBI GI
BLAST score
                   396
E value
                   1.0e-38
Match length
                   120
% identity
                   66
                   (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                   307202
Seq. No.
                   uC-zmf1b73235b08b2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g683475
BLAST score
                   34
E value
                   2.0e-09
Match length
                   58
                   90
% identity
NCBI Description H.vulgare mRNA for NADPH-protochlorophyllide oxidoreductase
                   307203
Seq. No.
                   uC-zmf1b73235d08b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3249064
                   258
BLAST score
                   3.0e-22
E value
Match length
                   121
% identity
                   52
```

NCBI Description (AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb_2245136 from A. thaliana chromosome 4

contig gb_Z97344. [Arabidopsis thaliana]

Seq. No. 307204

Seq. ID uC-zmflb73235d10b2

Method BLASTX NCBI GI g2832643 BLAST score 197



```
1.0e-19
E value
Match length
                  96
% identity
                  60
                  (AL021710) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  307205
Seq. No.
                  uC-zmflb73236b03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1946367
BLAST score
                  222
                  4.0e-18
E value
Match length
                  95
                  52
% identity
NCBI Description
                  (U93215) unknown protein [Arabidopsis thaliana]
                  307206
Seq. No.
                  uC-zmflb73236b07b1
Seq. ID
                  BLASTX
Method
                  g3746068
NCBI GI
                  150
BLAST score
                  1.0e-09
E value
Match length
                  40
                  70
% identity
                   (AC005311) unknown protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
                  307207
Seq. No.
                  uC-zmflb73236d07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4490297
BLAST score
                  308
                  3.0e-28
E value
Match length
                  120
                  54
% identity
NCBI Description
                  (AL035678) putative protein [Arabidopsis thaliana]
                  307208
Seq. No.
                  uC-zmflb73236f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2194119
                  185
BLAST score
E value
                  5.0e-14
Match length
                  87
% identity
                  47
NCBI Description
                  (AC002062) No definition line found [Arabidopsis thaliana]
Seq. No.
                  307209
Seq. ID
                  uC-zmflb73236f09b1
Method
                  BLASTX
NCBI GI
                  q2894569
BLAST score
                  169
                  7.0e-12
E value
Match length
                  46
% identity
                   67
```

Seq. No. 307210

NCBI Description

(AL021890) putative protein [Arabidopsis thaliana]

Seq. ID

Method

```
Seq. ID
                   uC-zmflb73236q08b1
Method
                   BLASTX
NCBI GI
                   q626042
BLAST score
                   147
E value
                    4.0e-19
Match length
                   70
% identity
                   73
NCBI Description
                   beta-glucosidase, root meristem (EC 3.2.1.-) precursor -
                   maize >gi_435313_emb_CAA52293 (X74217) beta-glucosidase
                    [Zea mays]
Seq. No.
                   307211
Seq. ID
                   uC-zmflb73236h04b1
Method
                   BLASTX
NCBI GI
                   q464846
BLAST score
                   623
E value
                   8.0e-65
Match length
                   128
% identity
                   93
                   TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178)
NCBI Description
                   alpha-tubulin #6 [Zea mays]
Seq. No.
                   307212
Seq. ID
                   uC-zmflb73237c03b2
Method
                   BLASTX
NCBI GI
                   q1673366
BLAST score
                   396
E value
                   1.0e-38
Match length
                   93
% identity
                   81
NCBI Description
                    (Z22673) cytosolic tRNA-Ala synthetase [Arabidopsis
                   thaliana]
Seq. No.
                   307213
Seq. ID
                   uC-zmflb73237c09b2
Method
                   BLASTX
NCBI GI
                   g2104535
BLAST score
                   419
E value
                   3.0e-41
Match length
                   109
% identity
                   73
NCBI Description
                   (AF001308) T10M13.13 [Arabidopsis thaliana]
Seq. No.
                   307214
Seq. ID
                   uC-zmflb73237c12b2
Method
                   BLASTX
NCBI GI
                   g3150407
BLAST score
                   286
E value
                   1.0e-25
Match length
                   63
% identity
                   81
NCBI Description
                   (AC004165) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   307215
```

43610

uC-zmflb73237g05b2

BLASTX

```
q1507699
 NCBI GI
 BLAST score
                   201
E value
                   1.0e-15
 Match length
                   46
                   76
 % identity
                    (L81119) COL2 [Arabidopsis thaliana] >gi 1507701 (L81120)
 NCBI Description
                   COL2 [Arabidopsis thaliana]
                   307216
 Seq. No.
                   uC-zmf1b73237h05b2
 Seq. ID
 Method
                   {\tt BLASTX}
 NCBI GI
                   g3132310
 BLAST score
                   389
 E value
                   4.0e-38
 Match length
                   82
 % identity
                   88
 NCBI Description
                   (AB012228) phosphoenolpyruvate carboxylase [Zea mays]
 Seq. No.
                   307217
 Seq. ID
                   uC-zmflb73238b03a1
 Method
                   BLASTX
 NCBI GI
                   g629844
 BLAST score
                   214
 E value
                   4.0e-17
 Match length
                   85
 % identity
                   58
 NCBI Description
                   heat shock protein hsp70-5 - maize (fragment)
                   >gi_498775_emb_CAA55184 (X78415) heat shock protein 70 kDa
                   [Zea mays]
 Seq. No.
                   307218
 Seq. ID
                   uC-zmflb73238b06b2
 Method
                   BLASTX
 NCBI GI
                   g3861449
 BLAST score
                   223
 E value
                   3.0e-18
 Match length
                   108
 % identity
                   41
 NCBI Description
                   (Z98596) SMC-family protein [Schizosaccharomyces pombe]
 Seq. No.
                   307219
 Seq. ID
                   uC-zmflb73238c09b2
Method -
                   BLASTX
NCBI GI
                   g3776023
BLAST score
                   489
E value
                   3.0e-49
Match length
                   141
 % identity
                   67
NCBI Description
                   (AJ010473) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   307220
Seq. ID
                   uC-zmflb73238d07b2
```

Method BLASTX
NCBI GI g2317910
BLAST score 222
E value 3.0e-18
Match length 99



% identity NCBI Description (U89959) CER1 protein [Arabidopsis thaliana] 307221 Seq. No. uC-zmf1b73238f07b2 Seq. ID BLASTX Method g4586308 NCBI GI 207 BLAST score 3.0e-16 E value 3. Match length 50 % identity 78 (AB025102) protoporphyrinogen IX oxidase [Glycine max] NCBI Description 307222 Seq. No. uC-zmflb73238g09a1Seq. ID Method BLASTN q596079 NCBI GI BLAST score 146 2.0e-76 E value Match length 276 % identity 97 Zea mays thiamine biosynthetic enzyme (thi1-2) mRNA, NCBI Description complete cds Seq. No. 307223 uC-zmflb73238h04b2 Seq. ID Method BLASTX NCBI GI g2435522 BLAST score 391 7.0e-38 E value Match length 132 58 % identity (AF024504) contains similarity to other AMP-binding enzymes NCBI Description [Arabidopsis thaliana] 307224 Seq. No. uC-zmflb73238h12b2 Seq. ID Method BLASTN NCBI GI g347843 BLAST score 173 2.0e-92 E value Match length 185 % identity 98 NCBI Description Zea mays globulin-1 gene, promoter region Seq. No. 307225 uC-zmflb73239a11b2 Seq. ID Method BLASTX NCBI GI g3335366 BLAST score 214 E value 2.0e-17

Match length 72 % identity 51

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 307226

Seq. ID uC-zmflb73239b07b2

```
BLASTX
Method
                    g2462825
  NCBI GI
                    226
  BLAST score
                    2.0e-18
  E value
  Match length
                    52
                    75
  % identity
                    (AF000657) contains Procite 'RNP1' putative RNA-binding
  NCBI Description
                    region [Arabidopsis thaliana]
  Seq. No.
                    307227
                    uC-zmflb73239f05b2
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g4580398
  BLAST score
                    161
                    7.0e-11
  E value
  Match length
                    94
                    45
  % identity
  NCBI Description
                    (AC007171) putative protein kinase APK1A [Arabidopsis
                    thaliana]
                    307228
  Seq. No.
                    uC-zmflb73239f10a1
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g2570505
  BLAST score
                    348
  E value
                    7.0e-33
  Match length
                    73
                    92
  % identity
                    (AF022735) proteasome component [Oryza sativa]
  NCBI Description
                    307229
  Seq. No.
  Seq. ID
                    uC-zmflb73239h07a1
  Method
                    BLASTX
  NCBI GI
                    q1707855
  BLAST score
                    212
  E value
                     5.0e-17
  Match length
                     65
                     63
  % identity
                     (Y09292) obtusifoliol 14-alpha-demethylase [Triticum
  NCBI Description
                     aestivum]
                     307230
  Seq. No.
                     uC-zmflb73240b12a2
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                     g22272
  BLAST score
                     97
  E value
                     3.0e-47
  Match length
                     140
  % identity
                     93
  NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
```

Seq. No. 307231

Seq. ID uC-zmflb73240c08a2

Method BLASTX
NCBI GI g4539452
BLAST score 197
E value 3.0e-15

```
Match length
% identity
                  71
                   (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                   [Arabidopsis thaliana]
                  307232
Seq. No.
                  uC-zmflb73240e08a2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168527
BLAST score
                  36
                  8.0e-11
E value
Match length
                  56
                  91
% identity
NCBI Description
                  Maize NADP-dependent malic enzyme (Mel) mRNA, complete cds
Seq. No.
                  307233
                  uC-zmflb73240f04a2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4455294
BLAST score
                  351
E value
                   3.0e-33
Match length
                  129
% identity
                   49
                  (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  307234
                  uC-zmflb73241d07b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3355465
BLAST score
                  148
                  2.0e-09
E value
Match length
                  50
% identity
                  52
                   (AC004218) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  307235
Seq. No.
```

8

Seq. ID uC-zmflb73241d08b2

Method BLASTX
NCBI GI g2369714
BLAST score 650
E value 3.0e-68
Match length 132
% identity 93

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 307236

Seq. ID uC-zmflb73241d09b2

Method BLASTX
NCBI GI g2984709
BLAST score 523
E value 2.0e-53
Match length 130
% identity 79

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

, ?÷

Seq. No. 307237



Seq. ID uC-zmflb73242a04a1

Method BLASTX
NCBI GI g548641
BLAST score 173
E value 2.0e-12
Match length 52
% identity 58

NCBI Description PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (FGAM SYNTHASE)

(FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT)

(ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE

SYNTHETASE) >gi 414423 (U00683) formylglycineamide ribotide

e ...

amidotransferase [Drosophila melanogaster]

Seq. No. 307238

Seq. ID uC-zmflb73242a11b2

Method BLASTN
NCBI GI g22091
BLAST score 233
E value 1.0e-128
Match length 315
% identity 66

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 307239

Seq. ID uC-zmflb73242b04b1

Method BLASTN
NCBI GI g1122438
BLAST score 50
E value 2.0e-19
Match length 94
% identity 88

NCBI Description Zea mays invertase (Ivr1) gene, complete cds

Seq. No. 307240

Seq. ID uC-zmflb73242b07a1

Method BLASTX
NCBI GI g3695392
BLAST score 154
E value 5.0e-10
Match length 59
% identity 46

NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]

Seq. No. 307241

Seq. ID uC-zmflb73242c06b1

Method BLASTX
NCBI GI g120670
BLAST score 481
E value 1.0e-48
Match length 91

% identity 99

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_100879_pir__S06879 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12) C - maize

>gi 295853 emb CAA33620 (X15596) GAPDH [Zea mays]

Seq. No. 307242



```
uC-zmflb73242d05b1
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g2914710
   BLAST score
                     331
   E value
                     5.0e-31
   Match length
                     105
                     50
   % identity
   NCBI Description
                     (AC003974) putative beta-D-galactosidase [Arabidopsis
                     thaliana]
                     307243
   Seq. No.
   Seq. ID
                     uC-zmflb73242d06b1
   Method
                     BLASTX
   NCBI GI
                     q1709970
   BLAST score
                     173
   E value
                     6.0e-13
   Match length
                     51
                     69
   % identity
   NCBI Description
                    60S RIBOSOMAL PROTEIN L10A
g Seq. No.
                     307244
                     uC-zmflb73242d07b1
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g422029
   BLAST score
                     256
   E value
                     5.0e-22
   Match length
                     124
   % identity
                     50
                     transcription factor OBF3.2, ocs element-binding - maize
   NCBI Description
                     >gi_297018_emb_CAA48904 (X69152) ocs-element binding
                     factor 3.2 [Zea mays]
   Seq. No.
                     307245
   Seq. ID
                     uC-zmflb73242d11a1
   Method
                     BLASTX
   NCBI GI
                     g2589164
   BLAST score
                     389
                     1.0e-37
   E value
   Match length
                     77
   % identity
                     90
   NCBI Description
                     (D88452) aldehyde oxidase-2 [Zea mays]
                     307246
   Seq. No.
   Seq. ID
                     uC-zmflb73242f09b1
   Method
                     BLASTX
   NCBI GI
                     g2511531
   BLAST score
                     382
   E value
                     5.0e-37
   Match length
                     73
   % identity
                     93
   NCBI Description
                     (AF008120) alpha tubulin 1 [Eleusine indica]
                     >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
                     [Eleusine indica]
```

Seq. No. 307247

Seq. ID uC-zmflb73242g02a1

Method BLASTX



```
NCBI GI g1888357
BLAST score 189
E value 3.0e-14
Match length 79
% identity 54
NCBI Description (X98130)
```

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

307248 Seq. No. uC-zmflb73242h07b2 Seq. ID Method BLASTX g116380 NCBI GI BLAST score 205 E value 3.0e-16 Match length 51 % identity 80

NCBI Description CHALCONE SYNTHASE C2 (NARINGENIN-CHALCONE SYNTHASE C2) >gi 66554 pir SYZMCC naringenin-chalcone synthase (EC

2.3.1.74) c2 - maize >gi_22218_emb_CAA42764_ (X60205)

chalcone synthase [Zea mays]

Seq. No. 307249

Seq. ID uC-zmflb73243h12a1

Method BLASTN
NCBI GI g22243
BLAST score 38
E value 4.0e-12
Match length 78
% identity 87

NCBI Description Zea mays Cin1 repeat from Cin1 middle repetitive family

Seq. No. 307250

Seq. ID uC-zmflb73244b01b2

Method BLASTX
NCBI GI g3193333
BLAST score 145
E value 5.0e-09
Match length 91
% identity 41

NCBI Description (AF069299) contains similarity to breast cancer susceptibility (Brca2) [Arabidopsis thaliana]

Seq. No. 307251

Seq. ID uC-zmflb73244b07b2

Method BLASTX
NCBI GI g3834304
BLAST score 241
E value 3.0e-20
Match length 107
% identity 73

NCBI Description (AC005679) Contains similarity to gi_1786244 hypothetical

24.9 kD protein in surA-hepA intergenic region yab0 from Escherichia coli genome gb_AE000116, and to hypothetical

YABO family PF 00849. [Arabidopsis thaliana]

Seq. No. 307252

**



```
uC-zmflb73245a05a1
Seq. ID
                   BLASTX
 Method
                   g2149640
 NCBI GI
                   283
 BLAST score
                   2.0e-25
 E value
 Match length
                   86
 % identity
                   64
 NCBI Description
                   (U91995) Argonaute protein [Arabidopsis thaliana]
 Seq. No.
                   307253
                   uC-zmflb73245a05b2
 Seq. ID
                   BLASTX
 Method
                   g2149640
 NCBI GI
 BLAST score
                   339
 E value
                   9.0e-32
 Match length
                   123
 % identity
                   63
                   (U91995) Argonaute protein [Arabidopsis thaliana]
 NCBI Description
                   307254
 Seq. No.
                   uC-zmflb73245a11a1
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   g3318612
 BLAST score
                   191
                   1.0e-103
 E value
 Match length
                   279
                   93
 % identity
                   Zea mays mRNA for mitochondrial phosphate transporter,
 NCBI Description
                   complete cds
 Seq. No.
                   307255
                   uC-zmflb73245b03a1
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   g949979
 BLAST score
                   189
 E value
                   1.0e-102
 Match length
                   213
 % identity
                   98
 NCBI Description Z.mays Glossy2 locus DNA
 Seq. No.
                   307256
                   uC\text{-}zmf1b73245b12b2\\
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q549732
 BLAST score
                   147
 E value
                   1.0e-09
 Match length
                   50
 % identity
                   48
                   HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION
 NCBI Description
                   >gi_481110_pir__S37791 hypothetical protein YKL160w - yeast
                    (Saccharomyces cerevisiae) >gi_407488_emb_CAA81494_
                    (Z26877) unknown [Saccharomyces cerevisiae]
                   >gi_486279_emb_CAA82002_ (Z28160) ORF YKL160w
                    [Saccharomyces cerevisiae] >gi_1582545_prf__2118404F ORF
                    [Saccharomyces cerevisiae]
```

Seq. No. 307257



```
Seq. ID
                  uC-zmflb73245d10b2
Method
                  BLASTN
NCBI GI
                  q2198852
BLAST score
                  134
E value
                  1.0e-69
Match length
                  150
                  98
% identity
NCBI Description
                  Zea mays cystathionine gamma-synthase (CGS1) gene, complete
                  cds
Seq. No.
                  307258
Seq. ID
                  uC-zmflb73245e06b2
Method
                  BLASTN
                  g551482
NCBI GI
BLAST score
                  115
                  6.0e-58
E value
Match length
                  223
% identity
                  95
NCBI Description
                  Zea mays ABA- and ripening-inducible-like protein mRNA,
                  complete cds
                  307259
Seq. No.
Seq. ID
                  uC-zmflb73245g04b2
Method
                  BLASTX
NCBI GI
                  g699621
BLAST score
                  570
                  8.0e-59
E value
Match length
                  136
% identity
                  88
NCBI Description
                  (D14578) glutamine synthetase [Zea mays]
Seq. No.
                  307260
Seq. ID
                  uC-zmflb73245h04a1
Method
                  BLASTX
NCBI GI
                  g3859116
BLAST score
                  338
                   9.0e-32
E value
Match length
                   97
% identity
                  73
NCBI Description
                  (AF031609) unknown [Oryza sativa]
Seq. No.
                  307261
Seq. ID
                  uC-zmflb73246g03b3
Method
                  BLASTX
NCBI GI
                  q3337356
BLAST score
                  233
E value
                  7.0e-20
Match length
                  61
% identity
NCBI Description
                  (AC004481) putative protein transport protein SEC61 alpha
                  subunit [Arabidopsis thaliana]
Seq. No.
                  307262
Seq. ID
                  uC-zmflb73247a02a2
```

Method BLASTX NCBI GI g729882 BLAST score 208



E value 2.0e-16
Match length 43
% identity 86
NCBI Description CASEIN

CBI Description CASEIN KINASE II BETA' CHAIN (CK II)

>gi 1076300 pir S47968 casein kinase II (EC 2.7.1.-) beta

chain CKB2 - Arabidopsis thaliana >gi_467975 (U03984) casein kinase II beta subunit CKB2 [Arabidopsis thaliana] >gi_2245122_emb_CAB10544_ (Z97343) unnamed protein product

[Arabidopsis thaliana]

Seq. No. 307263

Seq. ID uC-zmflb73247a04b3

Method BLASTX
NCBI GI g3643598
BLAST score 215
E value 7.0e-18
Match length 60
% identity 72

NCBI Description (AC005395) putative poly(A) polymerase [Arabidopsis

thaliana]

Seq. No. 307264

Seq. ID uC-zmflb73247b10b3

Method BLASTX
NCBI GI g3135268
BLAST score 185
E value 6.0e-14
Match length 98
% identity 29

NCBI Description (AC003058) putative RNA-binding protein [Arabidopsis

thaliana]

Seq. No. 307265

Seq. ID uC-zmflb73247h03b3

Method BLASTX
NCBI GI g3402690
BLAST score 147
E value 2.0e-09
Match length 59
% identity 51

NCBI Description (AC004697) hypothetical protein, 3' partial [Arabidopsis

thaliana]

Seq. No. 307266

Seq. ID uC-zmflb73248h08a2

Method BLASTN
NCBI GI g22346
BLAST score 38
E value 1.0e-12
Match length 102
% identity 86

NCBI Description Maize In2-1 mRNA

Seq. No. 307267

Seq. ID uC-zmflb73250g12a2

Method BLASTX NCBI GI g1707642

```
BLAST score
E value
                  2.0e-24
                  54
Match length
                  96
% identity
NCBI Description
                  (Y07748) TMK [Oryza sativa]
                  307268
Seq. No.
Seq. ID
                  uC-zmflb73251c10b3
Method
                  BLASTX
NCBI GI
                  g4191793
BLAST score
                  346
E value
                  1.0e-32
Match length
                  104
% identity
                   60
                   (AC005917) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
                  307269
Seq. No.
Seq. ID
                  uC-zmflb73251d05b3
Method
                  BLASTX
```

NCBI GI g2688842 BLAST score 281 E value 2.0e-26 Match length 126

% identity 54

NCBI Description (AF004830) serine palmitoyltransferase LCB2 subunit

[Cricetulus griseus]

307270 Seq. No. Seq. ID

uC-zmflb73251f11b3

Method BLASTX g1199467 NCBI GI BLAST score 269 E value 2.0e-23 95 Match length % identity 56

NCBI Description (D64155) possible aldehyde decarbonylase [Arabidopsis

thaliana]

Seq. No. 307271

Seq. ID uC-zmflb73252d04b3

Method BLASTX NCBI GI q4220462 BLAST score 498 E value 1.0e-50 Match length 135 77 % identity

(AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) NCBI Description

gene from Arabidopsis thaliana containing Homeobox PF_00046

and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No. 307272

uC-zmflb73252g01b3 Seq. ID

Method BLASTX NCBI GI g312179 BLAST score 485 E value 4.0e-49



Match length 92 % identity 100

NCBI Description (X73151)

(X73151) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi 1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Seq. No. 307273

Seq. ID uC-zmflb73252h10b3

Method BLASTX
NCBI GI g4559292
BLAST score 204
E value 1.0e-16
Match length 58
% identity 67

NCBI Description (AF124148) trehalase 1 GMTRE1 [Glycine max]

Seg. No. 307274

Seq. ID uC-zmflb73253a08b1

Method BLASTX
NCBI GI g961452
BLAST score 303
E value 1.0e-27
Match length 105
% identity 55

NCBI Description (D63880) KIAA0159 gene product is related to yeast protein

L8479.14. [Homo sapiens]

Seq. No. 307275

Seq. ID uC-zmflb73253a12a1

Method BLASTX
NCBI GI g3157943
BLAST score 174
E value 1.0e-12
Match length 97
% identity 38

NCBI Description (AC002131) Contains similarity to BAP31 protein gb X81816

from Mus musculus. [Arabidopsis thaliana]

Seq. No. 307276

Seq. ID uC-zmflb73253b07b1

Method BLASTX
NCBI GI g2492863
BLAST score 225
E value 2.0e-23
Match length 99
% identity 60

NCBI Description ORNITHINE AMINOTRANSFERASE (ORNITHINE--OXO-ACID

AMINOTRANSFERASE) >gi 4416517 gb AAB18259 (U74303)

ornithine transaminase [Emericella nidulans]

Seq. No. 307277

Seq. ID uC-zmflb73253e04a1

Method BLASTN NCBI GI g2735007 BLAST score 70



E value 5.0e-31 Match length 78 % identity 97

NCBI Description Zea mays kinase associated protein phosphatase (KAPP) mRNA,

complete cds

Seq. No. 307278

Seq. ID uC-zmflb73253g07b1

Method BLASTX
NCBI GI g3668087
BLAST score 195
E value 5.0e-15
Match length 94
% identity 44

NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No. 307279

Seq. ID uC-zmflb73253h03b1

Method BLASTX
NCBI GI g2305222
BLAST score 165
E value 7.0e-12
Match length 50
% identity 64

NCBI Description (AF012089) phenylalanyl tRNA synthetase [Drosophila

melanogaster]

Seq. No. 307280

Seq. ID uC-zmflb73255c04b1

Method BLASTX
NCBI GI g4539324
BLAST score 249
E value 3.0e-21
Match length 83
% identity 67

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 307281

Seq. ID uC-zmflb73255f10b1

Method BLASTX
NCBI GI g2459418
BLAST score 165
E value 2.0e-11
Match length 117
% identity 36

NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No. 307282

Seq. ID uC-zmflb73255g01b1

Method BLASTN
NCBI GI g1864000
BLAST score 134
E value 2.0e-69
Match length 299
% identity 33

NCBI Description Maize DNA for Fd III, complete cds



```
307283
Seq. No.
Seq. ID
                  uC-zmflb73256b01b1
Method
                  BLASTX
NCBI GI
                  q2499489
BLAST score
                  303
E value
                  2.0e-27
Match length
                  143
                  50
% identity
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                  BETA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                  (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                  (PPI-PFK) >gi_483536_emb_CAA83683 (Z32850)
```

307284

307285

pyrophosphate-dependent phosphofructokinase beta subunit

[Ricinus communis]

Seq. No. Seq. ID uC-zmflb73256d08b1 Method BLASTX NCBI GI g3128224 232 BLAST score E value 1.0e-19 Match lemgth 83 % identity 55

NCBI Description (AC004077) putative protein serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. Seq. ID uC-zmflb73256h10b1 Method BLASTX NCBI GI q419760 BLAST score 422 2.0e-41

E value Match length 123 % identity 67

NCBI Description P-glycoprotein atpgp1 - Arabidopsis thaliana

>gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein

[Arabidopsis thaliana]

Seq. No. 307286

Seq. ID uC-zmflb73257a05b3

Method BLASTX NCBI GI g4406781 BLAST score 155 E value 7.0e-11 Match length 65 % identity 52

NCBI Description (AC006532) putative Na+/H+ antiporter [Arabidopsis

thaliana]

Seq. No. 307287

Seq. ID uC-zmflb73257a07a2

Method BLASTX NCBI GI g4512657 BLAST score 180 E value 3.0e-13 66 Match length % identity 47



```
NCBI Description
                   (AC006931) putative APG protein [Arabidopsis thaliana]
                   >gi 4544463 gb AAD22370.1_AC006580_2 (AC006580) putative
                   APG isolog protein [Arabidopsis thaliana]
                   307288
Seq. No.
Seq. ID
                   uC-zmflb73257b03a2
Method
                   BLASTN
NCBI GI
                   g309560
BLAST score
                   272
E value
                   1.0e-151
Match length
                   332
% identity
                   95
                   Zea mays mitochondrial chaperonin 60 (mtcpn60II) mRNA,
NCBI Description
                   complete cds
                   307289
Seq. No.
Seq. ID
                   uC-zmflb73257b05a2
Method
                   BLASTN
NCBI GI
                   g1498596
BLAST score
                   233
E value
                   1.0e-128
Match length
                   233
% identity
                   100
                  Zea mays phospholipid transfer protein mRNA, complete cds
NCBI Description
Seq. No.
                   307290
Seq. ID
                   uC-zmflb73257e04b3
Method
                   BLASTX
NCBI GI
                   g3641837
BLAST score
                   347
E value
                   4.0e-33
Match length
                   90
% identity
                   78
NCBI Description
                   (AL023094) Nonclathrin coat protein gamma - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   307291
Seq. ID
                   uC-zmflb73257f04b3
Method
                   BLASTX
NCBI GI
                   q4521190
BLAST score
                   144
E value
                   2.0e-09
Match length
                   54
% identity
                   57
                   (AB013448) Pib [Oryza sativa] >gi_4521192_dbj_BAA76282.1_
NCBI Description
                   (AB013449) Pib [Oryza sativa]
Seq. No.
                   307292
Seq. ID
                  uC-zmflb73257f11a2
Method
                  BLASTX
NCBI GI
                  g2160544
```

BLAST score 156 E value 2.0e-10 Match length 99 % identity 38

NCBI Description (U63652) ent-kaurene synthase A [Pisum sativum]

BLAST score

Match length

E value

647

130

5.0e-68



```
Seq. No.
                   307293
Seq. ID
                  uC-zmflb73257h10b3
Method
                  BLASTX
NCBI GI
                  g2642157
BLAST score
                  190
E value
                  9.0e-15
Match length
                  60
% identity
                  58
NCBI Description
                  (AC003000) ankyrin-like protein [Arabidopsis thaliana]
                  307294
Seq. No.
Seq. ID
                  uC-zmflb73258b08b3
Method
                  BLASTX
NCBI GI
                  g3264596
BLAST score
                  221
                  3.0e-18
E value
Match length
                  60
% identity
                  80
NCBI Description
                  (AF057183) putative tonoplast aquaporin [Zea mays]
Seq. No.
                  307295
Seq. ID
                  uC-zmflb73258q03b3
Method
                  BLASTX
NCBI GI
                  g1653059
BLAST score
                  223
E value
                  3.0e-18
Match length
                  105
% identity
                  44
NCBI Description
                  (D90910) hypothetical protein [Synechocystis sp.]
                  307296
Seq. No.
Seq. ID
                  uC-zmflb73258h01b3
Method
                  BLASTN
NCBI GI
                  g2642323
BLAST score
                  110
E value
                  3.0e-55
Match length
                  178
% identity
                  89
NCBI Description Zea mays profilin (PRO4) mRNA, complete cds
Seq. No.
                  307297
Seq. ID
                  uC-zmflb73259b09a1
Method
                  BLASTX
NCBI GI
                  q4589852
BLAST score
                  242
E value
                  2.0e-20
Match length
                  71
% identity
                  63
                  (AB025968) cycloartenol synthase [Glycyrrhiza glabra]
NCBI Description
Seq. No.
                  307298
Seq. ID
                  uC-zmflb73260a09b2
Method
                  BLASTX
NCBI GI
                  q625509
```

```
% identity
NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment)
                  307299
Seq. No.
                  uC-zmflb73260d01b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3821793
                  270
BLAST score
                  1.0e-23
E value
                  49
Match length
                  96
% identity
NCBI Description
                 (Y11526) casein kinase II alpha subunit [Zea mays]
Seq. No.
                  307300
                  uC-zmflb73260f06b2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2921303 /
BLAST score
                  45
                  4.0e-16
E value
Match length
                  77
                  90
% identity
NGBI Description Zea mays herbicide safener binding protein (SBP1) mRNA,
                  complete cds
                  307301
Seq. No.
Seq. ID
                  uC-zmflb73260g05b2
Method
                  BLASTN
NCBI GI
                  q3819487
BLAST score
                  42
                  2.0e-14
E value
Match length
                  54
```

94 % identity

NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG2013.uni

307302 Seq. No.

Seq. ID uC-zmflb73260h06b2

Method BLASTX NCBI GI q1710841 BLAST score 325 E value 4.0e-30 Match length 124 % identity 85

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905)

S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]

Seq. No. 307303

Seq. ID uC-zmflb73261f09b3

Method BLASTX NCBI GI g1353193 BLAST score 198 2.0e-15 E value Match length 55 % identity 69

O-METHYLTRANSFERASE ZRP4 (OMT) >gi 542186 pir JQ2268 NGBI Description O-methyltransferase (EC 2.1.1.-) - maize >gi 404070

(L14063) O-methyltransferase [Zea mays]



```
Seq. No.
                  307304
                  uC-zmflb73262e10a2
Seq. ID
Method
                  BLASTN
                  q498774
NCBI GI
BLAST score
                  72
E value
                  1.0e-32
Match length
                  148
                  87
% identity
NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein
                  307305
Seq. No.
                  uC-zmflb73262f04a2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3641836
BLAST score
                  141
E value
                  8.0e-09
Match length
                  39
% identity
                  72
NCBI Description
                  (AL023094) putative serine/threonine protein kinase
                  [Arabidopsis thaliana]
                  307306
Seq. No.
Seq. ID
                  uC-zmflb73262f08b3
Method
                  BLASTN
NCBI GI
                  g951452
BLAST score
                  39
E value
                  3.0e-13
Match length
                  51
% identity
                  94
NCBI Description
                  Wheat (clone p80k-16) initiation factor isozyme 4F p82
                  subunit mRNA sequence
Seq. No.
                  307307
Seq. ID
                  uC-zmflb73263c01b1
Method
                  BLASTX
NCBI GI
                  g2827524
BLAST score
                  161
E value
                  3.0e-11
Match length
                  39
% identity
                  74
NCBI Description
                  (AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.
                  307308
Seq. ID
                  uC-zmflb73263c05b1
Method
                  BLASTX
NCBI GI
                  q1170767
BLAST score
                  171
E value
                  3.0e-12
Match length
                  60
% identity
                  58
NCBI Description
                  2.6S PROTEASE REGULATORY SUBUNIT 8 HOMOLOG (LET1 PROTEIN)
                  >gi_626074_pir__S45176 transcription factor SUG1 homolog -
                  fission yeast (Schizosaccharomyces pombe) >gi 406051
                  (U02280) Let1 [Schizosaccharomyces pombe]
```

>gi_4106689_emb_CAA22628_ (AL035065) 26s protease

regulatory subunit 8 homolog [Schizosaccharomyces pombe]



```
Seq. No.
                   307309
Seq. ID
                   uC-zmflb73263c10b1
Method
                   BLASTX
NCBI GI
                   g452593
BLAST score
                   405
E value
                   3.0e-47
Match length
                   124
% identity
                   69
NCBI Description
                  (D21814) ORF [Lilium longiflorum]
                   307310
Seq. No.
Seq. ID
                   uC-zmflb73263f12b1
Method
                   BLASTX
NCBI GI
                   g4455367
BLAST score
                   796
E value
                   3.0e-85
Match length
                   168
% identity
                   91
NCBI Description
                  (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                   307311
Seq. ID
                   uC-zmflb73264a09b1
Method
                  BLASTN
NCBI GI
                   g2781432
BLAST score
                   44
                   5.0e-16
E value
Match length
                  100
% identity
                  87
NCBI Description
                  Oryza sativa subsp. japonica RSW1-like cellulose synthase
                  catalytic subunit mRNA, partial cds
Seq. No.
                  307312
Seq. ID
                  uC-zmflb73264b06b1
Method
                  BLASTX
NCBI GI
                  g3962377
BLAST score
                  302
E value
                  1.0e-27
Match length
                  71
% identity
                  82
NCBI Description
                  (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
Seq. No.
                  307313
Seq. ID
                  uC-zmflb73264b08b1
Method
                  BLASTN
NCBI GI
                  g433040
BLAST score
                  37
E value
                  3.0e-11
Match length
                  53
% identity
                  92
NCBI Description
                  Zea mays W-22 clone PREM-1A retroelement PREM-1, partial
                  sequence
```

Seq. No. 307314

Seq. ID uC-zmflb73264e03b1

Method BLASTN NCBI GI g3511235



```
BLAST score
E value
                   8.0e-46
Match length
                   247
                   85
% identity
                  Zea mays starch branching enzyme IIb (ae) gene, complete
NCBI Description
Seq. No.
                  307315
Seq. ID
                  uC-zmflb73264f06b1
Method
                  BLASTX
NCBI GI
                  g3288704
BLAST score
                  215
E value
                  4.0e-20
Match length
                  120
% identity
                  41
NCBI Description
                  (AB008191) SRK29 [Brassica rapa]
                  307316
Seq. No.
Seq. ID
                  uC-zmflb73264f09b1
Method
                  BLASTN
NCBI GI
                  g293911
BLAST score
                  317
E value
                  1.0e-178
Match length
                  355
% identity
                  97
NCBI Description Zea mays (clone wusl1032) mRNA sequence
Seq. No.
                  307317
Seq. ID
                  uC-zmflb73264h03b1
Method
                  BLASTX
NCBI GI
                  g2894534
BLAST score
                  203
E value
                  1.0e-16
Match length
                  64
% identity
                  75
NCBI Description
                  (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  307318
Seq. ID
                  uC-zmflb73265d07b4
Method
                  BLASTX
NCBI GI
                  g4586250
BLAST score
                  142
E value
                  8.0e-09
Match length
                  43
% identity
                  63
NCBI Description
                  (AL049640) adenine DNA glycosylase like protein
                  [Arabidopsis thaliana]
Seq. No.
                  307319
Seq. ID
                  uC-zmflb73265e06b4
```

Method BLASTX NCBI GI q3063708 BLAST score 355 E value 8.0e-34 Match length 98 % identity 61

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

```
Seq. No.
                      307320
    Seq. ID
                      uC-zmflb73266a03a2
   Method
                      BLASTN
   NCBI GI
                      q4416300
   BLAST score
                      44
   E value
                      1.0e-15
   Match length
                      60
    % identity
                      31
   NCBI Description
                      Zea mays chromosome 4 22 kDa zein-associated intercluster
                      region, complete sequence
   Seq. No.
                      307321
   Seq. ID
                      uC-zmflb73266d11b2
   Method
                      BLASTN
NCBI GI
                      q4140643
   BLAST score
                      60
   E value
                      5.0e-25
   Match length
                      103
   % identity
                      90
   NCBI Description
                      Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                      complete sequence
   Seq. No.
                      307322
   Seq. ID
                      uC-zmflb73266g07b2
   Method
                      BLASTN
   NCBI GI
                      g18903
   BLAST score
                      35
   E value
                      4.0e-10
   Match length
                      51
   % identity
                      92
   NCBI Description Barley mRNA for aspartic proteinase
   Seq. No.
                      307323
   Seq. ID
                      uC-zmflb73267a09b2
   Method
                      BLASTX
   NCBI GI
                      q119355
   BLAST score
                      222
   E value
                      1.0e-18
   Match length
                      44
   % identity
                      100
                      ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
   NCBI Description
                      (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                      >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
                      4.2.1.11) - maize >gi_22273 emb CAA39454 (X55981) enolase
                      [Zea mays]
                      307324
   Seq. No.
   Seq. ID
                      uC-zmflb73267e04b2
   Method
                      BLASTX
   NCBI GI
                      g3510253
   BLAST score
                      164
   E value
                      1.0e-11
   Match length
```

(AC005310) hypothetical protein [Arabidopsis thaliana]

42

64

% identity

NCBI Description



```
Seq. No.
                  307325
Seq. ID
                  uC-zmflb73267f07b2
Method
                  BLASTX
NCBI GI
                  g131772
BLAST score
                  306
                  3.0e-28
E value
Match length
                  64
% identity
                  95
NCBI Description
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
                  >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                  maize
Seq. No.
                  307326
                  uC-zmflb73268a05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g602605
BLAST score
                  38
E value
                  3.0e-12
Match length
                  82
% identity
                  87
NCBI Description
                  Zea mays tandem genes for alphal-tubulin and alpha2-tubulin
                  307327
Seq. No.
                  uC-zmflb73270d10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169818
BLAST score
                  63
E value
                  3.0e-27
Match length
                  106
% identity
                  91
NCBI Description Rice 25S ribosomal RNA gene
                  307328
Seq. No.
                  uC-zmflb73270e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g419789
BLAST score
                  357
E value
                  6.0e-34
Match length
                  139
% identity
                  48
NCBI Description hypothetical protein - potato
Seq. No.
                  307329
Seq. ID
                  uC-zmflb73270e03b1
Method
                  BLASTX
                  g82665
NCBI GI
BLAST score
                  163
                  9.0e-12
E value
Match length
                  37
% identity
                  81
NCBI Description ADP, ATP carrier protein G1 - maize
```

Seq. No. 307330

Seq. ID uC-zmflb73270f04b1

Method BLASTX NCBI GI g135398 BLAST score 309



E value 8.0e-29 Match length 65 % identity 92

NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1

chain - maize >gi 22147 emb CAA33734 (X15704)

alphal-tubulin [Zea mays]

307331 Seq. No.

Seq. ID uC-zmflb73270f09b1

Method BLASTX NCBI GI q3269293 BLAST score 175 E value 4.0e-13 Match length 60

% identity 63

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 307332

uC-zmflb73270h03b1 Seq. ID

Method BLASTN NCBI GI g3264597 BLAST score 66 E value 9.0e-29 Match length 153 % identity 92

NCBI Description Zea mays trypsin inhibitor mRNA, complete cds

Seq. No. 307333

Seq. ID uC-zmflb73270h06b1

Method BLASTN NCBI GI g169133 BLAST score 59 E value 8.0e-25 Match length 111 % identity 88

NCBI Description Zea mays precursor of the oxygen evolving complex 17 kDa

protein mRNA, complete cds

307334

Seq. No. Seq. ID uC-zmflb73270h11b1

Method BLASTX NCBI GI g1769901 BLAST score 404 E value 2.0e-39 Match length 128 % identity

NCBI Description (X95737) proline transporter 1 [Arabidopsis thaliana]

>gi_2088642 (AF002109) proline transporter 1 [Arabidopsis

thaliana]

Seq. No. 307335

Seq. ID uC-zmflb73271c07a1

Method BLASTX NCBI GI g4585875 BLAST score 315 E value 4.0e-29 Match length 78



```
% identity
NCBI Description
                  (AC005850) Unknown protein [Arabidopsis thaliana]
                   307336
Seq. No.
Seq. ID
                  uC-zmflb73272c11a1
Method
                  BLASTN
NCBI GI
                  g22511
                  78
BLAST score
                  7.0e-36
E value
Match length
                  194
% identity
                  94
NCBI Description
                  Z.mays whp (white pollen) gene for chalcone synthase
                  307337
Seq. No.
                  uC-zmflb73272e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2384671
BLAST score
                  182
E value
                  3.0e-16
Match length
                  100
% identity
                  55
NCBÍ Description
                   (AF012657) putative potassium transporter AtKT2p
                  [Arabidopsis thaliana]
Seq. No.
                  307338
Seq. ID
                  uC-zmflb73272f05a1
Method
                  BLASTX
NCBI GI
                  g4006827
BLAST score
                  178
E value
                  5.0e-13
Match length
                  74
% identity
                  42
NCBI Description
                  (AC005970) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                  307339
Seq. ID
                  uC-zmflb73273g09a1
Method
                  BLASTN
NCBI GI
                  q600871
BLAST score
                  63
E value
                  4.0e-27
Match length
                  175
% identity
                  83
NCBI Description
                  Zea mays starch branching enzyme I (sbel) mRNA, complete
Seq. No.
                  307340
Seq. ID
                  uC-zmflb73274c07b1
Method
                  BLASTX
NCBI GI
                  q4455302
BLAST score
                  348
```

E value 2.0e-37 Match length 162 % identity 52

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 307341

Seq. ID uC-zmflb73274e11b1

```
Method
                     BLASTX
   NCBI GI
                     g4249380
   BLAST score
                     224
                     2.0e-18
   E value
   Match length
                     89
   % identity
                     51
   NCBI Description
                     (AC005966) ESTs gb Z37637, gb_AA042498 and gb_AA042269 come
                     from this gene. [Arabidopsis thaliana]
                     307342
   Seq. No.
   Seq. ID
                     uC-zmflb73274g06b1
                     {\tt BLASTX}
   Method
   NCBI GI
                     g1931643
   BLAST score
                     155
   E value
                     2.0e-10
   Match length
                     81
   % identity
                     40
   NCBI Description (U95973) DnaJ isolog [Arabidopsis thaliana]
   Seq. No.
                     307343
  Seq. ID
                     uC-zmflb73274h03b1
Method
                     BLASTX
  NCBI GI
                     g3688173
  BLAST score
                     303
  E value
                     1.0e-27
  Match length
                     88
   % identity
                     70
  NCBI Description
                     (AL031804) putative protein [Arabidopsis thaliana]
                     307344
  Seq. No.
  Seq. ID
                     uC-zmflb73274h04b1
  Method
                     BLASTX
  NCBI GI
                     g2462760
  BLAST score
                     179
  E value
                     5.0e-13
  Match length
                     122
  % identity
                     35
  NCBI Description
                    (AC002292) Hypothetical protein [Arabidopsis thaliana]
                     307345
  Seq. No.
  Seq. ID
                     uC-zmflb73275a07b1
  Method
                     BLASTN
  NCBI GI
                     g551482
  BLAST score
                     271
  E value
                     1.0e-151
  Match length
                     444
  % identity
                     95
  NCBI Description
                     Zea mays ABA- and ripening-inducible-like protein mRNA,
                     complete cds
  Seq. No.
                     307346
  Seq. ID
                     uC-zmflb73275d11a1
```

Method uc-zmith/32/3ditai

Method BLASTX
NCBI GI g4165488
BLAST score 251
E value 1.0e-21
Match length 54



% identity (AJ132399) alpha-tubulin 3 [Hordeum vulgare] NCBI Description

307347 Seq. No.

uC-zmflb73276a06b1 Seq. ID

Method BLASTX NCBI GI g516554 BLAST score 216 E value 1.0e-17 Match length 50 % identity 78

NCBI Description (U10079) cyclin IaZm [Zea mays]

Seq. No. 307348

Seq. ID uC-zmflb73276a10b1

Method BLASTX NCBI GI g4581164 BLAST score 194 E value 6.0e-22 Match length 98 58 % identity

NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No. 307349

uC-zmflb73276c11b1 Seq. ID

Method BLASTX NCBI GI g135411 BLAST score 361 E value 2.0e-34 Match length 90 % identity 80

TUBULIN ALPHA-2 CHAIN >gi_82732_pir__S15772 tubulin alpha-2 NCBI Description

chain - maize >gi_22148 emb CAA33733 (X15704)

. E.

alpha2-tubulin [Zea mays]

Seq. No. 307350

Seq. ID uC-zmflb73276d12b1

Method BLASTX NCBI GI g4371280 BLAST score 272 E value 5.0e-34 Match length 100 % identity 73

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 307351

Seq. ID uC-zmflb73276f06b1

Method BLASTX NCBI GI g3549654 BLAST score 291 E value 2.0e-26 Match length 108 % identity 57

NCBI Description (AL031394) metal-transporting P-type ATPase (fragment)

[Arabidopsis thaliana]

Seq. No. 307352

```
uC-zmflb73276f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455169
BLAST score
                  200
E value
                  1.0e-15
Match length
                  96
% identity
                  43
NCBI Description
                   (AL035521) putative aldehyde dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  307353
Seq. ID
                  uC-zmflb73276q01b1
Method
                  BLASTX
NCBI GI
                  q4584525
BLAST score
                  347
E value
                  9.0e-33
Match length
                  92
% identity
                  66
NCBI Description
                   (AL049607) protein phosphatase 2C-like protein [Arabidopsis
                  thaliana]
                  307354
Seq. No.
Seq. ID
                  uC-zmflb73276g08a1
Method
                  BLASTN
                  q416146
NCBI GI
BLAST score
                  49
                  5.0e-19
E value
Match length
                  101
% identity
                  87
NCBI Description Zea mays beta-6 tubulin (tub6) gene and mRNA, complete cds
Seq. No.
                  307355
Seq. ID
                  uC-zmflb73276h04b1
Method
                  BLASTX
NCBI GI
                  g3342802
BLAST score
                  329
E value
                  -9.0e-31
Match length
                  91
% identity
                  77
NCBI Description
                   (AF061838) putative cytosolic 6-phosphogluconate
                  dehydrogenase [Zea mays]
Seq. No.
                  307356
Seq. ID
                  uC-zmflb73276h05b1
Method
                  BLASTX
NCBI GI
                  g2088647
BLAST score
                  209
                  2.0e-16
E value
Match length
                  160
% identity
                  42
                  (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
```

uC-zmflb73277c12b1

307357

BLASTX

Seq. No. Seq. ID

Method



```
NCBI GI g542179
BLAST score 236
E value 2.0e-20
Match length 49
% identity 96
```

NCBI Description alpha tubulin - maize >gi_629837_pir__S39998 tubulin alpha chain - maize (fragment) >gi_393401 emb CAA52158 (X73980)

alpha tubulin [Zea mays]

Seq. No. 307358

Seq. ID uC-zmflb73278b06b1

Method BLASTX
NCBI GI g3202024
BLAST score 193
E value 9.0e-18
Match length 83
% identity 58

NCBI Description (AF069315) thylakoid-bound L-ascorbate peroxidase precursor

[Mesembryanthemum crystallinum]

Seq. No. 307359

Seq. ID uC-zmflb73278c07b1

Method BLASTX
NCBI GI g3236478
BLAST score 168
E value 6.0e-12
Match length 39
% identity 85

NCBI Description (AF071196) 26S protease regulatory subunit [Gossypium

hirsutum]

Seq. No. 307360

Seq. ID uC-zmflb73278c08b1

Method BLASTX
NCBI GI g1203832
BLAST score 594
E value 1.0e-61
Match length 146
% identity 78

NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII

[Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan

exohydrolase [Hordeum vulgare]

Seq. No. 307361

Seq. ID uC-zmflb73278e02a2

Method BLASTX
NCBI GI g4454051
BLAST score 190
E value 2.0e-14
Match length 68
% identity 54

NCBI Description (AL035394) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 307362

Seq. ID uC-zmflb73278e04b1

Method BLASTX

```
NCBI GI
                  q1711036
BLAST'score
                  169
                  7.0e-23
E value
Match length
                  69
                  73
% identity
NCBI Description
                  (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum
                  sativum]
                  307363
Seq. No.
                  uC-zmflb73278e06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3599491
BLAST score
                  227
E value
                  4.0e-19
Match length
                  71
% identity
                  62
```

(AF085149) putative aminotransferase [Capsicum chinense] NCBI Description

uC-zmflb73278f05b1 Seq. ID Method BLASTX NCBI GI g4512714 BLAST score 365 E value 9.0e-35 Match length 95 % identity 76

Seq. No.

307364

307365

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. Seq. ID uC-zmflb73278g01b1 Method BLASTX NCBI GI g3242783 BLAST score 471 E value 3.0e-47 Match length 133 % identity 63

NCBI Description (AF055354) respiratory burst oxidase protein B [Arabidopsis

thaliana]

307366 Seq. No.

uC-zmflb73278g05b1 Seq. ID

Method BLASTX g1707642 NCBI GI BLAST score 266 E value 4.0e-23 Match length 175 % identity 34

NCBI Description (Y07748) TMK [Oryza sativa]

Seq. No. 307367

Seq. ID uC-zmflb73278h10b1

Method BLASTX NCBI GI g1814403 BLAST score 686 E value 2.0e-72 Match length 168 % identity 82



NCBI Description (U84889) methionine synthase [Mesembryanthemum crystallinum]

Seq. No. 307368

Seq. ID uC-zmflb73279a04b1

Method BLASTN
NCBI GI g2341060
BLAST score 58
E value 5.0e-24
Match length 178
% identity 83

NCBI Description Zea mays translational initiation factor eIF-4A (tif-4A3)

mRNA, complete cds

Seq. No. 307369

Seq. ID uC-zmflb73279a06b1

Method BLASTX
NCBI GI g1806140
BLAST score 161
E value 1.0e-11
Match length 42
% identity 76

NCBI Description (X97314) cdc2MsC [Medicago sativa]

Seq. No. 307370

Seq. ID uC-zmflb73279a11a2

Method BLASTX
NCBI GI g2145356
BLAST score 222
E value 4.0e-18
Match length 63
% identity 63

NCBI Description (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474

(AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No. 307371

Seq. ID $uC-zmf_bb73279c01b1$

Method BLASTN
NCBI GI g607797
BLAST score 100
E value 9.0e-49
Match length 169
% identity 91

NCBI Description Zea mays FRB73 mitochondrion maturase-related protein

(mat-r) gene, complete cds, and NADH dehydrogenase subunit

I (nad1) gene, exon E, partial cds

Seq. No. 307372

Seq. ID uC-zmflb73279e08a2

Method BLASTX
NCBI GI g1172861
BLAST score 213
E value 2.0e-17
Match length 82
% identity 54

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR

(RUBISCO LARGE SUBUNIT) >gi_1363613 pir S58560 a





```
ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain
- maize chloroplast >gi_18036_emb_CAA78027_ (Z11973)
Ribulose bisphosphate carboxylase [Zea mays]
>gi_902230_emb_CAA60294_ (X86563) rubisco large subunit
[Zea mays]

307373
uC-zmf1b73279h09a2
BLASTX
g2347195
161
3.0e-11
87
39
```

% identity 39
NCBI Description (AC002338) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 307374

 Seq. ID
 uC-zmflb73279h10b1

 Method
 BLASTN

 NCBI GI
 g2921303

 BLAST score
 71

 E value
 4.0e-32

E value 4.0eMatch length 111
% identity 92

Seq. No. Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA, complete cds

Seq. No. 307375

Seq. ID uC-zmflb73280a04b2

Method BLASTX
NCBI GI g4056503
BLAST score 162
E value 3.0e-11
Match length 36
% identity 86

NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 307376

Seq. ID uC-zmflb73280a10b2

Method BLASTX
NCBI GI g1362162
BLAST score 359
E value 3.0e-34
Match length 88
% identity 76

NCBI Description beta-glucosidase BGQ60 precursor - barley >gi_804656

(L41869) beta-glucosidase [Hordeum vulgare]

Seq. No. 307377

Seq. ID uC-zmflb73280b04b2

Method BLASTX
NCBI GI g3928543
BLAST score 177
E value 3.0e-28
Match length 119
% identity 54

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis



thaliana]

```
307378
Seq. No.
Seq. ID
                  uC-zmflb73282q06a1
Method
                  BLASTX
NCBI GI
                  q516554
BLAST score
                  168
E value
                  9.0e-12
Match length
                  59
% identity
                  73
NCBI Description (U10079) cyclin IaZm [Zea mays]
Seq. No.
                  307379
                  uC-zmflb73283b05b2
Seq. ID
```

Method BLASTX g4510348 NCBI GI BLAST score 167 E value 1.0e-11 Match length 57 % identity 51

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

307380 Seq. No. Seq. ID uC-zmflb73283d09a1 Method BLASTX NCBI GI g4506489 BLAST score 203

E value 6.0e-16 Match length 78 % identity 51

NCBI Description replication factor C (activator 1) 3 (38kD)

>gi_3915601_sp_P40938_AC13 HUMAN ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD SUBUNIT) (A1 38 KD SUBUNIT)

(RF-C 38 KD SUBUNIT) (RFC38) >gi 1498259 (L07541) replication factor C, 38-kDa subunit [Homo sapiens]

Seq. No. 307381

Seq. ID uC-zmflb73283e11b2

Method BLASTX NCBI GI g3551960 BLAST score 277 E value 1.0e-24 Match length 116 % identity 50

NCBI Description (AF082033) senescence-associated protein 15 [Hemerocallis

hybrid cultivar]

Seq. No. 307382

Seq. ID uC-zmflb73284a06b1

Method BLASTX NCBI GI q4138265 BLAST score 213 E value 2.0e-17 Match length 49 % identity 84

NCBI Description (AJ006228) Avr9 elicitor response protein [Nicotiana

tabacum]

Method



```
307383
Seq. No.
Seq. ID
                   uC-zmflb73284a11b1
Method
                   BLASTX
NCBI GI
                   g4138265
BLAST score
                   183
E value
                   8.0e-14
Match length
                   53
                   68
% identity
NCBI Description
                   (AJ006228) Avr9 elicitor response protein [Nicotiana
                   tabacum]
Seq. No.
                   307384
                   uC-zmflb73284b09b1
Seq. ID
Method
                   BLASTN
                   g1839582
NCBI GI
BLAST score
                   90
                   5.0e-43
E value
Match length
                   145
                   92
% identity
NCBI Description
                  polyubiquitin homolog {clone CHEM 6} [Zea mays=maize, cv.
                   INRA 258, mercuric chloride-treated, leaves, mRNA Partial,
                   199 nt, segment 1 of 2]
Seq. No.
                   307385
                   uC-zmflb73284c03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4204260
BLAST score
                   152
E value
                   9.0e-10
                   77
Match length
% identity
                   44
NCBI Description
                  (AC005223) 25568 [Arabidopsis thaliana]
Seq. No.
                   307386
Seq. ID
                   uC-zmflb73284c07a1
Method
                   BLASTX
NCBI GI
                   q4539321
BLAST score
                   223
E value
                   3.0e-18
Match length
                   71
% identity
                   54
NCBI Description
                  (AL035679) putative protein [Arabidopsis thaliana]
Seq. No.
                   307387
Seq. ID
                   uC-zmflb73284c10b1
Method
                   BLASTX
NCBI GI
                   g3928142
BLAST score
                   452
E value
                   3.0e-45
                  96
Match length
                   97
% identity
NCBI Description
                  (AJ131045) protein phosphatase [Cicer arietinum]
                   307388
Seq. No.
Seq. ID
```

43643

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uC-zmflb73284d03b1

BLASTN

```
NCBI GI
                   q511665
BLAST score
                   42
E value
                   1.0e-14
Match length
                   146
                   84
% identity
NCBI Description
                  Rice gene for aspartic protease, complete cds
                   307389
Seq. No.
                  uC-zmflb73284e01a1
Seq. ID
Method ·
                  BLASTN
NCBI GI
                  g22091
BLAST score
                  187
E value
                   1.0e-101
Match length
                   303
% identity
                   91
NCBI Description
                  Z.diploperennis gene for hydroxyproline-rich glycoprotein
Seq. No.
                  307390
Seq. ID
                  uC-zmf1b73284e12a1
Method
                  BLASTX
NCBI GI
                  g1857256
BLAST score
                  307 -
E value
                   6.0e-28
Match length
                  128
% identity
                  48
NCBI Description
                  (U75360) MURAZC [Zea mays]
                  307391
Seq. No.
                  uC-zmflb73284f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539335
BLAST score
                  155
E value
                  2.0e-10
Match length
                  56
% identity
                  55
NCBI Description
                  (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                  307392
Seq. ID
                  uC-zmflb73285c12a1
Method
                  BLASTN
NCBI GI
                  g3925228
BLAST score
                  55
                  3.0e-22
E value
Match length
                  103
% identity
                  88
NCBI Description
                  Zea mays peroxidase J gene, partial cds
Seq. No.
                  307393
Seq. ID
                  uC-zmflb73285e02b1
```

Method BLASTX
NCBI GI g1040913
BLAST score 401
E value 5.0e-39
Match length 76
% identity 97

NCBI Description (U31381) ribulose-1,5-bisphosphate carboxylase/oxygenase

large subunit [Tristachya biseriata]

Seq. No.

Seq. ID

Method

NCBI GI

307399

BLASTN

g2737881

uC-zmflb73286b09b1

```
307394
Seq. No.
                  uC-zmf1b73285e06b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4539654
BLAST score
                  34
                  2.0e-09
E value
Match length
                  62
% identity
                  89
                  Sorghum bicolor 22 kDa kafirin cluster
NCBI Description
                  307395
Seq. No.
                  uC-zmflb73285f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706958
BLAST score
                  384
                  4.0e-37
E value
Match length
                  94
% identity
                  71
NCBI Description
                  (U58284) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  307396
Seq. ID
                  uC-zmflb73285g08b1
Method
                  BLASTN
NCBI GI
                  g4521194
BLAST score
                  73
E value
                  1.0e-32
Match length
                  153
% identity
                  87
NCBI Description
                  Oryza sativa DNA, centromere sequence RCB11
Seq. No.
                  307397
Seq. ID
                  uC-zmflb73285h08b1
Method
                  BLASTX
NCBI GI
                  g1076746
BLAST score
                  550
E value
                  2.0e-56
Match length
                  137
% identity
                  82
NCBI Description
                  heat shock protein 70 - rice (fragment)
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                  [Oryza sativa]
Seq. No.
                  307398
Seq. ID
                  uC-zmflb73286a10b1
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                  38
                  4.0e-12
E value
Match length
                  70
% identity
                  89
NCBI Description
                  Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
```

```
BLAST score
E value
                  6.0e-26
Match length
                  113
% identity
                  88
NCBI Description
                  Saccharum sp. polyphenol oxidase mRNA, complete cds
                  307400
Seq. No.
                  uC-zmflb73286c04b1
Seq. ID
                  BŁASTX
Method
NCBI GI
                  g2500497
BLAST score
                  319
E value
                  2.0e-29
Match length
                  61
% identity
                  100
NCBI Description
                  40S RIBOSOMAL PROTEIN S21 >gi 1419372 emb CAA67225
                  (X98656) ribosomal protein S21 [Zea mays]
                  307401
Seq. No.
                  uC-zmflb73286e04b1
                  BLASTX
```

 Seq. No.
 307401

 Seq. ID
 uC-zmflb73286e04b1

 Method
 BLASTX

 NCBI GI
 g3738337

 BLAST score
 242

 E value
 6.0e-26

 Match length
 179

 % identity
 38

NCBI Description (AC005170) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 307402 Seq. ID uC-zmflb73286e09b1 Method BLASTN

NCBI GI g1255684
BLAST score 34
E value 6.0e-10
Match length 50
% identity 92

NCBI Description Rice mRNA for aspartic protease, complete cds

Seq. No. 307403

Seq. ID uC-zmflb73286h01b1

Method BLASTN
NCBI GI g1864000
BLAST score 73
E value 7.0e-33
Match length 145
% identity 88

NCBI Description Maize DNA for Fd III, complete cds

``

Seq. No. 307404

Seq. ID uC-zmflb73287b02b1

Method BLASTX
NCBI GI g3548803
BLAST score 180
E value 5.0e-13
Match length 55
% identity 69

NCBI Description (AC005313) putative DNA-binding protein [Arabidopsis



thaliana] >gi_4335770_gb_AAD17447_ (AC006284) putative SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]

 Seq. No.
 307405

 Seq. ID
 uC-zmflb73287b03b1

 Method
 BLASTX

 NCBI GI
 g2623311

 BLAST score
 225

 E value
 1.0e-18

Match length 66 % identity 67

NCBI Description (AC002409) unknown protein [Arabidopsis thaliana]

>gi_3402720 (AC004261) unknown protein [Arabidopsis

thaliana]

Seq. No. 307406

Seq. ID uC-zmflb73287c02b1

Method BLASTX
NCBI GI g733454
BLAST score 145
E value 6.0e-09
Match length 29
% identity 93

NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor

[Zea mays]

Seq. No. 307407

Seq. ID uC-zmflb73287c07b1

Method BLASTN
NCBI GI g3769431
BLAST score 53
E value 6.0e-21
Match length 81
% identity 91

NCBI Description Zea mays RNA polymerase sigma factor 2 (sig2) mRNA, nuclear

mRNA encoding chloroplast protein, partial cds

Seq. No. 307408

Seq. ID uC-zmflb73287f09b1

Method BLASTX
NCBI GI g4584356
BLAST score 487
E value 4.0e-51
Match length 161
% identity 65

NCBI Description (AC006420) putative replication protein A [Arabidopsis

thaliana]

Seq. No. 307409

Seq. ID uC-zmflb73289b07b1

Method BLASTX:
NCBI GI g1293835
BLAST score 260
E value 3.0e-22
Match length 126
% identity 40

NCBI Description (U56965) C15H9.5 gene product [Caenorhabditis elegans]



```
307410
Seq. No.
                   uC-zmflb73289c01b1
Seq. ID
Method
                   BLASTX
                   g3252807
NCBI GI
                   378
BLAST score
                   2.0e-36
E value
Match length
                   131
% identity
                   60
                   (AC004705) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   307411
Seq. No.
                   uC-zmflb73291a01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q543063
BLAST score
                   176
                   2.0e-13
E value
Match length
                   60
                   57
% identity
NCBI Description
                  zinc-finger protein, BR140 - human
                   307412
Seq. No.
                   uC-zmflb73291d05b1
Seq. ID
Method
                   BLASTX
                   g4204300
NCBI GI
BLAST score
                   139
                   5.0e-09
E value
Match length
                   61
% identity
                   54
                   (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   307413
Seq. No.
                   uC-zmf1b73291g03a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g629844
BLAST score
                   214
E value
                   4.0e-17
Match length
                   85
% identity
                   58
                   heat shock protein hsp70-5 - maize (fragment)
NCBI Description
                   >gi 498775 emb CAA55184 (X78415) heat shock protein 70 kDa
                   [Zea mays]
                   307414
Seq. No.
Seq. ID
                   uC-zmflb73291g10b1
                   BLASTX
Method
                   g1708464
NCBI GI
BLAST score
                   231
E value
                   9.0e-20
Match length
                   63
% identity
                   62
NCBI Description
                   PUTATIVE DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD)
                   (2,3-DIHYDROXY ACID HYDROLYASE) >gi_1213255_emb_CAA93689_
```

Seq. No. 307415

Seq. ID uC-zmflb73291h02a1

(Z69795) unknown [Schizosaccharomyces pombe]

```
Method BLASTX
NCBI GI g4582436
BLAST score 139
E value 8.0e-09
Match length 59
% identity 56
NCBI Description (AC00719
```

NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]

Seq. No. 307416

Seq. ID uC-zmflb73292a09b1

Method BLASTN
NCBI GI g3309177
BLAST score 84
E value 3.0e-39
Match length 136
% identity 90

NCBI Description Zea mays starch branching enzyme I (sbel) gene, complete

cds

Seq. No. 307417

Seq. ID uC-zmflb73292a10a1

Method BLASTX
NCBI GI g3834304
BLAST score 204
E value 3.0e-16
Match length 67
% identity 67

NCBI Description (AC005679) Contains similarity to gi 1786244 hypothetical

24.9 kD protein in surA-hepA intergenic region yab0 from Escherichia coli genome gb AE000116, and to hypothetical

YABO family PF_00849. [Arabidopsis thaliana]

Seq. No. 307418

Seq. ID uC-zmflb73292a10b1

Method BLASTX
NCBI GI. g3834304
BLAST score 366
E value 7.0e-35
Match length 141
% identity 50

NCBI Description (AC005679) Contains similarity to gi_1786244 hypothetical

24.9 kD protein in surA-hepA intergenic region yab0 from Escherichia coli genome gb_AE000116, and to hypothetical

YABO family PF_00849. [Arabidopsis thaliana]

Seq. No. 307419

Seq. ID uC-zmflb73292b12b1

Method BLASTN
NCBI GI g22100
BLAST score 42
E value 1.0e-14
Match length 46
% identity 98

NCBI Description Z.mays 27kDa zein locus DNA

Seq. No. 307420

Seq. ID uC-zmflb73292d01a1

~.



```
Method
                     BLASTN
   NCBI GI
                     g507844
   BLAST score
                     130
   E value
                     8.0e-67
  Match length
                     338
                     86
   % identity
                     Zea mays A188 retrotransposon gag gene, complete cds
  NCBI Description
                     307421
Seq. No.
                     uC-zmflb73292d01b1
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g4416303
  BLAST score
                     315
  E value
                     6.0e-35
  Match length
                     91
                     88
   % identity
  NCBI Description
                     (AF105716) gag protein [Zea mays]
                     307422
  Seq. No.
                     uC-zmflb73292d06b1
  Seq. ID
  Method
                     BLASTX
                     g3985977
  NCBI GI
  BLAST score
                     141
  E value
                     3.0e-09
  Match length
                     36
   % identity
                     69
                     (AC005560) putative growth regulator protein [Arabidopsis
  NCBI Description
                     thaliana]
  Seq. No.
                     307423
   Seq. ID
                     uC-zmflb73292d07b1
  Method
                     BLASTX
  NCBI GI
                     g129232
  BLAST score
                     229
  E value
                     6.0e-19
  Match length
                     67
   % identity
                     75
  NCBI Description
                     ORYZAIN BETA CHAIN PRECURSOR >gi_67645 pir KHRZOB oryzain
                     (EC 3.4.22.-) beta precursor - rice
                     >gi_218183_dbj_BAA14403_ (D90407) oryzain beta precursor
                     [Oryza sativa]
  Seq. No.
                     307424
  Seq. ID
                     uC-zmflb73292f11b1
  Method
                     BLASTX
  NCBI GI
                     g2330863
  BLAST score
                     155
  E value
                     6.0e-10
  Match length
                     63
```

% identity 41

NCBI Description (Z98533) mrna 3'-end processing protein rna14.

[Schizosaccharomyces pombe]

307425 Seq. No.

Seq. ID uC-zmflb73292h02a1

Method BLASTN NCBI GI g217973



```
BLAST score
E value
                   2.0e-97
Match length
                   240
% identity
                   94
NCBI Description Zea mays gene for triosephosphate isomerase, complete cds
Seq. No.
                   307426
Seq. ID
                   uC-zmflb73294a12b1
Method
                   BŁASTX
NCBI GI
                   q2149640
BLAST score
                   447
E value
                   1.0e-44
Match length
                   112
% identity
                   75
NCBI Description
                  (U91995) Argonaute protein [Arabidopsis thaliana]
                   307427
Seq. No.
Seq. ID
                   uC-zmflb73294d04b1
Method
                   BLASTX
NCBI GI
                   g2984709
BLAST score
                   165
                   8.0e-12
E value .
Match length
                   37
% identity
                   89
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                   307428
Seq. ID
                   uC-zmflb73294f01b1
Method
                   BLASTX
NCBI GI
                   q2392895
BLAST score
                   307
E value
                   3.0e-28
Match length
                   91
% identity
                   65
NCBI Description
                   (AF017056) brassinosteroid insensitive 1 [Arabidopsis
                   thaliana]
Seq. No.
                   307429
Seq. ID
                   uC-zmflb73294q12b1
Method
                  BLASTX
NCBI GI
                   g3894157
BLAST score
                   197
E value
                   2.0e-28 ←
Match length
                   167
% identity
                   23
NCBI Description
                   (AC005312) putative protein kinase, 3' partial [Arabidopsis
                  thaliana]
                   307430
Seq. No.
Seq. ID
                  uC-zmflb73295d11b2
Method
                  BLASTX
NCBI GI
                  g2809251
                                                                         ~;,
BLAST score
                  294
E value
                  2.0e-29
Match length
                  137
% identity
                   48
```

43651

NCBI Description (AC002560) F21B7.20 [Arabidopsis thaliana]

Match length

NCBI Description

% identity

243 90



```
Seq. No.
                  307431
Seq. ID.
                  uC-zmflb73296c07b2
Method
                  BLASTX
NCBI GI
                  q135398
BLAST score
                  697
E value
                  1.0e-73
Match length
                  129
% identity
                  100
NCBI Description
                  TUBULIN ALPHA-1 CHAIN >gi 82731 pir S15773 tubulin alpha-1
                  chain - maize >gi 22147 emb CAA33734 (X15704)
                  alpha1-tubulin [Zea mays]
                  307432
Seq. No.
Seq. ID
                  uC-zmflb73296f01b2
Method
                  BLASTX
NCBI GI
                  q4539457
BLAST score
                  390
E value
                  9.0e-38
Match length
                  92
% identity
                  77
NCBI Description
                  (AL049500) heat shock transcription factor-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  307433
Seq. ID
                  uC-zmflb73296f08b2
Method
                  BLASTX
NCBI GI
                  g585202
BLAST score
                  472
E value
                  5.0e-54
                  110
Match length
% identity
                  98
                  GLUTAMINE SYNTHETASE ROOT ISOZYME 2 (GLUTAMATE--AMMONIA
NCBI Description
                  LIGASE) >qi 481807 pir S39478 qlutamate--ammonia liqase
                  (EC 6.3.1.2) 1-2, cytosolic - maize
                  >gi 434326 emb CAA46720 (X65927) glutamine synthetase [Zea
                  mays]
Seq. No.
                  307434
Seq. ID
                  uC-zmflb73296g06b2
Method
                  BLASTX
NCBI GI
                  q2244910
BLAST score
                  147
                  2.0e-09
E value
Match length
                  75
% identity
                  41
NCBI Description
                  (Z97339) unnamed protein product [Arabidopsis thaliana]
                  307435
Seq. No.
                  uC-zmflb73296g08b2
Seq. ID
Method
                  BLASTN
NCBI GI 🛴
                  g3341647
BLAST score
                  99
E value
                  3.0e-48
```

Zea mays Ama gene encoding single-subunit RNA polymerase



```
307436
Seq. No.
                  uC-zmflb73296g12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538896
BLAST score
                  197
                  3.0e-15
E value
Match length
                  113
                  38
% identity.
                   (AL049482) putative protein [Arabidopsis thaliana]
NCBI Description
                  307437
Seq. No.
                  uC-zmflb73296h02b2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2113846
BLAST score
                  51
                  7.0e-20
E value
                  107
Match length
                  87
% identity
                  Hordeum vulgare mRNA for hypothetical protein, partial,
NCBI Description
                   clone WL5
                   307438
Seq. No.
                   uC-zmflb73297d01a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2642212
BLAST score
                   36
                   8.0e-11
E value
Match length
                   92
                   85
% identity
                  Zea mays nitrate-induced NOI protein gene, complete cds
NCBI Description
                   307439
Seq. No.
                   uC-zmflb73297d04b2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2738247
BLAST score
                   37
E value
                   2.0e-11
Match length
                   65
% identity
                   89
                  Arabidopsis thaliana cobalamin-independent methionine
NCBI Description
                   synthase (ATCIMS) mRNA, complete cds
                   307440
Seq. No.
                   uC-zmflb73297d10b2
Seq. ID
Method
                   BLASTX
                   g3747048
NCBI GI
BLAST score
                   200
E value
                   4.0e-16
Match length
                   43
% identity
                   95
NCBI Description
                  (AF093539) methionine synthase [Zea mays]
```

Seq. ID uC-zmflb73298a03b1

Method BLASTX NCBI GI g2668742



```
BLAST score
                  2.0e-16
E value
Match length
                  77
% identity
                  62
NCBI Description
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
Seq. ID
                  uC-zmflb73298b07b1
Method
                  BLASTX
NCBI GI
                  q3850111
BLAST score
                  490
E value
                  2.0e-49
Match length
                  141
                  58
% identity
                  (AL033388) hypothetical integral membrane protein, putative
NCBI Description
                  involvement in lipid metabolism [Schizosaccharomyces pombe]
Seq. No.
                  307443
Seq. ID
                  uC-zmflb73298e12b1
Method
                  BLASTX
NCBI GI
                  g1946355
BLAST. score
                . 161
E value
                  6.0e-11
Match length
                  51
% identity
                  59
NCBI Description
                  (U93215) maize transposon MuDR mudrA protein isolog
                  [Arabidopsis thaliana] >gi 2880040 (AC002340) maize
                  transposon MuDR mudrA-like protein [Arabidopsis thaliana]
Seq. No.
                  307444
Seq. ID
                  uC-zmflb73298f12b1
Method
                  BLASTX
NCBI GI
                  g3850576
BLAST score
                  320
E value
                  1.0e-29
Match length
                  86
% identity
                  70
NCBI Description
                  (AC005278) Strong similarity to gb U04968 nucleotide
                  excision repair protein (ERCC2) from Cricetulus grisseus.
                  [Arabidopsis thaliana]
Seq. No.
                  307445
Seq. ID
                  uC-zmflb73298g04a1
Method
                  BLASTN
NCBI GI
                  g520581
BLAST score
                  37
E value
                  2.0e-11
Match length
                  81
% identity
                  86
NCBI Description
                  Barley gene for Ids3, complete cds
```

Seq. ID uC-zmflb73298g08a1

Method BLASTX
NCBI GI g209603
BLAST score 149
E value 9.0e-10



```
Match length
% identity
                   67
NCBI Description
                  (M31426) ubiquitin/relaxin fusion protein [Artificial gene]
Seq. No.
                   307447
Seq. ID
                  uC-zmflb73299a12a1
Method
                  BLASTN
NCBI GI
                  g498772
BLAST score
                  159
E value
                   3.0e-84
Match length
                  282
% identity
                  90
NCBI Description
                 Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
                  307448
Seq. No.
                  uC-zmflb73299h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4371285
BLAST score
                  171
E value
                  5.0e-12
Match length
                  47
% identity
                  66
NCBI Description
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  307449
Seq. ID
                  uC-zmflb73299h06b1
Method
                  BLASTN
NCBI GI
                  q576885
BLAST score
                  62
E value
                  4.0e-26
Match length
                  62
% identity
                  100
NCBI Description
                  Zea mays kaurene synthase A (An1) mRNA, complete cds
Seq. No.
                  307450
Seq. ID
                  uC-zmflb73300d07a1
Method
                  BLASTN
NCBI GI
                  g453188
BLAST score
                  131
E value
                  2.0e-67
Match length
                  190
% identity
                  91
NCBI Description Z.mays acp mRNA for acyl carrier protein
Seq. No.
                  307451
Seq. ID
                  uC-zmflb73300e06b1
Method
                  BLASTX
NCBI GI
                  g3785994
```

BLAST score 181 E value 3.0e-13Match length 90 % identity 44

(AC005499) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 307452

Seq. ID uC-zmflb73300e09a1

Method BLASTN



```
NCBI GI
                   g4220633
BLAST score
                   74
                   2.0e-33
E value
Match length
                  82
                   98
% identity
NCBI Description
```

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No. Seq. ID Method

307453 uC-zmflb73300f01a1

BLASTN NCBI GI g1335965 BLAST score 56 E value 5.0e-23 Match length 112 % identity 88

NCBI Description Zea mays acetyl CoA carboxylase mRNA, partial cds

Seq. No.

307454

Seq. ID uC-zmflb73300f02a1

Method BLASTX NCBI GI g4587525 BLAST score 175 E value 1.0e-12 Match length 87 % identity 38

NCBI Description (AC007060) Contains the PF_00650 CRAL/TRIO

phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene.

[Arabidopsis thaliana]

Seq. No.

307455

Seq. ID uC-zmflb73300h02b1 Method BLASTX

NCBI GI g3702352 BLAST score 169 E value 9.0e-12 Match length 42 % identity 76

NCBI Description (AC005397) putative mitochondrial carrier protein

[Arabidopsis thaliana]

Seq. No. 307456

Seq. ID uC-zmflb73300h10b1

Method BLASTX NCBI GI g2335097 BLAST score 472 E value 3.0e-47Match length 152 % identity 17

(AC002339) putative receptor-like protein kinase NCBI Description

[Arabidopsis thaliana]

Seq. No. 307457

Seq. ID uC-zmf1b73301e08b2

Method BLASTX NCBI GI g1001935

```
BLAST score
E value
                   7.0e-28
Match length
                   60
% identity
                  100
NCBI Description
                  (X81199) ZMM1 [Zea mays] >gi_1167914 (U31522) MADS box
                  protein [Zea mays]
Seq. No.
                  307458
Seq. ID
                  uC-zmflb73301f03b2
Method
                  BLASTX
NCBI GI
                  g3128168
BLAST score
                  458
E value
                  9.0e-46
Match length
                  143
                  59
% identity
NCBI Description
                   (AC004521) putative carboxyl-terminal peptidase
                   [Arabidopsis thaliana]
Seq. No.
                  307459
Seq. ID
                  uC-zmflb73302e05a1
Method
                  BLASTX
NCBI GI
                  g168570
BLAST score
                  213
E value
                  1.0e-17
Match length
                  56
% identity
                  84
NCBI Description
                  (M95077) phenylalanine ammonia lyase [Zea mays]
Seq. No.
                  307460
Seq. ID
                  uC-zmflb73303b05a2
Method
                  BLASTX
                  g1706082
NCBI GI
BLAST score
                  289
E value
                  3.0e-26
Match length
                  82
% identity
                  63
NCBI Description
                  SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)
                  >gi_629787_pir__S44191 serine-type carboxypeptidase (EC
                  3.4.16.1) II-3 - barley >gi_619350_bbs_153536
                  CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,
                  cv. Alexis, aleurone, Peptide, 516 aa]
                  >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3
                  [Hordeum vulgare]
Seq. No.
                  307461
Seq. ID
                  uC-zmflb73303d12b1
Method
                  BLASTX
NCBI GI
                  g4558591
BLAST score
                  215
E value
```

2.0e-17 Match length 75 % identity 52

NCBI Description (AC006555) putative beta-1,3-glucanase [Arabidopsis

thaliana]

Seq. No. 307462

Seq. ID uC-zmflb73303f01b1



```
Method
                  BLASTN
NCBI GI
                  g459267
BLAST score
                  127
E value
                   3.0e-65
Match length
                  155
% identity
                   96
NCBI Description
                  Z.mays gene for HMG protein
Seq. No.
                  307463
Seq. ID
                  uC-zmflb73303f03a2
Method
                  BLASTX
NCBI GI
                  g3036805
BLAST score
                  229
E value
                  2.0e-19
Match length
                  76
% identity
                  54
NCBI Description
                  (AL022373) thaumatin-like protein [Arabidopsis thaliana]
Seq. No.
                  307464
Seq. ID
                  uC-zmflb73303f12b1
Method
                  BLASTX
NCBI GI
                  q1169544
BLAST score
                  452
E value
                  3.0e-47
Match length
                  131
% identity
                  72
NCBI Description
                  ERD1 PROTEIN PRECURSOR >gi 541859 pir JN0901 ERD1 protein
                  - Arabidopsis thaliana >gi 497629 dbj BAA04506 (D17582)
                  ERD1 protein [Arabidopsis thaliana]
Seq. No.
                  307465
                  uC-zmflb73304f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4098521
BLAST score
                  187
                 _2.0e-14
E value
Match length
                  46
% identity
                  76
NCBI Description
                  (U79160) HMG-CoA synthase [Arabidopsis thaliana]
                  >gi 4098523 (U79161) HMG-CoA synthase [Arabidopsis
                  thaliana]
Seq. No.
                  307466
                  uC-zmf1b73304f12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1931647
BLAST score
                  410
```

E value 4.0e-40 Match length 123 % identity 64

NCBI Description (U95973) endomembrane protein EMP70 precusor isolog

[Arabidopsis thaliana]

Seq. No. 307467

Seq. ID uC-zmflb73304g12b1

Method BLASTN NCBI GI g1532072 2.9h



```
BLAST score
E value
                   1.0e-39
Match length
                   207
                   87
% identity
                  Z.mays mRNA for S-adenosylmethionine decarboxylase
NCBI Description
                   307468
Seq. No.
                   uC-zmflb73304h06a1
Seq. ID
Method 🛫
                   BLASTN
                   g3004949
NCBI GI
BLAST score
                   135
E value
                   4.0e-70
Match length
                   156
% identity
                   97
NCBI Description
                   Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,
                   complete cds
                   307469
Seq. No.
                   uC-zmflb73304h09b1
Seq. ID
Method
                   BLASTX
                   g3688398
NCBI GI
BLAST score
                   207
                   8.0e-17
E value
Match length
                   41
% identity
                   95
NCBI Description
                   (AJ006358) ascorbate peroxidase [Hordeum vulgare]
                   307470
Seq. No.
                   uC-zmflb73305a05b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1707364
BLAST score
                   156
E value
                   2.0e-10
Match length
                   36
 % identity
                   83
NCBI Description (X94626) AATP2 [Arabidopsis thaliana]
Seq. No.
                   307471
                   uC-zmflb73305a11b2
Seq. ID
Method
                   BLASTX
                   g3831457
NCBI GI
BLAST score
                   349
E value
                   7.0e-33
Match length
                   93
                   71
% identity
                   (AC005700) putative ion channel protein [Arabidopsis
                   thaliana]
```

NCBI Description

Seq. No. 307472

Seq. ID uC-zmf1b73305c05b2

Method BLASTX NCBI GI q4220521 BLAST score 163 E value 1.0e-11 Match length 44 % identity 61

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

```
Seq. No.
                   307473
Seq. ID
                   uC-zmflb73305d10b2
Method
                   BLASTX
NCBI GI
                   g2914703
BLAST score
                   399
E value
                   6.0e-39
Match length
                   118
                   58
% identity
NCBI Description
                  (AC003974) unknown protein [Arabidopsis thaliana]
Seq. No.
                   307474
Seq. ID
                  uC-zmflb73305f12b2
Method
                  BLASTX
NCBI GI
                  g2190549
BLAST score
                  275
E value
                  2.0e-25
Match length
                  96
% identity
                   66
NCBI Description
                  (AC001229) No definition line found [Arabidopsis thaliana]
                  307475
Seq. No.
Seq. ID
                  uC-zmf1b73305h03b2
Method
                  BLAŞTX
NCBI GI
                  g2129549
BLAST score
                  240
E value
                  3.0e-20
Match length
                  97
% identity
                  52
NCBI Description
                  calcium-dependent protein kinase (EC 2.7.1.-) CDPK19 -
                  Arabidopsis thaliana >gi 2129551 pir S71778
                  calcium-dependent protein kinase 19 - Arabidopsis thaliana
                  >gi 836942 (U20624) calcium-dependent protein kinase
                   [Arabidopsis thaliana] >gi 836948 (U20627)
                  calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.
                  307476
Seq. ID
                  uC-zmflb73305h05a1
Method
                  BLASTX
NCBI GI
                  g2462925
BLAST score
                  236
E value
                  5.0e-20
Match length
                  62
% identity
                  79
NCBI Description
                  (AJ000053) GTP cyclohydrolase II /
                  3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                  thaliana]
Seq. No.
                  307477
Seq. ID
                  uC-zmflb73305h07b2
Method
                  BLASTX
NCBI GI
                  g3334147
BLAST score
                  161
E value
                  7.0e-22
Match length
                  110
% identity
                  45
NCBI Description ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I
```

E value

Match length

% identity

4.0e-29 90

96



chitinase [Gossypium hirsutum]

Seq. No. 307478 Seq. ID uC-zmflb73306a06a1 Method BLASTN NCBI GI g4416300 BLAST score 34 E value 1.0e-09 Match length 58 % identity 45 NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence Seq. No. 307479 Seq. ID uC-zmflb73306b01b1 Method BLASTN NCBI GI g1209674 BLAST score 45 E value 2.0e-16 Match length 45 100 % identity NCBI Description Murine MAP kinase kinase 6c mRNA, complete cds Seq. No. 307480 Seq. ID uC-zmflb73306b03b1 Method -BLASTX NCBI GI g1711492 BLAST score 452 E value 3.0e-45 Match length 85 % identity 99 NCBI Description ARGININE DECARBOXYLASE (ARGDC) (ADC) >gi 478412 pir JQ2341 arginine decarboxylase (EC 4.1.1.19) - tomato >qi_295350 (L16582) arginine decarboxylase [Lycopersicon esculentum] Seq. No. 307481 Seq. ID uC-zmflb73306b04b1 Method BLASTX NCBI GI g115806 BLAST score 305 E value 2.0e-28 Match length 54 % identity 100 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-5) (LHCP) >gi_100198_pir__S10858 chlorophyll a/b-binding protein precursor - tomato >gi 170392 (M17559) chlorophyll a/b-binding protein precursor [Lycopersicon esculentum] 307482 Seq. No. Seq. ID uC-zmflb73306b05b1 Method BLASTN NCBI GI g170521 BLAST score 66



NCBI Description Tomato leaf wound-induced proteinase inhibitor II mRNA, complete cds

Seq. No. 307483

Seq. ID uC-zmflb73306c02b1

Method BLASTX
NCBI GI g1352734
BLAST score 159
E value 3.0e-11
Match length 37
% identity 89

NCBI Description PROBABLE PECTATE LYASE P56 PRECURSOR

>gi_551656_emb_CAA33524_ (X15500) P56 protein [Lycopersicon

esculentum]

Seq. No. 307484

Seq. ID uC-zmflb73306c04b1

Method BLASTN
NCBI GI g1103688
BLAST score 166
E value 1.0e-88
Match length 174
% identity 99

NCBI Description L.esculentum mRNA for metallothionein-like protein

Seq. No. 307485

Seq. ID uC-zmflb73306c06b1

Method BLASTX
NCBI GI g3785996
BLAST score 192
E value 4.0e-15
Match length 64
% identity 58

NCBI Description (AC005499) putative annexin [Arabidopsis thaliana]

Seq. No. 307486

Seq. ID uC-zmflb73306c08b1

Method BLASTN
NCBI GI g4468776
BLAST score 47
E value 1.0e-17
Match length 62
% identity 95

NCBI Description Urechis caupo mRNA for cytoplasmic intermediate filament

protein

Seq. No. 307487

Seq. ID uC-zmflb73306c09b1

Method BLASTX
NCBI GI g3024020
BLAST score 220
E value 2.0e-18
Match length 42
% identity 98

NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)

>gi_2225881 dbj BAA20877 (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

307493

```
Seq. No.
                   307488
Seq. ID
                   uC-zmflb73306c10b1
Method
                   BLASTN
NCBI GI
                   g1042033
BLAST score
                   52
E value
                   2.0e-20
Match length
                   56
% identity
                   98
                   1-phosphatidy \verb|Pinositol-4-phosphate| 5-kinase isoform C
NCBI Description
                   [human, peripheral blood leukocytes, mRNA, 1835 nt]
Seq. No.
                   307489
Seq. ID
                   uC-zmflb73306c11b1
Method
                   BLASTN
NCBI GI
                   g2921800
BLAST score
                   50
E value
                   2.0e-19
Match length
                   54
                   98
% identity
NCBI Description
                   Danio rerio stem cell leukemia protein (tal-1) mRNA,
                   complete cds
Seq. No.
                   307490
Seq. ID
                   uC-zmflb73306d01b1
Method
                   BLASTN
NCBI GI
                   g4324406
BLAST score
                   42
E value
                   1.0e-14
Match length
                   42
                   100
% identity
NCBI Description
                   Gallus gallus peptide elongation factor 1-beta mRNA,
                   complete cds
Seq. No.
                   307491
Seq. ID
                   uC-zmflb73306d02b1
Method
                   BLASTN
NCBI GI
                   g2921800
BLAST score
                   43
E value
                   3.0e-15
Match length
                   43
% identity
                   100
NCBI Description
                   Danio rerio stem cell leukemia protein (tal-1) mRNA,
                   complete cds
Seq. No.
                   307492
Seq. ID
                   uC-zmflb73306d03b1
Method
                   BLASTN
NCBI GI
                   g1042033
BLAST score
                   48
E value
                   7.0e-18
Match length
                   52
% identity
                   98
NCBI Description
                   1-phosphatidylinositol-4-phosphate 5-kinase isoform C
```

43663

[human, peripheral blood leukocytes, mRNA, 1835 nt]

```
Seq. ID
                   uC-zmflb73306d05b1
Method
                   BLASTX
NCBI GI
                   q2642434
BLAST score
                   206
E value
                   3.0e-16
Match length
                   63
% identity
                   60
NCBI Description
                   (AC002391) putative Rerl protein [Arabidopsis thaliana]
                   307494
Seq. No.
Seq. ID
                   uC-zmflb73306d06b1
Method
                   BLASTX
NCBI GI
                   q2765081
BLAST score
                   182
E value
                   5.0e-29
Match length
                   101
% identity
                   67
NCBI Description
                   (Y10557) g5bf [Arabidopsis thaliana]
Seq. No.
                   307495
Seq. ID
                   uC-zmflb73306d08b1
Method
                   BLASTN
NCBI GI
                   q1042033
BLAST score
                   58
E value
                   4.0e-24
Match length
                   69
% identity
                   96
NCBI Description
                   1\hbox{-phosphatidylinositol-}4\hbox{-phosphate }5\hbox{-kinase isoform C}
                   [human, peripheral blood leukocytes, mRNA, 1835 nt]
Seq. No.
                   307496
Seq. ID
                   uC-zmflb73306d09b1
Method
                   BLASTX
NCBI GI
                   q731511
BLAST score
                   171
                   9.0e-13
E value
Match length
                   54
% identity
                   65
NCBI Description
                   HYPOTHETICAL 29.7 KD PROTEIN IN RSP5-PAK1 INTERGENIC REGION
                   >gi_539138_pir__S43218 hypothetical protein YER126c - yeast
                   (Saccharomyces cerevisiae) >gi 603365 (U18916) Yer126cp
                   [Saccharomyces cerevisiae]
Seq. No.
                   307497
Seq. ID
                   uC-zmflb73306d12b1
Method
                   BLASTN
NCBI GI
                   q4324406
BLAST score
                   46
E value
                   9.0e-17
Match length
                   54
% identity
                   96
NCBI Description
                   Gallus gallus peptide elongation factor 1-beta mRNA,
                   complete cds
Seq. No.
                   307498
Seq. ID
                   uC-zmflb73306e01b1
Method
                   BLASTN
```



```
g1042033
NCBI GI
BLAST score
                  49
E value
                  1.0e-18
Match length
                  53
                  98
% identity
NCBI Description
                  1-phosphatidylinositol-4-phosphate 5-kinase isoform C
                  [human, peripheral blood leukocytes, mRNA, 1835 nt]
                  307499
Seq. No.
                  uC-zmflb73306e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g170404
BLAST score
                  288
E value
                  5.0e-26
Match length
                  60
% identity
                  88
NCBI Description
                  (M14444) chlorophyll a/b-binding protein Cab-3C
                  [Lycopersicon esculentum]
Seq. No.
                  307500
                  uC-zmflb73306e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g462243
BLAST score
                  379
E value
                  1.0e-36
Match length
                  77
% identity
                  100
NCBI Description
                  HISTONE H4 >gi 421921 pir S32769 histone H4 - tomato
                  >gi 297150 emb CAA48923 (X69179) histone H4 [Lycopersicon
                  esculentum] >gi 297152 emb CAA48924 (X69180) histone H4
                  [Lycopersicon esculentum] >qi 2746721 (AF038387) histone H4
                  [Capsicum annuum]
Seq. No.
                  307501
Seq. ID
                  uC-zmflb73306e05b1
Method
                  BLASTX
NCBI GI
                  g1076776
                  161
BLAST score
E value
                  6.0e-11
Match length
                  33
% identity
                  94
NCBI Description
                  histone H2A - wheat >gi 536888 dbj BAA07276 (D38087)
                protein H2A [Triticum aestivum] >gi_1095224_prf__2108279A
                  histone H2A:ISOTYPE=2 [Triticum aestivum]
Seq. No.
                  307502
Seq. ID
                  uC-zmflb73306e06b1
Method
                  BLASTN
NCBI GI
                  g2369713
BLAST score
                  46
```

E value 1.0e-16

Match length 50 % identity 98

NCBI Description Beta vulgaris cDNA for elongation factor

Seq. No. 307503

uC-zmflb73306e07b1 Seq. ID



```
Method
                   BLASTN
NCBI GI
                   q1399459
BLAST score
                   33
E value
                   2.0e-09
                   37
Match length
% identity
                   97
NCBI Description Human mariner-like element-containing mRNA, clone pcHMT1
Seq. No.
                   307504
Seq. ID
                   uC-zmflb73306e10b1
Method
                   BLASTN
NCBI GI
                   g1217641
BLAST score
                   149
E value
                   3.0e-78
Match length
                   237
% identity
                   91
NCBI Description L.esculentum mRNA for 10kDa polypeptide precursor of
                   photosystem II
Seq. No.
                   307505
Seq. ID
                   uC-zmflb73306e11b1
Method
                   BLASTN
NCBI GI
                   g3820481
BLAST score
                   48
E value
                   5.0e-18
Match length
                   52
% identity
                   98
NCBI Description
                  Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c)
                  mRNA, complete cds
Seq. No.
                   307506
Seq. ID
                   uC-zmflb73306e12b1
Method
                   BLASTX
NCBI GI
                   g974850
BLAST score
                   182
E value
                   1.0e-13
Match length
                   38
% identity
                   87
NCBI Description
                  (X89023) LHCII type I protein [Hordeum vulgare]
Seq. No.
                   307507
Seq. ID
                  uC-zmflb73306f01b1
Method
                  BLASTN
NCBI GI
                  g1017801
BLAST score
                  52
E value
                  2.0e-20
Match length
                  52
% identity
                  100
NCBI Description Shuttle expression vector pBKCMV
                  307508
Seq. No.
Seq. ID
                  uC-zmflb73306f02b1
Method
                  BLASTN
NCBI GI
```

43666

g2369713

2.0e-20

52

52

BLAST score

Match length

E value



```
% identity
NCBI Description Beta vulgaris cDNA for elongation factor
Seq. No.
                  307509
Seq. ID
                  uC-zmflb73306f03b1
Method
                  BLASTX
NCBI GI
                  q4587562
BLAST score
                  300
E value
                  1.0e-27
Match length
                  60
% identity
NCBI Description
                   (AC006550) Belongs to PF 00583 Acetyltransfersase (GNAT)
                  family. [Arabidopsis thaliana]
Seq. No.
                  307510
Seq. ID
                  uC-zmflb73306f05b1
Method
                  BLASTX
NCBI GI
                  g2129921
BLAST score
                  193
E value
                  7.0e-15
Match length
                  51
% identity
                  75
NCBI Description
                  hypothetical protein 1 - Madagascar periwinkle >gi 758694
                   (U12573) putative [Catharanthus roseus]
Seq. No.
                  307511
Seq. ID
                  uC-zmflb73306f06b1
Method
                  BLASTX
NCBI GI
                  q717142
BLAST score
                  466
E value
                  1.0e-46
Match length
                  94
% identity
                  100
NCBI Description
                  (U21801) alcohol dehydrogenase homolog [Solanum
                  lycopersicum]
Seq. No.
                  307512
Seq. ID
                  uC-zmflb73306f08b1
Method
                  BLASTX
NCBI GI
                  q2129579
BLAST score
                  205
E value
                  2.0e-16
Match length
                  68
% identity
                  60
NCBI Description
                  Dwarfl protein - Arabidopsis thaliana >gi 516043 (U12400)
                  Dwarf1 [Arabidopsis thaliana]
Seq. No.
                  307513
Seq. ID
                  uC-zmflb73306q01b1
Method
                  BLASTN
NCBI GI
                  q3820481
BLAST score
                  37
```

E value 1.0e-11

Match length 37 % identity 100

NCBI Description Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c)

mRNA, complete cds

55

NCBI Description (D29641) KIAA0052 [Homo sapiens]

```
307514
Seq. No.
Seq. ID
                   uC-zmflb73306g11b1
Method
                  BLASTX
NCBI GI
                   g543841
BLAST score
                   225
                   7.0e-19
E value
Match length
                   47
% identity
                   98.÷
NCBI Description
                  ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875
                  ADP-ribosylation factor 1 - Arabidopsis thaliana >qi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                  >gi 2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                  thaliana] >gi_4630747_gb_AAD26597.1 AC007236 2 (AC007236)
                  ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.
                  307515
                  uC-zmflb73306h11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22312
BLAST score
                  55
E value
                  2.0e-22
Match length
                  134
% identity
                  87
NCBI Description
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
                  abscisic acid)
Seq. No.
                  307516
Seq. ID
                  uC-zmflb73306h12b1
Method
                  BLASTN
NCBI GI
                  g3617765
BLAST score
                  40
                  1.0e-13
E value
Match length
                  40
% identity
                  100
NCBI Description Anopheles gambiae mRNA for ICHIT protein
Seq. No.
                  307517
Seq. ID
                  uC-zmflb73307e02b1
Method
                  BLASTX
NCBI GI
                  q2252854
BLAST score
                  192
E value
                  1.0e-14
Match length
                  92
% identity
                  47
NCBI Description
                  (AF013294) similar to auxin-induced protein [Arabidopsis
                  thaliana]
Seq. No.
                  307518
Seq. ID
                  uC-zmflb73307e12b1
Method
                  BLASTX
NCBI GI
                  q473933
BLAST score
                  418
E value
                  4.0e-41
Match length
                  139
```

84



```
307519
Seq. No.
Seq. ID
                   uC-zmflb73307h03b1
Method
                   BLASTX
NCBI GI
                   g1587206
BLAST score
                   395
E value
                   2.0e-38
Match length
                   87
% identity
                   91
NCBI Description
                  T complex protein [Cucumis sativus]
Seq. No.
                   307520
Seq. ID
                   uC-zmflb73307h11b1
Method
                   BLASTX
NCBI GI
                   g1619602
BLAST score
                   167
E value
                   3.0e-12
                                     4
Match length
                   75
% identity
                   47
NCBI Description
                  (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                   307521
Seq. ID
                   uC-zmflb73317a03b1
Method
                   BLASTX
NCBI GI
                   g312179
BLAST score
                   254
E value
                   6.0e-25
Match length
                   84
% identity
                   77
NCBI Description
                   (X73151) glyceraldehyde 3-phosphate dehydrogenase
                   (phosphorylating) [Zea mays] >qi 1184772 (U45855) cytosolic
                   glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                   >gi 1185554 (U45858) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays]
Seq. No.
                   307522
Seq. ID
                  uC-zmflb73317a04b1
Method
                  BLASTX
NCBI GI
                  g1706328
BLAST score
                   402
                   4.0e-39
E value
Match length
                   113
% identity
                   73
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi_1009710 (U27350)
NCBI Description
                  pyruvate decarboxylase 2 [Oryza sativa] >qi 1777455
                   (U38199) pyruvate decarboxylase 2 [Oryza sativa]
Seq. No. Seq. ID
                  307523
                  uC-zmflb73317a08b1
Method
                  BLASTX
NCBI GI
                  g3264596
BLAST score
                  225
E value
                  7.0e-19
Match length
                  56
```

NCBI Description (AF057183) putative tonoplast aquaporin [Zea mays]



```
Seq. No.
                   307524
                   uC-zmflb73317d07b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2326946
BLAST score
                   161
                   1.0e-85
E value
                   169
Match length
% identity
                   99
NCBI Description
                   Z.mays mRNA for chlorophyll a/b-binding protein CP29
Seq. No.
                   307525
                   uC-zmflb73317f02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2826900
BLAST score
                   164
E value
                   1.0e-11
Match length
                   50
% identity
                   64
NCBI Description
                   (AB004461) DNA polymerase alpha catalytic subunit [Oryza
                   satival
                   307526
Seq. No.
                   uC-zmflb73317f06b1
Seq. ID
                   BLASTN
Method
                   g168508
NCBI GI
BLAST score
                   38
                   5.0e-12
E value
Match length
                   74
% identity
                   88
NCBI Description
                   Maize oleosin KD18 (KD18; L2) gene, complete cds
                   307527
Seq. No.
                   uC-zmflb73317q03b1
Seq. ID
Method
                   {\tt BLASTX}
NCBI GI
                   g2149051
                   Ī51
BLAST score
                   3.0e-14
E value
Match length
                   48
% identity
                   72
NCBI Description
                   (U73810) small Ras-like GTP-binding protein [Arabidopsis
                   thaliana]
Seq ... No.
                   307528
Seq. ID
                   uC-zmflb73317h02b1
Method
                   BLASTX
NCBI GI
                   g3122572
                   303
BLAST score
E value
                   1.0e-27
Match length
                   80
```

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I

SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi 758340 emb CAA59818 (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]



Seq. ID uC-zmflb73318a12b1

Method BLASTX
NCBI GI g2498882
BLAST score 231
E value 4.0e-19
Match length 128
% identity 40

NCBI Description SPLICEOSOME ASSOCIATED PROTEIN 114 (SAP 114) (SF3A120)

>gi_2146975_pir__S60735 splicing factor SF3a 120K chain human >gi_899298_emb_CAA59494_ (X85237) human splicing
factor [Homo sapiens] >gi_3212998 (AC004997) spliceosome

associated protein 114 (SF3a) [Homo sapiens]

Seq. No. 307530

Seq. ID uC-zmflb73318e03b1

Method BLASTX
NCBI GI g3236249
BLAST score 227
E value 1.0e-18
Match length 76
% identity 55

NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]

Seq. No. 307531

Seq. ID uC-zmflb73318f10b1

Method BLASTX
NCBI GI g1172932
BLAST score 156
E value 2.0e-10
Match length 80
% identity 40

NCBI Description RIBOFLAVIN-SPECIFIC DEAMINASE >qi 1075214 pir H64103

riboflavin biosynthesis protein (ribG) homolog -Haemophilus influenzae (strain Rd KW20) >gi 1573964 (U32775) riboflavin biosynthesis protein (ribD)

[Haemophilus influenzae Rd]

Seq. No. 307532

Seq. ID uC-zmflb73318g12b1

Method BLASTX g2618693
BLAST score 150
E value 2.0e-09
Match length 154
% identity 34

NCBI Description (AC002510) putative zinc-finger protein [Arabidopsis

thaliana]

Seq. No. 307533

Seq. ID uC-zmflb73319a04b1

Method BLASTX NCBI GI g129916 BLAST score 212 E value 5.0e-17 Match length 71 % identity 69



PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY NCBI Description phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum] 307534 Seq. No. uC-zmflb73319b06b1 Seq. ID Method BLASTX NCBI GI g129916 390

BLAST score 1.0e-39 E value Match length 105 % identity 88

PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY NCBI Description phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi 21835 emb CAA33302 (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

307535 Seq. No.

Seq. ID uC-zmflb73319c02b1

BLASTX Method NCBI GI g3435196 205 BLAST score 6.0e-16 E value Match length 107 % identity 40

NCBI Description (AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]

307536 Seq. No.

uC-zmflb73319d04b1 Seq. ID

Method BLASTX NCBI GI g421929 BLAST score 287 E value 2.0e-27 Match length 111 10 % identity

ubiquitin - toma\o >gi_312160_emb_CAA51679_ (X73156) NCBI Description

ubiquitin [Lycopersicon esculentum]

307537 Seq. No.

uC-zmflb73319e06b1 Seq. ID

BLASTX Method q541824 NCBI GI 340 BLAST score E value 5.0e-32 99 Match length % identity 67

protein kinase - spinach >gi 457709 emb CAA82991 (Z30330) NCBI Description

protein kinase [Spinacia oleracea]

Seq. No. 307538

Seq. ID uC-zmflb73319g05b1

Method BLASTX NCBI GI g425194 BLAST score 308 E value 2.0e-28 Match length 79



% identity NCBI Description (L26243) heat shock protein [Spinacia oleracea] >gi 2660772 (AF034618) cytosolic heat shock 70 protein [Spinacia oleracea] Seq. No. 307539

Seq. ID uC-zmflb73324b11a1 Method BLASTN NCBI GI g168460 BLAST score 211 E value 1.0e-115 239

Match length % identity 97

NCBI Description Zea mays cyclophilin (CyP) mRNA, complete cds

307540 Seq. No.

Seq. ID uC-zmflb73326a02a1

Method BLASTX NCBI GI g3643607 BLAST score 240 E value 2.0e-28 Match length 83

% identity 77

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 307541

Seq. ID uC-zmflb73333e03a1

Method BLASTN g435542 NCBI GI BLAST score 149 E value 2.0e-78 Match length 208 % identity 94

NCBI Description Z.mays mRNA for calmodulin

Seq. No. 307542

Seq. ID uC-zmflb73333e11a1

Method BLASTN NCBI GI g2642323 BLAST score 320 E value 1.0e-180 Match length 320 % identity 100

NCBI Description Zea mays profilin (PRO4) mRNA, complete cds

Seq. No. 307543

Seq. ID uC-zmflb73333h05a1

Method BLASTX NCBI GI g2462936 BLAST score 187 E value 7.0e-14 Match length 108 % identity 43

NCBI Description (Y12321) open reading frame 2 [Brassica oleracea]

Seq. No. 307544

Seq. ID uC-zmflb73333h07a1



```
Method
                   BLASTX
NCBI GI
                   q3426064
BLAST score -
                   193
E value
                   6.0e-15
Match length
                   87
                   53
% identity
NCBI Description
                   (AJ007588) monooxygenase [Arabidopsis thaliana]
                   >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2)
                   [Arabidopsis thaliana]
                   307545
Seq. No.
Seq. ID
                  uC-zmflb73337d02a1
Method
                  BLASTX
NCBI GI
                  g3776084
BLAST score
                  175
E value
                  1.0e-12
Match length
                  59
% identity
                  54
NCBI Description
                  (Y18251) NtN2 [Medicago truncatula]
Seq. No.
                  307546
Seq. ID
                  uC-zmflb73342e04a2
Method
                  BLASTN
NCBI GI
                  g293911
BLAST score
                  211
E value
                  1.0e-115
Match length
                  231
% identity
                  98
NCBI Description Zea mays (clone wus11032) mRNA sequence
                  307547
Seq. No.
Seq. ID
                  uC-zmflb73344c06a2
Method
                  BLASTX
NCBI GI
                  g2130137
BLAST score
                  405
E value
                  1.0e-39
Match length
                  124
% identity
                  72
NCBI Description
                  homeotic protein Hox2b - maize >gi 1143707 emb CAA61910
                  (X89761) Hox2b [Zea mays]
Seq. No.
                  307548
Seq. ID
                  uC-zmflb73345c11a2
Method
                  BLASTN
NCBI GI
                  g2984708
BLAST score
                  41
E value
                  7.0e-14
Match length
                  90
% identity
                  84
NCBI Description
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
```

5.

Seq. No. 307549

Seq. ID uC-zmflb73346b10a2

Method BLASTX NCBI GI g3142297 BLAST score 339



```
E value
                   9.0e-32
Match length
                   126
% identity -.
                   55
NCBI Description
                   (AC002411) Contains similarity to serine/threonine protein
                   phosphatase gb_X83099 from S. cerevisiae. [Arabidopsis
                   thaliana]
Seq. No.
                   307550
Seq. ID
                   uC-zmflb73346e12a2
Method
                   BLASTN
NCBI GI
                   g312180
BLAST score
                   133
E value
                   1.0e-68
Match length
                   198
% identity
                   91
NCBI Description
                  Z.mays GapC4 gene
Seq. No.
                   307551
Seq. ID
                   uC-zmflb73346h05a2
                   BLASTX
Method
NCBI GI
                   g553073
BLAST score
                   588
E value
                   1.0e-73
Match length
                   152
% identity
                   91
NCBI Description
                   (M94481) reverse transcriptase [Zea mays]
Seq. No.
                   307552
Seq. ID
                   uC-zmflb73347g09a1
Method
                   BLASTX
NCBI GI
                   g3096920
BLAST score
                   208
                   1.0e-16
E value
Match length
                   64
% identity
NCBI Description
                   (AL023094) putative ketoacyl-CoA synthase [Arabidopsis
                   thaliana]
Seq. No.
                   307553
Seq. ID
                   uC-zmflb73347h06a1
Method
                   BLASTN
NCBI GI
                   q22476
BLAST score
                   90
E value
                   4.0e-43
Match length
                   98
% identity
                   98
NCBI Description
                  Z.mays ruq66 transposon
Seq. No.
                  307554
Seq. ID
                  uC-zmflb73348h09a3
```

Method BLASTN NCBI GI g4105718

BLAST score 38 E value 3.0e-12 Match length 98 % identity 85

NCBI Description Zea mays cell wall invertase Incw2 gene, complete cds

```
Seq. No.
                  307555
Seq. ID
                  uC-zmflb73349c08a2
Method
                  BLASTX
NCBI GI
                  q4427003
BLAST score
                  520
E value
                  4.0e-53
Match length
                  108
% identity
                  89
NCBI Description
                  (AF127664) NBD-like protein [Arabidopsis thaliana]
Seq. No.
                  307556
Seq. ID
                  uC-zmflb73349d01a2
Method
                  BLASTX
NCBI GI
                  q2104538
BLAST score
                  159
E value
                  2.0e-20
Match length
                  108
% identity
                  56
NCBI Description (AF001308) AtKAP alpha [Arabidopsis thaliana]
Seq. No.
                  307557
Seq. ID
                  uC-zmflb73349d08a2
Method
                  BLASTX
NCBI GI
                  g2827718
BLAST score
                  291
E value
                  3.0e-26
Match length
                  84
% identity
                  (AL021684) retrotransposon - like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  307558
Seq. ID
                  uC-zmflb73349e02a2
Method
                  BLASTX
NCBI GI
                  g3929221
BLAST score
                  149
E value
                  1.0e-09
Match length
                  99
% identity
                  37
NCBI Description
                  (AF082557) TRF1-interacting ankyrin-related ADP-ribose
                  polymerase [Homo sapiens]
Seq. No.
                  307559
Seq. ID
                  uC-zmflb73349e03a2
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2388582
BLAST score 150
E value 8.0e-10
Match length 51
% identity 53

NCBI Description (AC000098) Contains similarity to Rattus O-GlcNAc

transferase (gb_U76557). [Arabidopsis thaliana]

Seq. No. 307560

Seq. ID uC-zmflb73349g02a2

Method BLASTX



```
g480450
NCBI GI
BLAST score
                   369
E value
                   2.0e-35
Match length
                   98
                   72
% identity
NCBI Description
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
                  thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                   reductoisomerase [Arabidopsis thaliana]
Seq. No.
                   307561
                   uC-zmflb73349g09a2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g100484
BLAST score
                   326
E value
                   3.0e-30
Match length
                   152
% identify
                   47
NCBI Description
                  hypothetical protein - garden snapdragon
Seq. No.
                  307562
Seq. ID
                  uC-zmflb73349q12a2
Method
                  BLASTX
NCBI GI
                  g3738284
BLAST score
                  251
E value
                  2.0e-21
Match length
                  59
% identity
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
                  307563
Seq. No.
                  uC-zmflb73350g12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4650841
BLAST score
                  34
E value
                  1.0e-09
Match length
                  70
                  87
% identity
NCBI Description
                  Lithospermum erythrorhizon mRNA for elongation factor 2,
                  partial cds
Seq. No.
                  307564
Seq. ID
                  uC-zmflb73353a01a1
Method
                  BLASTX
NCBI GI
                  q461736
BLAST score
                  196
E value
                  4.0e-15
Match length
                  62
                  68
% identity
NCBI Description
                  MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR
                  >gi_478786 pir S29316 chaperonin 60 - cucurbit
                  >gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita
                  sp.]
```

Seq. ID uC-zmflb73353a09a1

Method BLASTX NCBI GI g1370182

```
BLAST score
E value
                   2.0e-24
Match length
                   69
 % identity
                   70
NCBI Description (Z73940) RAB7A [Lotus japonicus]
Seq. No.
                   307566
Seq. ID
                   uC-zmflb73353e01a1
Method
                   BLASTX
NCBI GI
                   g4455233
BLAST score
                   242
E value
                   1.0e-20
Match length
                   65
% identity
                   68
NCBI Description
                   (AL035523) hypothetical protein [Arabidopsis thaliana]
                   307567
Seq. No.
                   uC-zmflb73354b06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4582787
BLAST score
                   341
                                                             ī,
E value
                   3<sub>3</sub>0e-32
Match length
                   69
% identity
                   91
NCBI Description (AJ012281) adenosine kinase [Zea mays]
                   307568
Seq. No.
Seq. ID
                   uC-zmflb73354e11a1
Method
                   BLASTN
NCBI GI
                   g517492
BLAST score
                   59
E value
                   2.0e-24
Match length
                   99
% identity
                   90
NCBI Description Z.Mays Zm38 gene, intron
Seq. No.
                   307569
Seq. ID
                   uC-zmflb73354g11a1
Method
                   BLASTX
NCBI GI
                   g4204315
BLAST score
                   225
E value
                   2.0e-18
Match length
                   61
% identity
                   62
NCBI Description
                   (AC003027) Unknown protein [Arabidopsis thaliana]
```

 Seq. No.
 307570

 Seq. ID
 uC-zmflb73356e10a2

 Mathod
 BLAGEN

Method BLASTN NCBI GI g871985 BLAST score 51

E value 9.0e-20 Match length 91 89

NCBI Description A.sativa Aspkl1 mRNA

Seq. No. 307571

```
Seq. ID
                    uC-zmflb73359b04a2
  Method
                    BLASTX
  NCBI GI
                    g4006867
  BLAST score
                    370
  E value
                    9.0e-36
  Match length
                    89
                    74
  % identity
  NCBI Description
                    (Z99707) putative protein [Arabidopsis thaliana]
                    307572
  Seq. No.
                    uC-zmflb73359b07a2
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g542179
  BLAST score
                    583
  E value
                    1.0e-60
  Match length
                    108
  % identity
                    100
  NCBI Description
                    alpha tubulin - maize >gi 629837 pir S39998 tubulin alpha
                    chain - maize (fragment) >gi 393401 emb CAA52158 (X73980)
                    alpha tubulin [Zea mays]
                    307573
  Seq. No.
Seq. ID
                    uC-zmflb73359b09a2
  Method
                    BLASTX
  NCBI GI
                    g4454032
  BLAST score
                    215
                    3.0e-17
  E value
  Match length
                    99
  % identity
                    48
  NCBI Description
                    (AL035394) putative protein [Arabidopsis thaliana]
  Seq. No.
                    307574
  Seq. ID
                    uC-zmflb73359d02a2
  Method
                    BLASTX
  NCBI GI
                    q71634
  BLAST score
                    307
  E value
                    5.0e-28
  Match length
                    59
  % identity
                    98
  NCBI Description
                    actin 1 - rice
                    307575
  Seq. No.
  Seq. ID
                    uC-zmflb73359e01a2
  Method
                    BLASTN
  NCBI GI
                    g4185305
  BLAST score
                    120
  E value
                    9.0e-61
  Match length
                    398
  % identity
                    85
  NCBI Description
                    Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                    (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                    protein, polyprotein, and copia protein genes, complete
                    cds; and unknown genes
```

Seq. ID uC-zmflb73359f02a2

Method BLASTX

43679

- Mr.

```
NCBI GI
                   g4567273
BLAST score
                   187
E value
                   9.0e-19
Match length
                   103
% identity
                   50
NCBI Description
                   (AC006841) putative vacuolar proton ATPase subunit
                   [Arabidopsis thaliana]
Seq. No.
                  307577
                  uC-zmflb73359g07a2
Seq. LA z.
Method
                  BLASTX
NCBI GI
                  g122083
BLAST score
                  302
E value
                  7.0e-28
Match length
                   63
% identity
                  97
NCBI Description
                  HISTONE H3 >gi_70751_pir  HSEAH3 histone H3 - Altenstein's
                  bread tree >gi 224865 prf 1202289A histone H3
                   [Encephalartos sp.]
                  307578
Seq. No.
Seq. ID
                  uC-zmflb73360f11a1
Method
                  BLASTX
NCBI GI
                  g1762309
BLAST score
                  147
E value
                  2.0e-09
Match length
                  39
% identity
                  82
NCBI Description
                  (U53345) AP-1 Golgi-related complex component; clathrin
                  coated vesicles; clathrin assembly protein [Camptotheca
                  acuminata]
                  307579
Seq. No.
Seq. ID
                  uC-zmflb73361a01a2
Method
                  BLASTX
NCBI GI
                  g4646203
BLAST score
                  176
E value
                  1.0e-12
Match length
                  62
% identity
                  48
NCBI Description
                  (AC007230) Belongs to PF 00026 Eukaryotic aspartyl protease
                  family. [Arabidopsis thaliana]
Seq. No.
                  307580
Seq. ID
                  uC-zmflb73361a12a2
Method
                  BLASTX
NCBI GI
                  g2760323
BLAST score
                  173
                  2.0e-12
E value
```

Match length 34 % identity 79

NCBI Description (AC002130) F1N21.8 [Arabidopsis thaliana]

Seq. No. 307581

Seq. ID uC-zmflb73361h08a2

Method BLASTX NCBI GI g131192

```
BLAST score
E value
                  9.0e-48
Match length
                  110
% identity
                  81
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
                   (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi 100606 pir S20937
                  photosystem I chain V precursor - barley
                  >gi 19091 emb CAA42727 (X60158) photosystem I polypeptide
                  PSI-G precursor [Hordeum vulgare]
Seq. No.
                  307582
Seq. ID
                  uC-zmf1b73362a06a2
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  373
E value
                  6.0e-36
Match length
                  71
                  100
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  307583
Seq. No.
                  .uC-zmflb73362a07a2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2105430
BLAST score
                  472
E value
                  3.0e-47
Match length
                  170
% identity
                  54
NCBI Description (U97079) U5-116kD [Mus musculus]
                  307584
Seq. No.
                  uC-zmflb73362d12a2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4584685
BLAST score
                  391
E value
                  6.0e-38
Match length
                  109
% identity
                  68
NCBI Description
                  (AJ237754) putative lectin [Hordeum vulgare]
Seq. No.
                  307585
Seq. ID
                  uC-zmflb73362g08a2
Method
                  BLASTX
NCBI GI
                  g3309243
BLAST score
                  494
E value
                  5.0e-50
Match length
                  122
                  75
% identity
NCBI Description
                  (AF073507) aconitase-iron regulated protein 1 [Citrus
                  limon]
```

Seq. ID uC-zmflb73363d04a1

Method BLASTN
NCBI GI g2341060
BLAST score 198
E value 1.0e-107

```
Match length
                   311
                   90
% identity
NCBI Description
                   Zea mays translational initiation factor eIF-4A (tif-4A3)
                   mRNA, complete cds
Seq. No.
                   307587
Seq. ID
                   uC-zmflb73363d10a1
Method
                   BLASTX
NCBI GI
                   g4098272
BLAST score
                   176
E value
                   7.0e-13
Match length
                   38
% identity
                   84
NCBI Description
                   (U76558) alpha-tubulin [Triticum aestivum]
Seq. No.
                   307588
Seq. ID.
                   uC-zmflb73363g08a1
Method
                   BLASTN
NCBI GI
                   q998429
BLAST score
                   269
E value
                   1.0e-150
Match length
                   345
% identity
                   94
NCBI Description
                   GRF1=general regulatory factor [Zea mays, XL80, Genomic,
                   5348 nt]
Seq. No.
                   307589
Seq. ID
                   uC-zmflb73365d01a1
Method
                   BLASTN
NCBI GI
                   q498772
BLAST score
                   52
E value
                   2.0e-20
Match length
                   151
% identity
                   84
NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
Seq. No.
                   307590
                   uC-zmflb73366b08a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1695697
BLAST score
                   50
E value
                   4.0e-19
                                  3
Match length
                   98
% identity
                   88
NCBI Description Oryza sativa mRNA for C-type cyclin, complete cds
Seq. No.
                   307591
                  uC-zmflb73366g04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2499819
BLAST score
                  154
E value
                   4.0e-10
Match length
                  35
```

43682

>gi_2130068_pir__S66516 aspartic proteinase 1 precursor rice >gi_1030715 dbj BAA06876 (D32165) aspartic protease

ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR

77

% identity

NCBI Description



[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]

Seq. No. 307592

Seq. ID uC-zmflb73367c11a1

Method BLASTN
NCBI GI g1049252
BLAST score 62
E value 2.0e-26

Match length 125 % identity 88

NCBI Description Zea mays vacuolar ATPase 69 kDa subunit mRNA, partial cds

Seq. No. 307593

Seq. ID uC-zmflb73369h04a1

Method BLASTX
NCBI GI g2275207
BLAST score 176
E value 9.0e-13
Match length 113
% identity 42

NCBI Description (AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 307594

Seq. ID uC-zmflb73371h12a1

Method BLASTN
NCBI GI g19052
BLAST score 65
E value 4.0e-28
Match length 109
% identity 90

NCBI Description H.vulgare Myb1 gene

Seq. No. 307595

Seq. ID uC-zmflb73372g01a1

Method BLASTX
NCBI GI g2739000
BLAST score 213
E value 4.0e-17
Match length 124
% identity 35

NCBI Description (AF022459) CYP71D10p [Glycine max]

Seq. No. 307596

Seq. ID uC-zmflb73376c07a2

Method BLASTN
NCBI GI g168436
BLAST score 276
E value 1.0e-154
Match length 328
% identity 97

NCBI Description Zea mays catalase (Cat3) gene, complete cds

Seq. No. 307597

Seq. ID uC-zmflb73376g05a2

Method BLASTN NÇBI GI g998429

Match length

% identity

110

89

```
BLAST score
E value
                  6.0e-60
Match length
                  214
% identity
                  89
NCBI Description
                  GRF1=general regulatory factor [Zea mays, XL80, Genomic,
                  5348 nt]
                  307598
Seq. No.
                  uC-zmflb73376g11a2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g902585
BLAST score
                  81
                  5.0e-38
E value
Match length
                  152
% identity
                  89
NCBI Description
                  Zea mays clone MubG9 ubiquitin gene, complete cds
                  307599
Seq. No.
                  uC-zmflb73378b02a2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4325369
BLAST score
                  179
E value
                  3.0e-13
Match length
                  54
% identity
                  59
NCBI Description
                  (AF128396) T3H13.3 gene product [Arabidopsis thaliana]
Seq. No.
                  307600
Seq. ID
                  uC-zmflb73378c11a2
Method
                  BLASTN
NCBI GI
                  q498772
BLAST score
                  277
E value
                  1.0e-154
Match length
                  370
                  95
% identity
NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
Seq. No.
                  307601
                  uC-zmflb73378g12a2
Seq. ID
Method
                  BLASTN
                  g514945
NCBI GI
BLAST score
                  102
E value
                  1.0e-50
Match length
                  150
                  92
% identity
NCBI Description Zea mays sucrose synthase (Sus1) mRNA, complete cds
Seq. No.
                  307602
Seq. ID
                  uC-zmflb73379a12a1
Method
                  BLASTN
                  g602605
NCBI GI
BLAST score
                  62
                  7.0e-27
E value
```

43684

NCBI Description Zea mays tandem genes for alphal-tubulin and alpha2-tubulin

```
307603
Seq. No.
                  uC\text{-}zmf1b73379b11a1\\
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2921303
BLAST score
                   65
                   1.0e-28
E value
                  93
Match length
                   92
% identity
                   Zea mays herbicide safener binding protein (SBP1) mRNA,
NCBI Description
                   complete cds
                   307604
Seq. No.
                   uC-zmflb73379d12a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3925363
BLAST score
                   436
                   4.0e-43
E value
                   146
Match length
% identity
                   58
                   (AF067961) homeodomain protein [Malus domestica]
NCBI Description
Seq. No.
                   307605
                   uC-zmflb73379g09a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g558364
BLAST score
                   46
                   2.0e-17
E value
Match length
                   97
                   88
% identity
                  Z.mays mRNA for ADP-glucose pyrophosphorylase
NCBI Description
                   307606
Seq. No.
                   uC-zmflb73387h12a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3212863
BLAST score
                   239
                   2.0e-20
E value
Match length
                   76
% identity
                   66
                   (AC004005) putative translation initiation factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   307607
                   uC-zmflb73389b06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2262105
BLAST score
                   241
                   1.0e-20
E value
Match length
                   79
```

(AC002343) unknown protein [Arabidopsis thaliana] NCBI Description

307608 Seq. No.

uC-zmflb73395g11a2 Seq. ID

Method BLASTN NCBI GI g1532072 BLAST score 38



```
E value 4.0e-12
Match length 62
% identity 90
NCBI Description Z.mays
```

NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 307609

Seq. ID uC-zmflb73397g07a1

Method BLASTX
NCBI GI g1168609
BEAST score 339
E value 7.0e-32
Match length 99
% identity 71

NCBI Description AUXIN-RESISTANCE PROTEIN AXR1 >gi_479664_pir__S35071

auxin-resistance protein AXR1 - Arabidopsis thaliana >gi_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana] >gi_448755 prf_1917337A ubiquitin-activating enzyme E1

[Arabidopsis thaliana]

Seq. No. 307610

Seq. ID uC-zmflb73401h06a1

Method BLASTN
NCBI GI g2984708
BLAST score 66
E value 9.0e-29
Match length 147
% identity 85

NCBI Description Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete

cds

Seq. No. 307611

Seq. ID uC-zmflb73402f04a2

Method BLASTX
NCBI GI g3036804
BLAST score 187
E value 1.0e-14
Match length 41
% identity 73

NCBI Description (AL022373) thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 307612

Seq. ID uC-zmflb73404h12a1

Method BLASTX
NCBI GI g3377941
BLAST score 220
E value 7.0e-18
Match length 97
% identity 43

NCBI Description (AL021960) putative protein (fragment) [Arabidopsis

thaliana]

Seq. No. 307613

Seq. ID uC-zmflb73405c04a2

Method BLASTX NCBI GI g1931652



BLAST score 205 E value 3.0e-16 Match length 69 % identity 52 NCBI Description (U95973

NCBI Description (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog

[Arabidopsis thaliana]

Seq. No. 307614

Seq. ID uC-zmflb73407b11a2

Method BLASTN
NCBI GI g4185305
BLAST score 49
E value 4.0e-19
Match length 105
% identity 87

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 307615

Seq. ID uC-zmflb73411a01a1

Method BLASTX
NCBI GI g3024506
BLAST score 165
E value 1.0e-11
Match length 46
% identity 76

NCBI Description RAS-RELATED PROTEIN RAB11A >gi 623582 (L29271) Nt-Rab11a

gene product [Nicotiana tabacum]

Seq. No. 307616

Seq. ID uC-zmflb73411d08a1

Method BLASTX
NCBI GI g4454459
BLAST score 172
E value 3.0e-12
Match length 58

% identity 60

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 307617

Seq. ID uC-zmflb73411h12a1

Method BLASTN
NCBI GI g949979
BLAST score 74
E value 1.0e-33
Match length 130
% identity 89

NCBI Description Z.mays Glossy2 locus DNA

Seq. No. 307618

Seq. ID uC-zmflb73412e05a1

MethodBLASTXNCBI GIg4406757BLAST score375E value5.0e-36

```
Match length
                  105
% identity
                  70
NCBI Description
                  (AC006836) putative integral membrane protein A3
                  [Arabidopsis thaliana]
```

Seq. ID uC-zmflb73414c07a1 Method BLASTN NCBI GI g1895083 BLAST score 114 E value 1.0e-57 Match length 133

% identity NCBI Description Zea mays golgi associated protein se-wap41 mRNA, complete

97

Seq. No. 307620

Seq. ID uC-zmflb73414g10a1

Method BLASTN NCBI GI g2257755 BLAST score 269 E value 1.0e-150 Match length 338 % identity 95

NCBI Description Zea mays nucleolar histone deacetylase HD2-p39 mRNA,

complete cds

307621 Seq. No.

Seq. ID uC-zmflb73415c12a1

Method BLASTX NCBI GI g1699024 BLAST score 279 E value 8.0e-25 Match length 77 % identity 64

NCBI Description (U78866) gene1000 [Arabidopsis thaliana] >gi_1699057

(U78870) unknown [Arabidopsis thaliana]

307622 Seq. No.

Seq. ID uC-zmflb73416a03a1

Method BLASTX NCBI GI g4240031 236 BLAST score E value 6.0e-20 Match length 101 % identity 47

NCBI Description (AB018422) DNA binding zinc finger protein (Pspzf) [Pisum

sativum]

307623 Seq. No.

Seq. ID uC-zmflb73416b10a1

Method BLASTN NCBI GI g902200 BLAST score 51 E value 8.0e-20 Match length 155 % identity 42



```
NCBI Description Z.mays complete chloroplast genome

Seq. No. 307624
Seq. ID 2072mflb73417g05a1
```

Method BLASTN
NCBI GI g312178
BLAST score 79
E value 2.0e-36
Match length 139
% identity 56

NCBI Description Z.mays GapC2 gene

Seq. No. 307625

Seq. ID uC-zmflb73418d03a1

Method BLASTN
NCBI GI g3452306
BLAST score 266
E value 1.0e-148
Match length 282
% identity 99

NCBI Description Zea mays retrotransposon Opie-3 5' LTR, partial sequence

Seq. No. 307626

Seq. ID uC-zmflb73418e12a1

Method BLASTX
NCBI GI 9987267
BLAST score 356
E value 6.0e-34
Match length 66
% identity 100

NCBI Description (U32579) DWARF3 [Zea mays]

Seq. No. 307627

Seq. ID uC-zmflb73418g11a1

Method BLASTN
NCBI GI g987266
BLAST score 83
E value 4.0e-39
Match length 172
% identity 85

NCBI Description Zea mays DWARF3 (dwarf3) mRNA, complete cds

Seq. No. 307628

Seq. ID uC-zmflm017016a01b1

Method BLASTX
NCBI GI g2231149
BLAST score 219
E value 7.0e-18
Match length 52
% identity 83

NCBI Description (L81152) integral membrane protein [Oryza sativa]

Seq. No. 307629

Seq. ID uC-zmflm017016a08b1

Method BLASTX
NCBI GI g3075394
BLAST score 282

... 2.0e-25 E value 95 Match length % identity 60

(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis NCBI Description thaliana] >gi 3559809 emb CAA09311_ (AJ010713) fiddlehead

protein [Arabidopsis thaliana]

307630 Seq. No.

Seq. ID uC-zmflm017016d09b1

Method BLASTX g2500345 NCBI GI BLAST score 150 4.0e-10 E value Match length 46 % identity 63

NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY NCBI Description

GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG)

>gi 2618578 dbj BAA23363 (D50420) OTK27 [Homo sapiens]

>gi 3859990 (AF091076) OTK27 [Homo sapiens]

>qi 1589072 prf 2210268A nuclear protein-NHP2-like protein

[Homo sapiens]

307631 Seq. No.

uC-zmflm017016g09b1 Seq. ID

Method BLASTX NCBI GI g3915826 BLAST score 280 E value 4.0e-25 Match length 75 % identity 73

60S RIBOSOMAL PROTEIN L5 NCBI Description

307632 Seq. No.

uC-zmflm017018a11b1 Seq. ID

Method BLASTN NCBI GI g22340 BLAST score 58 3.0e-24 E value Match length 162 % identity 85

NCBI Description Maize gene for heat shock protein 70 exon 1 (hsp70; clone

pMON 9502)

307633 Seq. No.

uC-zmflm017018a12b1 Seq. ID

Method BLASTN NCBI GI g1498596 BLAST score 76 4.0e-35 E value Match length 124 % identity 90

NCBI Description Zea mays phospholipid transfer protein mRNA, complete cds

Seq. No.

307634

uC-zmflm017018h04b1 Seq. ID

Method BLASTX NCBI GI g135060

% identity

NCBI Description

52

unguiculata]

```
BLAST score
E value
                  3.0e-18
Match length
                  82
% identity
                  56
NCBI Description
                  SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
                   (SHRUNKEN-1) >gi_66570_pir _YUZMS sucrose synthase (EC
                  2.4.1.13) - maize >gi_22486 emb CAA26247 (X02400) sucrose
                  synthase [Zea mays] >gi 22488 emb CAA26229 (X02382)
                  sucrose synthase [Zea mays]
Seq. No.
                  307635
Seq. ID
                  uC-zmflm017025g10b1
Method
                  BLASTX
NCBI GI
                  q2244898
BLAST score
                  450
E value
                  2.0e-45
Match length
                  148
% identity
                  64
NCBI Description
                  (Z97338) strong similarity to protein phosphatase 2A
                  regulatory chain, 74K [Arabidopsis thaliana]
                 307636
Seq. No.
Seq. ID
                  uC-zmflm017025h09b1
Method
                  BLASTX
NCBI GI
                  g100490
BLAST score
                  791
E value
                  1.0e-84
Match length
                  173
% identity
                  28
NCBI Description
                  polyubiquitin - garden snapdragon (fragment)
                  >gi_16071_emb_CAA48140 (X67957) ubiquitin [Antirrhinum
                  majus]
Seq. No.
Seq. ID
                  307637
                  uC-zmflm017026b06b1
Method
                  BLASTX
NCBI GI
                  q135398
BLAST score
                  515
E value
                  2.0e-52
Match length
                  98
% identity
                  96
                  TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1
NCBI Description
                  chain - maize >gi_22147_emb_CAA33734 (X15704)
                  alpha1-tubulin [Zea mays]
Seq. No.
                  307638
Seq. ID
                  uC-zmflm017026b07b1
Method
                  BLASTX
NCBI GI
                  q2498098
BLAST score
                  338
                  1.0e-31
E value
Match length
                  124
```

>gi 938300_emb_CAA62086_ (X90487) unknown [Vigna

A3 PROTEIN >gi 2129909 pir S58310 gene A3 protein - cowpea

Seq. ID

307644

uC-zmflm017026h05b1



```
Seq. No.
Seq. ID
                   uC-zmflm017026c10b1
Method
                   BLASTX
NCBI GI
                   g4454026
BLAST score
                   292
                   2.0e-26
E value
Match length
                   95
% identity
                   61
                   (AL035394) phosphatase like protein [Arabidopsis thaliana]
NCBI Description
                   307640
Seq. No.
Seq. ID
                   uC-zmflm017026d09b1
Method
                   BLASTX
NCBI GI
                   g1706260
BLAST score
                   381
                   5.0e-37
E value
                   94
Match length
% identity
                   81
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__$59597
NCBI Description
                   cysteine proteinase 1 precursor - maize
                   >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                   mays]
                   307641
Seq. No.
Seq. ID
                   uC-zmflm017026e07b1
Method
                   BLASTX
NCBI GI
                   q1488297
                   278
BLAST score
                   7.0e-25
E value
Match length
                   100
                   59
% identity
NCBI Description
                  (U63530) osRAD23 [Oryza sativa]
Seq. No.
                   307642
Seq. ID
                   uC-zmflm017026f07b1
Method
                   BLASTX
NCBI GI
                   g548770
                   232
BLAST score
E value
                   2.0e-19
Match length
                   84
% identity
                   62
                   60S RIBOSOMAL PROTEIN L3 >gi_481228 pir S38359 ribosomal
NCBI Description
                   protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                   ribosomal protein L3 [Oryza sativa]
Seq. No.
                   307643
Seq. ID
                   uC-zmflm017026f10b1
Method
                   BLASTX
NCBI GI
                   q1817584
BLAST score
                   145
E value
                   4.0e-09
Match length
                   44
% identity
NCBI Description
                  (Y08991) adaptor protein [Homo sapiens]
```

```
Method
                  BLASTX
NCBI GI
                  g2583128
BLAST score
                  203
                  3.0e-16
E value
Match length
                  68
% identity
                  56
                  (AC002387) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seg. No.
                  307645
                  uC-zmflm017026h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  289
E value
                  5.0e-26
Match length
                  62
% identity
                  90
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
                  307646
Seq. No.
                  uC-zmflm017082b08b1
Seq. ID
                  BLASTX
Method
                  g3024657
NCBI GI
BLAST score
                  183
E value
                   3.0e-18
Match length
                  72
                   69
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi 2668740 (AF034944) translation initiation factor; GOS2
                   [Zea mays]
                   307647
Seq. No.
                   uC-zmflm017082c01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1076746
                   329
BLAST score
                   5.0e-31
E value
Match length
                   85
% identity
                   79
                  heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                   [Oryza sativa]
                   307648
Seq. No.
                   uC-zmflm017082f03b1
Seq. ID
                   BLASTN
Method
                   g22332
NCBI GI
                   237
BLAST score
                   1.0e-131
E value
Match length
                   328
% identity
                   93
NCBI Description
                   Z.mays HRGP gene
```

307649

uC-zmflm017082h08b1

Seq. No.

Seq. ID

Seq. ID Method

NCBI GI BLAST score BLASTX g112994

323

```
BLASTX
Method
NCBI GI
                   g3024432
BLAST score
                   248
                   2.0e-21
E value
Match length
                   69
% identity
                   72
NCBI Description PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
                   COMPLEX ALPHA SUBUNIT) >qi 1930070 (U92540) proteasome
                alpha subunit [Oryza sativa]
Seq. No.
                   307650
                  uC-zmflm017084g04b1
Seq. ID
                   BLASTX
Method
                   g2129533
NCBI GI
                   203
BLAST score
E value
                   6.0e-16
Match length
                   77
% identity
                   60
                   adenine nucleotide translocase - Arabidopsis thaliana
NCBI Description
                   >gi 1051109 emb_CAA89201 (Z49227) adenine nucleotide
                   translocase [Arabidopsis thaliana]
                   307651
Seq. No.
                   uC-zmflm017084h07b1
Seq. ID
                   BLASTX
Method
                   g1673456
NCBI GI
BLAST score
                   180
                   8.0e-14
E value
                   53
Match length
% identity
                   72
                  (Y09214) rubisco small subunit [Zea mays]
NCBI Description
Seq. No.
                   307652
                   uC-zmflm017086a11b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4007864
                                                                    4 _S.
BLAST score
                   273
E value
                   1.0e-152
Match length
                   316
% identity
                   35
NCBI Description Zea mays HRGP gene, AC1503 line
                   307653
Seq. No.
                   uC-zmflm017086d07b1
Seq. ID
                   BLASTX
Method
                   g1800281
NCBI GI
BLAST score
                   571
                   5.0e-59
E value
                   122
Match length
% identity
                   21
                  (U82086) polyubiquitin [Fragaria x ananassa]
NCBI Description
                   307654
Seq. No.
                   uC-zmflm017086h03b1
```



```
3.0e-30
E value
                  76
Match length
% identity
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf. 1410284A abscisic acid inducible gene [Zea
                  mays]
14
                  307655
Seq. No.
Seq. ID
                  uC-zmflm017086h11b1
                  BLASTX
Method
                  g1332579
NCBI GI
BLAST score
                  432
                  2.0e-44
E value
Match length
                  123
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                   307656
Seq. No.
Seq. ID
                  uC-zmflm017089a05b1
Method
                  BLASTX
                   g3882211
NCBI GI
                  163
BLAST score
                   3.0e-16
E value
                   139
Match length
% identity
                   39
NCBI Description (AB018288) KIAA0745 protein [Homo sapiens]
                   307657
Seq. No.
                   uC-zmflm017089a12b1
Seq. ID
Method
                   BLASTN
                   q945021
NCBI GI
                   62
BLAST score
                   3.0e-26
E value
                   70
Match length
                   97
% identity
NCBI Description
                   Z.mays DNA for tbpl gene
                   307658
Seq. No.
                   uC-zmflm017089b03b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1498596
BLAST score
                   109
                   3.0e-54
E value
                   226
Match length
                   95
% identity
                   Zea mays phospholipid transfer protein mRNA, complete cds
NCBI Description
                   307659
Seq. No.
                   uC-zmflm017089e06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3913427
```

43695

194

86

5.0e-15

BLAST score

E value Match length

```
% identity
                     S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                     (SAMDC) >gi 1532073 emb CAA69075 (Y07767)
                     S-adenosylmethionine decarboxylase [Zea mays]
                     307660
Seq. No.
                     uC-zmflm017089f06b1
Seq. ID
Method
                     BLASTX
NCBI GI
                     g1172836
BLAST score
                     352
                     2.0e-33
 E value
                     75
 Match length
 % identity
                     85
                     GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)
 NCBI Description
                     small ras-related protein [Nicotiana tabacum]
 Seq. No.
                     307661
                     uC-zmflm017089g06b1
 Seq. ID
 Method
                     BLASTX
 NCBI GI
                     g1172836
BLAST score
                     240
                     3.0e-20
∢E value
Match length
                     66
 % identity
                     70
                     GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)
 NCBI Description
                     small ras-related protein [Nicotiana tabacum]
 Seq. No.
                     307662
                     uC-zmflm017089h06b1
 Seq. ID
                     BLASTX
 Method
                     q135060
 NCBI GI
 BLAST score
                     257
                     2.0e-22
 E value
                     105
 Match length
 % identity
                     55
                     SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
 NCBI Description
                     (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose
                     synthase [Zea mays] >\overline{gi}_224\overline{8}8\underline{emb}_CAA262\overline{2}9\underline{} (X02382)
                     sucrose synthase [Zea mays]
 Seq. No.
                     -307663
                     uC-zmflm017092c05b1
 Seq. ID
 Method
                     BLASTX
 NCBI GI
                     q4263791
 BLAST score
                     214
                     2.0e-17
 E value
 Match length
                     82
 % identity
                     (AC006068) putative receptor protein kinase [Arabidopsis
 NCBI Description
                     thaliana]
```

Seq. ID uC-zmflm017093d09b1

Method BLASTN NCBI GI g22332 BLAST score 291



```
E value 1.0e-163
Match length 425
% identity 93
```

NCBI Description Z.mays HRGP gene

Seq. No. 307665

Seq. ID uC-zmflm017205b10b1

Method BLASTX
NCBI GI g1732517
BLAST score 296
E value 8.0e-27
Match length 97
% identity 63

NCBI Description (U62745) putative cytoskeletal protein [Arabidopsis

thaliana]

Seq. No. 307666

Seq. ID uC-zmflm017205c11b1

Method BLASTX
NCBI GI g2760084
BLAST score 186
E value 6.0e-14
Match length 109
% identity 39

NCBI Description (Y16045) leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No. 307667

Seq. ID uC-zmflm017205c12b1

Method BLASTX
NCBI GI g4314362
BLAST score 252
E value 2.0e-21
Match length 78
% identity 60

NCBI Description (AC006340) putative D-amino acid dehydrogenase [Arabidopsis

thaliana]

Seq. No. 307668

Seq. ID uC-zmflm017205e04b1

Method BLASTN
NCBI GI g3851002
BLAST score 68
E value 1.0e-29
Match length 83
% identity 95

NCBI Description Zea mays pyruvate dehydrogenase E1 beta subunit isoform 3

mRNA, nuclear gene encoding mitochondrial protein, complete

cds

Seq. No. 307669

Seq. ID uC-zmflm017205f04b1

Method BLASTX
NCBI GI g3193284
BLAST score 230
E value 8.0e-19
Match length 140
% identity 39

```
(AF069298) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  uC-zmflm017207a02b1
Seq. ID
                  BLASTX
Method
                  g1076385
NCBI GI
BLAST score
                  177
                  1.0e-12
E value
                  57
Match length
                   65
% identity
                  protein kinase (EC 2.7.1.37) tousled - Arabidopsis thaliana
NCBI Description
                  >gi 433052 (L23985) protein kinase [Arabidopsis thaliana]
Seq. No.
                   307671
                   uC-zmflm017207a04b1
Seq. ID
                   BLASTX
Method
                   q3789942
NCBI GI
                   452
BLAST score
                   3.0e-45
E value
                   103
Match length
                   19
% identity
                   (AF093505) polyubiquitin [Saccharum hybrid cultivar
NCBI Description
                   H32-8560]
                   307672
Seq. No.
```

uC-zmflm017207e06b1 Seq. ID

BLASTN Method q4140643 NCBI GI 50 BLAST score 5.0e-19 E value 178 Match length 83 % identity

Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description

complete sequence

307673 Seq. No.

uC-zmflm017207e09b1 Seq. ID

BLASTX Method q4138137 NCBI GI BLAST score 393 E value 5.0e-38 153 Match length % identity 51

(AJ012796) ss-galactosidase [Lycopersicon esculentum] NCBI Description

307674 Seq. No.

uC-zmflm017207f02b1 Seq. ID

BLASTN Method NCBI GI g4416300 50 BLAST score 5.0e-19 E value 113 Match length 86 % identity

Zea mays chromosome 4 22 kDa zein-associated intercluster NCBI Description

region, complete sequence

307675 Seq. No.

Method

NCBI GI

BLASTX

q4539404



```
uC-zmflm017207f07b1
Seq. ID
                  BLASTX
Method
                  g131754
NCBI GI
                  183
BLAST score
                  2.0e-13
E value
                  59
Match length
                  58
% identity
                  PPLZ02 PROTEIN >gi 99973 pir S11881 hypothetical protein
NCBI Description
                   (clone pPLZ2) - large-leaved lupine >gi_19507_emb_CAA36069_
                   (X51767) put. pPLZ2 product (AA 1-164) [Lupinus
                  polyphyllus]
                  307676
Seq. No.
                  uC-zmflm017209b01b1
Seq. ID
                  BLASTX
Method
                  g4581149
NCBI GI
                                                   *
BLAST score
                  171
                  5.0e-12
E value
                  125
Match length
% identity
                  38
                  (AC006919) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  307677
                  uC-zmflm017209b02b1
Seq. ID
Method
                  BLASTX
                  q2766448
NCBI GI
                  350
BLAST score
E value
                  4.0e-33
                  92
Match length
                  76
% identity
                  (AF029856) cytochrome P450 CYP98A1 [Sorghum bicolor]
NCBI Description
Seq. No.
                  307678
                  uC-zmflm017209b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739387 🔩
BLAST score
                  205
                   6.0e-16
E value
                  111
Match length
                   42
% identity
                  (AC002505) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   307679
Seq. No.
Seq. ID
                  uC-zmflm017209b10b1
Method
                  BLASTX
                   g4204695
NCBI GI
BLAST score
                   370
E value
                   2.0e-35
Match length
                  116
                   59
% identity
                   (AF117062) putative inositol polyphosphate 5-phosphatase
NCBI Description
                  At5P1 [Arabidopsis thaliana]
                   307680
Seq. No.
Seq. ID
                   uC-zmflm017209b12b1
```



```
BLAST score
                  2.0e-12
E value
                  104
Match length
                  37
% identity
                  (AL049524) putative protein [Arabidopsis thaliana]
NCBI Description
                  307681
Seq. No.
Seq. ID
                  uC-zmf1m017209c07b1
                                                                     3
Method
                  BLASTX
NCBI GI
                  g3790581
BLAST score
                  225
                  2.0e-18
E value
                  54
Match length
% identity
                  63
                   (AF079179) RING-H2 finger protein RHB1a [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  307682
Seq. ID
                  uC-zmflm017209c11b1
Method
                  BLASTX
NCBI GI
                  g1655930
BLAST score
                  278
                  2.0e-24
E value
Match length
                  101
% identity
                  52
                   (U66564) RUSH-lalpha [Oryctolagus cuniculus]
NCBI Description
Seq. No.
                  307683
Seq. ID
                  uC-zmflm017209d07b1
Method
                  BLASTX
                  g2623298
NCBI GI
BLAST score
                  315
E value
                  6.0e-29
Match length
                  123
% identity
NCBI Description
                   (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis
                  thaliana]
                  307684
Seq. No.
Seq. ID
                  uC-zmflm017209d10b1
Method
                  BLASTX
NCBI GI
                  g118104
BLAST score
                  698
E value
                  8.0e-74
Match length
                  147
                  90
% identity
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
```

uC-zmflm017209d12b1 Seq. ID

Method BLASTN NCBI GI q168406 BLAST score 92



```
E value
                   4.0e-44
Match length
                   128
% identity
                   93
```

NCBI Description Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,

complete cds

Seq. No. 307686

Seq. ID uC-zmflm017209f07b1

Method BLASTX NCBI GI q4154352 BLAST score 214 E value 3.0e-17 Match length 128 38 % identity

NCBI Description (AF110333) PrMC3 [Pinus radiata]

307687 Seq. No.

Seq. ID uC-zmflm017211a05b1

Method BLASTX NCBI GI q4115373 BLAST score 203 E value 6.0e-16 Match length 83 28

% identity NCBI Description (AC005967) receptor-like protein kinase [Arabidopsis

thaliana]

307688 Seq. No.

uC-zmflm017211b01b1 Seq. ID

Method BLASTX NCBI GI q135103 BLAST score 221 E value 4.0e-18 Match length 79 47 % identity

MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [CONTAINS: NCBI Description

GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (PROLINE--TRNA LIGASE)]

>gi_103253_pir__S18644 multifunctional amino acid--tRNA ligase (EC 6.1.1.-) - fruit fly (Drosophila melanogaster)

>gi 157564 (M74104) transfer RNA-Glu-Pro aminoacyl

synthetase [Drosophila melanogaster] >gi 1871360 (U59923) glutamyl-prolyl-tRNA synthetase [Drosophila melanogaster]

307689 Seq. No.

Seq. ID uC-zmflm017211c08b1

Method BLASTX NCBI GI g2213594 BLAST score 158 E value 1.0e-23 Match length 90 71 % identity

NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

307690 Seq. No.

Seq. ID uC-zmflm017211d04b1

Method BLASTX



```
NCBI GI
                   g3924602
BLAST score
                  152
E value
                  2.0e-10
Match length
                   63
% identity
                  54
NCBI Description
                  (AF069442) predicted OR23 protein of unknown function
                   [Arabidopsis thaliana]
Seq. No.
                  307691
Seq. ID
                  uC-zmflm017211e07b1
Method
                  BLASTX
NCBI GI
                  q3881836
BLAST score
                  498
E value
                  2.0e-50
Match length
                  137
% identity
                  70
NCBI Description
                  (Z78019) Similarity to Yeast LPG22P protein (TR:G1151240);
                  cDNA EST EMBL: T00686 comes from this gene; cDNA EST
                  EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728
                  comes from this gene; cDNA EST EMBL:C10626 comes from this
                  ge
Seq. No.
                  307692
Seq. ID
                  uC-zmflm017211g01b1
Method
                  BLASTX
NCBI GI
                  g1711618
BLAST score
                  427
E value
                  4.0e-42
Match length
                  144
% identity
                  60
NCBI Description
                  LOW AFFINITY SULPHATE TRANSPORTER 3 >gi 1085993 pir S51765
                  low affinity sulphate transporter - Stylosanthes hamata
                  >gi_607188_emb_CAA57831_ (X82454) low affinity sulphate
                  transporter [Stylosanthes hamata]
Seq. No.
                  307693
Seq. ID
                  uC-zmflm017211g08b1
Method
                  BLASTX
NCBI GI
                  g3157928
BLAST score
                  588
E value
                  7.0e-61
Match length
                  153
```

% identity 70

NCBI Description (AC002131) Similar to fumarylacetoacetate hydrolase,

gb_L41670 from Emericella nidulans. [Arabidopsis thaliana]

Seq. No. 307694

Seq. ID uC-zmflm017211g09b1

Method BLASTX NCBI GI q4539662 BLAST score 273 E value 4.0e-24 Match length 131 % identity 50

NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 307695

43702

. .

Seq. ID

307700

uC-zmflm017214a01b1

```
uC-
```

```
Seq. ID
                    uC-zmflm017211h09b1
 Method
                   BLASTX
NCBI GI
                    g283045
 BLAST score
                   167
 E value
                    8.0e-12
 Match length
                   86
 % identity
                    45
 NCBI Description
                   hydroxyproline-rich glycoprotein - maize
                   >gi 22333 emb CAA44844 (X63134) hydroxyproline-rich
                    glycoprotein [Zea mays] >gi_228936_prf__1814452A Hyp-rich
                   glycoprotein [Zea mays]
 Seq. No.
                   307696
 Seq. ID
                   uC-zmflm017212b10b1
 Method
                   BLASTX
 NCBI GI
                   g3549626
 BLAST score
                   161
 E value
                   2.0e-15
 Match length
                   101
 % identity
                   48
 NCBI Description
                   (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
 Seq. No.
                   307697
 Seq. ID
                   uC-zmflm017212c10b1
 Method
                   BLASTX
 NCBI GI
                   g2494:144
 BLAST score
                   150
 E value
                   1.0e-09
 Match length
                   47
 % identity
                   68
 NCBI Description
                   (AC002329) predicted leucine-rich protein [Arabidopsis
                   thaliana]
 Seq. No.
                   307698
 Seq. ID
                   uC-zmflm017212g04b1
 Method
                   BLASTX
NCBI GI
                   g3603353
 BLAST score
                   195
E value
                   7.0e-15
Match length
                   57
 % identity
                   63
NCBI Description
                   (AF074843) peroxisomal targeting signal type 1 receptor
                   [Arabidopsis thaliana]
Seq. No.
                   307699
Seq. ID
                   uC-zmflm017212h09b1
Method
                   BLASTX
NCBI GI
                   q1657619
BLAST score
                   399
E value
                   8.0e-39
Match length
                   134
% identity
                   54
                   (U72504) G5p [Arabidopsis thaliana] >gi 3068710 (AF049236)
NCBI Description
                   putative transmembrane protein G5p [Arabidopsis thaliana]
```

```
Method
                   BLASTN
                   g22332 💂
NCBI GI
BLAST score
                   273
E value
                   1.0e-152
Match length
                   407
% identity
                   92
NCBI Description
                  Z.mays HRGP gene
Seq. No.
                   307701
Seq. ID
                   uC-zmflm017214b02b1
Method
                   BLASTX
NCBI GI
                   g3264596
BLAST score
                   175
E value
                   1.0e-12
Match length
                   81
% identity
                   46
NCBI Description
                  (AF057183) putative tonoplast aquaporin [Zea mays]
Seq. No.
                   307702
Seq. ID
                   uC-zmflm017214b11b1
Method
                  BLASTX
NCBI GI
                   q1086111
BLAST score
                   185
E value
                   1.0e-26
Match length
                   116
% identity
                  59
NCBI Description
                  peroxidase (EC 1.11.1.7) - Spirodela polyrrhiza
                  >gi_438245_emb_CAA80502 (Z22920) peroxidase [Spirodela
                  polyrrhiza]
Seq. No.
                  307703
Seq. ID
                  uC-zmflm017214e05b1
Method
                  BLASTN
NCBI GI
                  g288611
BLAST score
                  34
E value
                  2.0e-09
Match length
                  50
% identity
                  92
NCBI Description
                  Z.mays PG gene for polygalacturonase
Seq. No.
                  307704
Seq. ID
                  uC-zmflm017214g01b1
Method
                  BLASTX
NCBI GI
                  q4433620
BLAST score
                  499
E value
                  8.0e-54
Match length
                  136
% identity
                  82
NCBI Description
                  (AF107586) putative cell division control protein
                  [Dendrobium grex Madame Thong-IN]
Seq. No.
                  307705
```

Seq. ID uC-zmflm017214h03b1

Method BLASTX
NCBI GI g1352679
BLAST score 278
E value 7.0e-25



Match length 107 % identity 59 NCBI Description PROTEIN PHOSPHATASE 2C ABI1 (PP2C) >gi 2129699 pir A54588 protein phosphatase ABI1 - Arabidopsis thaliana >gi 509419_emb_CAA55484_ (X78886) ABI1 [Arabidopsis thaliana] 307706 Seq. No. Seq. ID uC-zmflm017214h09b1 Method BLASTX NCBI GI g4096786 BLAST score 183 E value 4.0e-14 Match length 67 % identity 58 NCBI Description (U39958) NADP-malic enzyme [Zea mays] 307707 Seq. No. uC-zmflm017233a07b1 Seq. ID Method BLASTX NCBI GI g1076763 BLAST score 162 E value 6.0e-11 Match length 131 % identity 34 AWJL218 protein - wheat >gi_551212_emb_CAA57134_ (X81369) NCBI Description AWJL218 [Triticum aestivum] 307708 Seq. No. Seq. ID uC-zmflm017233b07b1 Method BLASTX NCBI GI g2829894 BLAST score 290 E value 5.0e-26 Match length 102 % identity 61 NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana] Seq. No. 307709 Seq. ID uC-zmflm017233c02b1 Method BLASTX NCBI GI g82696 BLAST score 298 E value 3.0e-27 Match length 75 % identity 79 NCBI Description glycine-rich protein - maize >gi 22293 emb CAA43431 (X61121) glycine-rich protein [Zea mays]

Seq. No. 307710

Seq. ID uC-zmflm017233c03b1

Method BLASTX NCBI GI q4115926 BLAST score 275 E value 3.0e-24Match length 89 % identity 57



NCBI Description (AF118222) similar to the subtilase family of serine

proteases (Pfam: PF00082, Score=50.7, E=4.7e-13, n=3) [Arabidopsis thaliana] >gi 4539413 emb CAB40046.1

(AL049524) putative subtilisin-like protease [Arabidopsis

thaliana]

Seq. No. 307711

Seq. ID uC-zmflm017233c04b1

Method 3 BLASTX g127243 NCBI GI BLAST score 149 E value 1.0e-20 Match length 149 % identity 42

NCBI Description AUTONOMOUS TRANSPOSABLE ELEMENT EN-1 MOSAIC PROTEIN

(SUPPRESSOR-MUTATOR SYSTEM PROTEIN) (SPM)

>gi_320621_pir_S28365 gene 1 protein - maize transposon

En-1 >gi 168640 (M25427) mosaic protein [Zea mays]

>gi 225007 prf 1206239C gene 1 [Zea mays]

Seq. No. 307712

uC-zmflm017233d08b1 Seq. ID

Method BLASTX NCBI GI g2979554 BLAST score 734 E value 5.0e-78 Match length 168 % identity 83

NCBI Description (AC003680) CDC4 like protein [Arabidopsis thaliana]

Seq. No. 307713

Seq. ID uC-zmflm017233d11b1

Method BLASTX NCBI GI g115771 BLAST score 631 E value 5.0e-66 Match length 128 % identity 90

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll

a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

Seq. No. 307714

Seq. ID uC-zmflm017233h10b1

Method BLASTX NCBI GI g2245021 BLAST score 223 E value 3.0e-18 Match length 121 % identity 44

NCBI Description (Z97341) heat shock protein 110 homolog [Arabidopsis

thaliana]

Seq. No. 307715

Seq. ID uC-zmflmo17001a09b1

```
Method
NCBI GI
                  g22192
BLAST score
                  71
                  1.0e-31
E value
Match length
                  135
                  89
% identity
NCBI Description Z.mays B-I gene for B transcriptional activator
                  307716
Seq. No.
                  uC-zmflmo17001a12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1931651
BLAST score
                  190
E value
                  2.0e-14
Match length
                  85
                  47
% identity
                  (U95973) membrane-associated salt-inducible protein isolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  307717
Seq. ID
                  uC-zmflmo17001c03b1
Method
                  BLASTN
NCBI GI
                  g22332
BLAST score
                  198
                  1.0e-107
E value
Match length
                  329
                  90
% identity
NCBI Description Z.mays HRGP gene
Seq. No.
                  307718
Seq. ID
                  uC-zmflmo17001d11b1
Method
                  BLASTX
NCBI GI
                  q3258456
BLAST score
                  248
E value
                  2.0e-21
Match length
                  86
% identity
                  58
NCBI Description (AB015655) chitinase [Cucurbita sp.]
                  307719
Seq. No.
Seq. ID
                  uC-zmflmo17001d12b1
Method
                  BLASTX
NCBI GI
                  g2286113
BLAST score
                  176
                  1.0e-12
E value
Match length
                  69
% identity
                  58
NCBI Description
                  (U78892) MADS box protein [Oryza sativa]
                  307720
Seq. No.
Seq. ID
                  uC-zmflmo17001e09b1
                                                                       ٠,٠
```

Method BLASTX NCBI GI g118104

BLAST score 329
E value 2.0e-51
Match length 132
% identity 80



NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) maize >gi_168461 (M55021) cyclophilin [Zea mays] >gi 829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays] Seq. No. 307721 Seq. ID uC-zmflmo17001e11b1 Method BLASTX NCBI GI g421929 BLAST score 321 E value 1.0e-29 Match length 131 % identity 10 NCBI Description ubiquitin - tomato >gi_312160_emb_CAA51679 (X73156) ubiquitin [Lycopersicon esculentum] Seq. No. 307722 Seq. ID uC-zmflmo17001h02b1 Method BLASTX NCBI GI g4176530 BLAST score 152 E value 1.0e-09 Match length 182 % identity 24 NCBI Description (AL035263) putative condensin subunit [Schizosaccharomyces pombe] Seq. No. 307723 Seq. ID uC-zmflmo17010b08a1 Method BLASTN NCBI GI g22312 BLAST score 139 E value 3.0e-72 Match length 232 % identity 77 NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid) Seq. No. 307724 Seq. ID uC-zmflmo170112a09b1 Method BLASTX NCBI GI g3540194 BLAST score 218 E value 8.0e-18 Match length 66 % identity 67 NCBI Description (AC004260) AtVPS45p [Arabidopsis thaliana] Seq. No. 307725

Seq. ID uC-zmflmo170112a10b1

Method BLASTN NCBI GI g1532072 BLAST score 75 E value 3.0e - 34Match length 151 % identity 87



NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 307726

Seq. ID uC-zmflmo170112a12b1

Method BLASTX
NCBI GI g629641
BLAST score 165
E value 1.0e-11
Match length 87
% identity 51

NCBI Description PsHSC71.0 protein - garden pea >gi_1076530 pir_S53500

HSC71.0 protein - garden pea >gi_473217_emb_CAA83548_

(Z32537) PsHSC71.0 [Pisum sativum]

Seq. No. 307727

Seq. ID uC-zmflmo170112b05b1

Method BLASTX
NCBI GI g400803
BLAST score 301
E value 3.0e-27
Match length 144
% identity 58

NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE

(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_283033_pir__A42807 phosphoglycerate mutase (EC 5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize >gi_168588 (M80912) 2,3-bisphosphoglycerate-independent

phosphoglycerate mutase [Zea mays]

Seq. No. 307728

Seq. ID uC-zmflmo170112b09b1

Method BLASTX
NCBI GI g3281868
BLAST score 657
E value 3.0e-70
Match length 153
% identity 83

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 307729

Seq. ID uC-zmflmo170112b12b1

Method BLASTX
NCBI GI g4217999
BLAST score 155
E value 2.0e-10
Match length 53
% identity 58

NCBI Description (AC006135) putative ubiquitin--protein ligase

(ubiquitin-conjugating enzyme) [Arabidopsis thaliana]

Seq. No. 307730

Seq. ID uC-zmflmo170112c05b1

Method BLASTX
NCBI GI g2244866
BLAST score 280
E value 7.0e-25
Match length 107

```
% identity
 NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                    307731
  Seq. No.
                    uC-zmflmo170112c11b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3122234
                    279
 BLAST score
. E value
                    1.0e-24
 Match length
                    128
                    49
 % identity
                    EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT
 NCBI Description
                    (EIF-2-BETA) (P38) >gi_2306768 (U87163) eIF-2 beta subunit
                    [Triticum aestivum]
                    307732
 Seq. No.
 Seq. ID
                    uC-zmflmo170112d06b1
 Method
                    BLASTX
 NCBI GI
                    q2347098
 BLAST score
                    475
                    8.0e-50
 E value
 Match length
                    129
 % identity
                    84
 NCBI Description
                    (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
                    >gi 4490742 emb CAB38904.1 (AL035708) ubiquitin-specific
                    protease (AtUBP3) [Arabidopsis thaliana]
  × .
 Seq. No.
                    307733
 Seq. ID
                    uC-zmflmo170112e07b1
 Method
                    BLASTX
 NCBI GI
                    g4158230
 BLAST score
                    471
                    3.0e-47
 E value
 Match length
                    134
 % identity
                    69
 NCBI Description
                   (Y18625) amylogenin [Triticum aestivum]
 Seq. No.
                    307734
 Seq. ID
                    uC-zmflmo170112f04b1
 Method
                    BLASTX
 NCBI GI
                    q3256035
 BLAST score
                    186
 E value
                    6.0e-14
 Match length
                    84
 % identity
                    48
 NCBI Description
                    (Y14274) putative serine/threonine protein kinase [Sorghum
                    bicolor]
 Seq. No.
                    307735
 Seq. ID
                    uC-zmflmo170112f05b1
 Method
                    BLASTX
```

NCBI GI q4105798 BLAST score 176 E value 1.0e-12 Match length 43 % identity 67

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]



307736 Seq. No. uC-zmflmo170112f09b1 Seq. ID Method BLASTX NCBI GI g4512667 BLAST score 327 2.0e-30 E value Match length 123 % identity 59 (AC006931) putative MAP kinase [Arabidopsis thaliana] NCBI Description 307737 Seq. No. uC-zmflmo170113c08b1 Seq. ID BLASTX Method NCBI GI q4490736 BLAST score 201 E value 2.0e-19 Match length 92 % identity 39 NCBI Description (AL035708) putative protein [Arabidopsis thaliana] 307738 Seq. No. uC-zmflmo170113f01b1 Seq. ID Method BLASTX g1890575 NCBI GI BLAST score 396 E value 1.0e-38 Match length 115 % identity 65 (X93174) xyloglucan endotransglycosylase (XET) [Hordeum NCBI Description vulgare] 307739 Seq. No. uC-zmflmo170113g01b1 Seq. ID Method BLASTN g2668739 NCBI GI BLAST score 50 E value 9.0e-20 Match length 70 96 % identity NCBI Description Zea mays translation initiation factor GOS2 (TIF) mRNA, complete cds 307740 Seq. No. uC-zmflmo170114a08b1 Seq. ID Method BLASTX

g115771 NCBI GI BLAST score 720 E value 5.0e-81 Match length 167 % identity 92

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900 (X14794) chlorophyll a/b-binding
preprotein (AA 1 - 262) [Zea mays]

```
307741
Seq. No.
Seq. ID
                  uC-zmflmo170114a09b1
Method
                  BLASTN
NCBI GI
                   g22292
BLAST score
                   211
E value
                   1.0e-115
Match length
                   365.
% identity
                   94
NCBI Description Z.mays mRNA for glycine-rich protein
                   307742
Seq. No.
Seq. ID
                  uC-zmflmo170114a12b1
Method
                  BLASTX
NCBI GI
                   g2959767
BLAST score
                   235
E value
                   2.0e-19
Match length
                  120
% identity
                   44
NCBI Description
                   (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi 3738292
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
Seq. No.
                   307743
Seq. ID
                  uC-zmflmo170114b07b1
Method
                  BLASTX
NCBI GI
                   g3273243
BLAST score
                   468
E value
                  7.0e-47
Match length
                  124
                   81
% identity
NCBI Description
                   (AB004660) NLS receptor [Oryza sativa]
                  >gi 3273245 dbj BAA31166 (AB004814) NLS receptor [Oryza
                   sat\overline{i}va
Seq. No.
                   307744
Seq. ID
                  uC-zmflmo170114c02b1
Method
                  BLASTX
NCBI GI
                   g4587533
BLAST score
                   393
                   5.0e-38
E value
Match length
                  165
% identity
                   50
                   (AC007060) EST gb AA721821 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. ID uC-zmflmo170114c07b1

Method BLASTX NCBI GI g2760345 BLAST score 503 E value 6.0e-52 Match length 136 % identity 20

NCBI Description (U84967) ubiquitin [Arabidopsis thaliana]

Seq. No. 307746

Seq. ID uC-zmflmo170114c09b1



```
Method
                  BLASTX
NCBI GI
                  g4415996
BLAST score
                  720
                  2.0e-76
E value
                  137
Match length
                  99
% identity
                  (AF059290) beta-tubulin 4 [Eleusine indica]
NCBI Description
Seq. No.
                  307747
                  uC-zmflmo170114c11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4056568
BLAST score
                  426
E value
                  5.0e-42
Match length
                  127
% identity
                  71
NCBI Description
                  (U90944) PDI-like protein [Zea mays]
                  307748
Seq. No.
Seq. ID
                  uC-zmflmo170114d03b1
Method
                  BLASTX
NCBI GI
                  g1632831
BLAST score
                  511
E value
                  6.0e-52
Match length
                  123
% identity
                  78
                  (Z49698) orf [Ricinus communis]
NCBI Description
                  307749
Seq. No.
                  uC-zmflmo170114d05b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4185305
BLAST score
                  47
                  3.0e-17
E value
Match length
                  63
% identity
                  94
NCBI Description
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
Seq. No.
                  307750
                  uC-zmflmo170114d08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4321977
BLAST score
                  132
E value
                  6.0e-68
Match length
                  224
                  90
% identity
NCBI Description Zea mays beta-amylase (Amy2) gene, complete cds
```

307751

Seq. ID uC-zmflmo170114e02b1

Method BLASTX NCBI GI q1592812 BLAST score 183 2.0e-13 E value



Match length 127 % identity 38

NCBI Description (X95957) 22 kDa polypeptide [Nicotiana tabacum]

Seq. No. 307752

Seq. ID uC-zmflmo170114e06b1

Method BLASTX
NCBI GI g4204912
BLAST score 369
E value 2.0e-35
Match length 133
% identity 56

NCBI Description (U58918) MEK kinase [Arabidopsis thaliana]

Seq. No. 307753

Seq. ID uC-zmflmo170114e08b1

Method BLASTX
NCBI GI g1255430
BLAST score 208
E value 3.0e-16
Match length 121
% identity 40

NCBI Description (U53155) No definition line found [Caénorhabditis elegans]

Seq. No. 307754

Seq. ID uC-zmflmo170114e10b1

Method BLASTX
NCBI GI g2407800
BLAST score 485
E value 8.0e-49
Match length 109
% identity 89

NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No. 307755

Seq. ID uC-zmflmo170114e11b1

Method BLASTX
NCBI GI g3080420
BLAST score 384
E value 4.0e-37
Match length 130
% identity 59

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No. 307756

Seq. ID uC-zmflmo170114e12b1

Method BLASTX
NCBI GI g4165861
BLAST score 177
E value 9.0e-13
Match length 122
% identity 22

NCBI Description (AF006603) histone deacetylase mHDA2 [Mus musculus]

Seq. No. 307757

Seq. ID uC-zmflmo170114f09b1

```
BLASTX
Method
                   g2198851
NCBI GI
BLAST score
                   147
                   2.0e-09
E value
                   33
Match length
                   94
% identity
                   (AF007785) cystathionine gamma-synthase [Zea mays]
NCBI Description
Seq. No.
                   307758
                   uC-zmflmo170114f10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115923
BLAST score
                   212
E value
                   2.0e-17
Match length
                   62
                   83
% identity
                   CELL DIVISION CONTROL PROTEIN 2 HOMOLOG >gi 168511 (M60526)
NCBI Description
                   protein cdc2 kinase [Zea mays]
Seq. No.
                   307759
                   uC-zmflmo170114g01b1
Seq. ID
                   BLASTX
Method
NCBI GÌ
                   g3367576
BLAST score
                   392
                   7.0e-38
E value
Match length
                   124
% identity
                   (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]
NCBI Description
                   307760
Seq. No.
Seq. ID
                   uC-zmflmo170114h02b1
Method
                   BLASTX
                   g2262105
NCBI GI
BLAST score
                   199
E value
                   1.0e-23
                   148
Match length
% identity
                   42
NCBI Description
                   (AC002343) unknown protein [Arabidopsis thaliana]
                   307761
Seq. No.
Seq. ID
                   uC-zmflmo170114h08b1
Method
                   BLASTX
NCBI GI
                   g2499819
BLAST score
                   576
E value
                   2.0e-59
Match length
                   158
% identity
                   72
                   ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR
NCBI Description
                   >gi_2130068_pir__S66516 aspartic proteinase 1 precursor -
                   rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic
                   protease [Oryza sativa]
```

Seq. No. 307762 Seq. ID uC-zmflmo17011b04b1

Method BLASTX NCBI GI g2492504



BLAST score 448
E value 2.0e-44
Match length 110
% identity 42

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG

>gi 1669660 emb CAA70565 (Y09396) protein of AAA family

2.4%

[Capsicum annuum]

Seq. No. 307763

Seq. ID uC-zmflmo17011c10b1

Method BLASTX
NCBI GI g2506470
BLAST score 583
E value 2.0e-60
Match length 125
% identity 85

NCBI Description ALPHA-1,4 GLUCAN PHOSPHORYLASE, L ISOFORM PRECURSOR (STARCH

PHOSPHORYLASE L) >gi 1616637 emb CAA85354 (Z36880)

alpha-1,4 Glucan Phosphorylase, L isoform precursor [Vicia

faba]

Seq. No. 307764

Seq. ID uC-zmflmo17011f11b1

Method BLASTX
NCBI GI g2262111
BLAST score 172
E value 3.0e-12
Match length 73
% identity 51

NCBI Description (AC002343) ribitol dehydrogenase isolog [Arabidopsis

thaliana]

Seq. No. 307765

Seq. ID uC-zmflmo17011f12b1

Method BLASTX
NCBI GI g1890575
BLAST score 232
E value 2.0e-19
Match length 101
% identity 48

NCBI Description (X93174) xyloglucan endotransglycosylase (XET) [Hordeum

vulgare]

Seq. No. 307766

Seq. ID uC-zmflmo17011g01b1

Method BLASTN
NCBI GI g6598437
BLAST score 33
E value 3.0e-09
Match length 57
% identity 89

NCBI Description Arabidopsis thaliana chromosome II BAC F13M22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 307767

Seq. ID uC-zmflmo17011g07a1

Method BLASTX

```
g4206306
NCBI GI
BLAST score
                  346
E value
                  5.0e-33
Match length
                  90
% identity
                  76
NCBI Description (AF049110) prpol [Zea mays]
                  307768
Seq. No.
                  uC-zmflmo17011q12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g399942
BLAST score
                  553
E value
                  6.0e-57
Match length
                  119
% identity
                  91
NCBI Description
                  CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN
                  PRECURSOR >gi 421881 pir S32818 heat shock protein, 70K,
                  chloroplast - garden pea >gi 169023 (L03299) 70 kDa heat
                  shock protein [Pisum sativum] >gi 871515_emb_CAA49147
                  (X69213) Psst70 (stress 70 protein) [Pisum sativum]
Seq. No.
                  307769
Seq. ID
                  uC-zmflmo17011h02b1
Method
                  BLASTX
NCBI GI
                  g4204265
BLAST score
                 ~.171
E value
                  2.0e-12
Match length
                  65
% identity
                  57
NCBI Description
                  (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                  307770
                  uC-zmflmo17012a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417360
BLAST score
                  200
E value
                  1.0e-15
Match length
                  106
% identity
                  42
NCBI Description
                  HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2
                  >gi_2131280 pir S67767 high mobility group-like protein
                  NHP2 - yeast (Saccharomyces cerevisiae)
                  >gi_666101_emb_CAA40885_ (X57714) high mobility group-like
                  nuclear protein 2 [Saccharomyces cerevisiae]
                  >gi 1429348 emb CAA67483 (X99000) high-mobility-group-like
                  protein [Saccharomyces cerevisiae]
                  >gi 1431346 emb CAA98786 (Z74256) ORF YDL208w
                  [Saccharomyces cerevisiae]
```

Seq. ID uC-zmflmo17012a07b1

Method BLASTX NCBI GI g3858935 BLAST score 148 E value 4.0e-19 Match length 118 % identity 53



NCBI Description (AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No. 307772

Seq. ID uC-zmflmo17013b02b1

Method BLASTN
NCBI GI g257040
BLAST score 64
E value 1.0e-27
Match length 88
% identity 93

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 307773

Seq. ID uC-zmflmo17015e04b1

Method BLASTX
NCBI GI g479413
BLAST score 160
E value 5.0e-22
Match length 132
% identity 55

NCBI Description myosin-like protein - Arabidopsis thaliana

Seq. No. 307774

Seq. ID uC-zmflmo17016d07a1

Method BLASTX
NCBI GI g2842482
BLAST score 161
E value 6.0e-11
Match length 44
% identity 75

NCBI Description (AL021749) protein phosphatase 2C-like protein [Arabidopsis

thaliana]

Seq. No. 307775

Seq. ID uC-zmflmo17017a05b1

Method BLASTX
NCBI GI g4218014
BLAST score 242
E value 2.0e-20
Match length 51
% identity 92

NCBI Description (AC006135) putative spliceosomal protein (RNA binding

protein) [Arabidopsis thaliana]

Seq. No. 307776

Seq. ID uC-zmflmo17017b04b1

Method BLASTX
NCBI GI g4416302
BLAST score 484
E value 7.0e-49
Match length 134
% identity 73

NCBI Description (AF105716) copia-type pol polyprotein [Zea mays]

```
Seq. No.
                   307777
Seq. ID
                  uC-zmflmo17017c03b1
Method
                  BLASTX
NCBI GI
                   q2244866
BLAST score
                   148
E value
                   1.0e-10
Match length
                   108
% identity
                   39
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  uC-zmflmo17017c06b1
Method
                  BLASTX
NCBI GI
                  q435942
BLAST score
                   162
E value
                   4.0e-11
Match length
                  44
% identity
                   66
NCBI Description
                  (U04295) DNA-binding factor of bZIP class [Oryza sativa]
Seq. No.
                  307779
Seq. ID
                  uC-zmflmo17017d02b1
Method
                  BLASTX
NCBI GI
                  q4586401
BLAST score
                  168
E value
                  8.0e-12
Match length
                  121
% identity
NCBI Description (D88208) hSgt1p [Homo sapiens]
                  307780
Seq. No.
Seq. ID
                  uC-zmflmo17017d05b1
Method
                  BLASTX
NCBI GI
                  g2129559
BLAST score
                  223
                 , 3.0e-18
E value
Match length
                  63
                  79
% identity
                  cellulase homolog OR16pep - Arabidopsis thaliana
NCBI Description
                  >gi 1022807 (U37702) cellulase [Arabidopsis thaliana]
                  >gi 3493633 (AF074092) cellulase [Arabidopsis thaliana]
                  >gi 3598956 (AF074375) cellulase [Arabidopsis thaliana]
                  >gi 3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
                   [Arabidopsis thaliana]
Seq. No.
                  307781
Seq. ID
                  uC-zmflmo17017d10b1
Method
                  BLASTX
NCBI GI
                  g2369766
BLAST score
                  309
                  2.0e-28
E value
Match length
                  113
% identity
NCBI Description
                 (AJ001304) hypothetical protein [Citrus x paradisi]
```

Seq. ID uC-zmflmo17017h06b1

307782

Seq. No.

E value

Match length

7.0e-28

70

```
BLASTX
Method
NCBI GI
                  q2832686
BLAST score
                   255
                   2.0e-23
E value
Match length
                  81
                  72
% identity
NCBI Description
                  (AL021712) putative protein [Arabidopsis thaliana]
                 5 307783
Seq. No.
                  uC-zmflmo17017h07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                   34
                   9.0e-10
E value
Match length
                   34
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   307784
                  uC-zmflmo17018a10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4008008
BLAST score
                   211
E value
                   8.0e-17
Match length
                   122
% identity
                   39
                   (AF084035) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   307785
Seq. No.
                   uC-zmflmo17019c01a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g717080
BLAST score
                   73
E value
                   9.0e-33
Match length
                   224
% identity
                   84
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase (GapC4)
NCBI Description
                   gene, promoter region
Seq. No.
                   307786
Seq. ID
                   uC-zmflmo17019f01a1
Method
                   BLASTN
NCBI GI
                   q902583
BLAST score
                   41
E value
                   6.0e-14
Match length
                   125
                   83
% identity
NCBI Description Zea mays clone MubG1 ubiquitin gene, complete cds
                   307787
Seq. No.
                   uC-zmflmo17020a06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2511531
BLAST score
                   304
```

141



% identity NCBI Description

(AF008120) alpha tubulin 1 [Eleusine indica]

>gi 3163944 emb CAA06618 (AJ005598) alpha-tubulin 1

[Eleusine indica]

307788 Seq. No.

uC-zmflmo17020c02b1 Seq. ID

Method BLASTX NCBI GI g1235565 BLAST score 316 E value 4.0e-29 Match length 108 % identity 64

NCBI Description (X96681) DNA-binding protein [Oryza sativa]

Seq. No.

307789 uC-zmflmo17020c04b1 Seq. ID

BLASTX Method NCBI GI q4104929 BLAST score 501 9.0e-51 E value 133

Match length % identity 73

NCBI Description (AF042195) auxin response factor 7 [Arabidopsis thaliana]

307790 Seq. No.

Seq. ID uC-zmflmo17020d03b1

BLASTX Method NCBI GI g266578 BLAST score 259 2.0e-22 E value Match length 56 % identity 82

NCBI Description METALLOTHIONEIN-LIKE PROTEIN 1 >gi 100898 pir S17560

metallothionein-like protein - maize >gi_236730_bbs_57629 (S57628) metallothionein homologue [Zea mays, Peptide, 76

aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186)

metallothionein- like protein [Zea mays]

>gi_228095_prf__1717215A metallothionein-like protein [Zea

mays]

Seq. No. 307791

Seq. ID uC-zmflmo17020e07a1

Method BLASTN NCBI GI q736358 BLAST score 87 E value 2.0e-41 Match length 125 % identity 93

NCBI Description Zea mays cell wall invertase mRNA, complete cds

307792 Seq. No.

uC-zmflmo17020f06a1 Seq. ID

Method BLASTX NCBI GI q629844 BLAST score 254 E value 6.0e-22



Match length 66 % identity 79

NCBI Description heat shock protein hsp70-5 - maize (fragment)

>gi 498775 emb CAA55184 (X78415) heat shock protein 70 kDa

[Zea mays]

Seq. No. 307793

Seq. ID uC-zmflmo17020f09b1

Method BLASTX
NCBI GI g585338
BLAST score 424
E value 7.0e-42
Match length 106
% identity 75

NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)

>gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza

J. -

satīva]

Seq. No. 307794

Seq. ID uC-zmflmo17020f12b1

Method BLASTX
NCBI GI g4581164
BLAST score 236
E value 1.0e-19
Match length 136
% identity 40

NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No. 307795

Seq. ID uC-zmflmo17020g07b1

Method BLASTX
NCBI GI g282994
BLAST score 395
E value 2.0e-38
Match length 87
% identity 79

NCBI Description Sipl protein - barley >gi_167100 (M77475) seed imbibition

protein [Hordeum vulgare]

Seq. No. 307796

Seq. ID uC-zmflmo17020g10a1

Method BLASTN
NCBI GI g3695004
BLAST score 195
E value 1.0e-106
Match length 259
% identity 99

NCBI Description Zea mays pyruvate dehydrogenase kinase isoform 2 mRNA,

nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 307797

Seq. ID uC-zmflmo17020h08b1

Method BLASTN
NCBI GI g3004949
BLAST score 137
E value 5.0e-71
Match length 253

```
% identity
                  Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,
NCBI Description
                  complete cds
                  307798
Seq. No.
Seq. ID
                  uC-zmflmo17021b05b1
Method
                  BLASTX
NCBI GI
                  q4567197
BLAST score
                  179
E value
                  4.0e-13
Match length
                  128
% identity
                  36
NCBI Description
                  (AC007168) unknown protein [Arabidopsis thaliana]
                  307799
Seq. No.
Seq. ID
                  uC-zmflmo17021c11b1
Method
                  BLASTX
NCBI GI
                  g4104931
BLAST score
                  295
E value
                  1.0e-26
Match length
                  65
% identity
                  82
NCBI Description
                  (AF042196) auxin response factor 8 [Arabidopsis thaliana]
                  307800
                  uC-zmflmo17021d11b1
                  BLASTX
                  q3821793
                  187
                  5.0e-14
                  36
```

Seq. No. Seq. ID Method

NCBI GI BLAST score E value Match length 100 % identity

NCBI Description (Y11526) casein kinase II alpha subunit [Zea mays]

Seq. No. 307801 Seq. ID

uC-zmflmo17021q07b1

Method BLASTX g1203832 NCBI GI BLAST score 334 E value 4.0e-31 Match length 137 % identity 87

NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII

[Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan

exohydrolase [Hordeum vulgare]

Seq. No. 307802

Seq. ID uC-zmflmo17021h02b1

BLASTX Method NCBI GI q1890575 BLAST score 202 7.0e-16 E value 58 Match length 64 % identity

(X93174) xyloglucan endotransglycosylase (XET) [Hordeum NCBI Description

vulgare]



Seq. No. 307803

Seq. ID uC-zmflmo17021h10b1

Method BLASTX NCBI GI g3176687 BLAST score 276 E value 1.0e-24 Match length 106 % identity 51

NCBI Description (AC003671) Strong similarity to trehalose-6-phosphate

synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

307804 Seq. No.

Seq. ID uC-zmflmo17021h12b1

Method BLASTN NCBI GI g257040 BLAST score 76 8.0e-35 E value Match length 151 % identity

hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt] NCBI Description

Seq. No. 307805

uC-zmflmo17022a02b1 Seq. ID

Method BLASTN q4007864 NCBI GI 286 BLAST score E value 1.0e-160 386 Match length

37 % identity

Zea mays HRGP gene, AC1503 line NCBI Description

Seq. No. 307806

Seq. ID uC-zmflmo17022c12a1

Method BLASTN NCBI GI q4140643 BLAST score 265 E value 1.0e-147 Match length 461 % identity

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

307807 Seq. No.

Seq. ID uC-zmflmo17022d07b1

Method BLASTX NCBI GI q422248 BLAST score 343 3.0e-32 E value Match length 102 % identity 15

ubiquitin - basidiomycete (Phanerochaete chrysosporium) NCBI Description

>gi 395056 emb CAA80851 (Z24723) ubiquitin [Phanerochaete

chrysosporium]

Seq. No. 307808

```
uC-zmflmo17022f05b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4185305
BLAST score
                  103
                  1.0e-50
E value
                  179
Match length
                  90
% identity
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
                  307809
Seq. No.
                  uC-zmflmo17022f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2655098
BLAST score
                  300
                  5.0e-30
E value
Match length
                  81
% identity
                  81
```

NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

307810 Seq. No. uC-zmflmo17023a05b1 Seq. ID Method BLASTX NCBI GI g445¥470 BLAST score 148 E value 2.0e-09 Match length 91 41 % identity

(AC006234) putative sugar transporter [Arabidopsis NCBI Description

thaliana]

307811 Seq. No.

uC-zmflmo17023a07b1 Seq. ID

Method BLASTX g4455324 NCBI GI BLAST score 202 1.0e-15 E value Match length 54 % identity 57

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

307812 Seq. No.

Seq. ID uC-zmflmo17023b01b1

Method BLASTX g2191175 NCBI GI BLAST score 421 E value 2.0e-41 102 Match length % identity 73

NCBI Description (AF007270) A_IG002P16.24 gene product [Arabidopsis

thaliana]

Seq. No. 307813

Seq. ID uC-zmflmo17023c06b1

Method BLASTX

43725

```
g1019946
NCBI GI
BLAST score
                  321
E value
                  1.0e-29
Match length
                  69
                  87
% identity
                  (U37060) ascorbate peroxidase [Gossypium hirsutum]
NCBI Description
                  307814
Seq. No.
                  uC-zmflmo17023d03b1
Seq. ID
                  BLASTX
Method
                  g4102839
NCBI GI
BLAST score
                  438
                  3.0e-43
E value
                  109
Match length
% identity
                  72
NCBI Description
                  (AF016713) LeOPT1 [Lycopersicon esculentum]
                  307815
Seq. No.
                  uC-zmflmo17023g10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4190952
BLAST score
                  271
E value
                  8.0e-24
Match length
                  92
% identity
                  51
NCBI Description
                  (AB022689) similar to hsr203J [Lycopersicon esculentum]
Seq. No.
                  307816
Seq. ID
                  uC-zmflmo17023g12b1
Method
                  BLASTX
NCBI GI
                  q4559356
BLAST score
                  146
                  4.0e-09
E value
Match length
                  126
% identity
                  27
NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  307817
                  uC-zmflmo17024b03a1
Seq. ID
Method
                  BLASTX
                  g2660670
NCBI GI
BLAST score
                  203
E value
                  5.0e-16
Match length
                  64
% identity
                  61
NCBI Description
                  (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
                  thaliana]
                  307818
Seq. No.
Seq. ID
                  uC-zmflmo17024b10a1
Method
                  BLASTN
NCBI GI
                  q22229
BLAST score
                  41
E value
                  7.0e-14
Match length
                  181
% identity
                  79
```

NCBI Description Z.mays cab-m7 gene for light harvesting chlorophyll a/b

NCBI Description



binding protein

```
Seq. No.
                   307819
Seq. ID
                   uC-zmflmo17027e09a1
Method
                   BLASTX
NCBI GI
                   q1711355
BLAST score
                   296
E value
                   8.0e-27
Match length
                   98
% identity
                   59
NCBI Description
                   SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE
                   >gi_421786_pir__S34678 short-chain alcohol dehydrogenase -
                   Norway spruce >gi_395223_emb_CAA52213_ (X74115) short-chain
                   alcohol dehydrogenase [Picea abies]
Seq. No.
                   307820
Seq. ID
                   uC-zmflmo17027h03a1
Method
                   BLASTN
NCBI GI
                   g22212
BLAST score
                   38
E value
                   6.0e-12
Match length
                  70
% identity
                   89
NCBI Description
                  Z.mays DNA for c1 locus
Seq. No.
                  307821
Seq. ID
                  uC-zmflmo17028d04a1
Method
                  BLASTX
NCBI GI
                  g3548810
BLAST score
                  175
E value
                  8.0e-13
Match length
                  69
% identity
                  51
NCBI Description
                  (AC005313) putative chloroplast nucleoid DNA binding
                  protein [Arabidopsis thaliana]
Seq. No.
                  307822
Seq. ID
                  uC-zmflmo17029a09b1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  274
E value
                  2.0e-24
                                                                       *
Match length
                  82
% identity
                  68
NCBI Description
                  PHENYLALANINE AMMONIA-LYASE >gi 295824_emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  307823
Seq. ID
                  uC-zmflmo17029a12b1
Method
                  BLASTX
NCBI GI
                  g498643
BLAST score
                  470
E value
                  3.0e-47
Match length
                  82
% identity
```

(U10270) G-box binding factor 1 [Zea mays]

```
307824
Seq. No.
                  uC-zmflmo17029b03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1532072
BLAST score
                  48
                  6.0e-18
E value
Match length
                 `152
% identity
                  83
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase
                  307825
Seq. No.
                  uC-zmflmo17029b12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  307826 .
                  uC-zmflmo17029c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913427
BLAST score
                  309
E value
                  6.0e-32
Match length
                  134
% identity
                  57
NCBI Description
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                  (SAMDC) >gi 1532073 emb CAA69075 (Y07767)
                  S-adenosylmethionine decarboxylase [Zea mays]
                  307827
Seq. No.
                  uC-zmflmo17029d10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4160401
BLAST score
                  62
                  3.0e-26
E value
Match length
                  66
% identity
                  98
NCBI Description
                  Zea mays eIF-5 gene, exons 1-2
                  307828
Seq. No.
                  uC-zmflmo17029f02b1
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI 9421845
BLAST score 500
E value 9.0e-51
Match length 115
% identity 86

NCBI Description RecA homolog - Arabidopsis thaliana (fragment) >gi 166841

(M98039) replicase [Arabidopsis thaliana]

Seq. No. 307829

Seq. ID uC-zmflmo17029g08b1

Method BLASTX NCBI GI g1143705

```
BLAST score
                   3.0e-52
E value
Match length
                   122
% identity
                   51
NCBI Description
                  (X89760) Hox2a [Zea mays]
Seq. No.
                   307830
                   uC-zmflmo17029h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4204859
BLAST score
                   261
E value
                   8.0e-23
Match length
                   84
                   67
% identity
NCBI Description
                  (U55859) heat shock protein 80 [Triticum aestivum]
Seq. No.
                   307831
Seq. ID
                   uC-zmflmo17030c02b1
Method
                   BLASTX
NCBI GI
                   q3096949
BLAST score
                   347
E value
                   1.0e-32
Match length
                   107
                   63
% identity
                   (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana] >gi 3894399 (AF067798) cyclic
                   nucleotide-gated cation channel [Arabidopsis thaliana]
Seq. No.
                   307832
Seq. ID
                   uC-zmflmo17030c06b1
Method
                   BLASTN
NCBI GI
                   g22466
BLAST score
                   96
E value
                   2.0e-46
Match length
                   119
% identity
                   48
NCBI Description Zea mays rcy: Mu7 Cy transposable element system
                   307833
Seq. No.
                   uC-zmflmo17030e01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1313909
BLAST score
                   182
                   2.0e-13
E value
Match length
                   66
% identity
                   58
                  (D84508) CDPK-related protein kinase [Zea mays]
NCBI Description
                   307834
Seq. No.
                   uC-zmflmo17030e02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g728863
BLAST score
                   633
                   3.0e-66
E value
Match length
                   128
% identity
                   93
```

-segar

43729

NCBI Description LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN

HYDROXYLASE) >gi_100871_pir__ S12043 gene A2 protein - maize >gi_22104_emb_CAA39022_ (X55314) A2 [Zea mays]

in the

Seq. No. 307835 Seq. ID 11C-zmf

Seq. ID uC-zmflmo17030e08b1 Method BLASTX

NCBI GI g3377836
BLAST score 170
E value 7.0e-12
Match length 80
% identity 40

NCBI Description (AF075598) contains similarity to reverse transcriptases

[Arabidopsis thaliana]

Seq. No. 307836

Seq. ID uC-zmflmo17030f01b1

Method BLASTX
NCBI GI g3775993
BLAST score 284
E value 3.0e-25
Match length 72
% identity 75

NCBI Description (AJ010460) RNA helicase [Arabidopsis thaliana]

Seq. No. 307837

Seq. ID uC-zmflmo17030g05b1

Method BLASTX
NCBI GI g1084454
BLAST score 144
E value 1.0e-09
Match length 86
% identity 50

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp1 - rice

>gi_600765 (L29471) cyclophilin 1 [Oryza sativa]

Seq. No. 307838

Seq. ID uC-zmflmo17030h09b1

Method BLASTX
NCBI GI g4558484
BLAST score 207
E value 3.0e-18
Match length 75
% identity 71

NCBI Description (AF097363) heat shock protein 101 [Triticum aestivum]

Seq. No. 307839

Seq. ID uC-zmflmo17030h12b1

Method BLASTX
NCBI GI g2511541
BLAST score 547
E value 4.0e-56
Match length 145
% identity 77

NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]

Seq. No. 307840

Seq. ID uC-zmflmo17031a05b1

43730



```
BLASTX
Method
                   q3075394
NCBI GI
BLAST score
                   174
E value
                   1.0e-12
Match length
                   55
                   62
% identity
```

NCBI Description (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead

protein [Arabidopsis Thaliana]

Seq. No. 307841

Seq. ID uC-zmflmo17031b05b1

Method BLASTX NCBI GI q2668744 BLAST score 158 E value 7.0e-11 Match length 41 76 % identity

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No. 307842

uC-zmflmo17031c07b1 Seq. ID

Method BLASTX g123656 NCBI GI BLAST score 438 E value 1.0e-43 Match length 107 80

% identity

NCBI Description CHLOROPLAST ENVELOPE MEMBRANE 70 KD HEAT SHOCK-RELATED PROTEIN >gi 285407 pir A42582 heat shock protein SCE70 -

spinach >gi_21338 emb_CAA43711 (X61491) 70 kDa heat shock

protein [Spinacia oleracea]

Seq. No. 307843

Seq. ID uC-zmflmo17031d08b1

Method BLASTX NCBI GI g4510383 BLAST score 165 E value 2.0e-11 Match length 51 % identity 65

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 307844

Seq. ID uC-zmflmo17031g10b1

Method BLASTN NCBI GI q4007864 BLAST score 95 E value 5.0e-46 Match length 263 % identity

NCBI Description Zea mays HRGP gene, AC1503 line

Seq. No. 307845

Seq. ID uC-zmflmo17031g12b1

Method BLASTX NCBI GI g3337350



```
BLAST score
E value
                  1.0e-31
Match length
                  142
% identity
                  50
NCBI Description
                  (AC004481) putative permease [Arabidopsis thaliana]
Seq. No.
                  307846
Seq. ID
                  uC-zmflmo17031h11b1
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  172
E value
                  3.0e-12
Match length
                  50
% identity
                  74
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi_226091_prf 1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  307847
Seq. ID
                  uC-zmflmo17033b08b2
Method
                  BLASTX
                  g120670
NCBI GI
BLAST score
                  147
E value
                  4.0e-14
Match length
                  60
% identity
                  88
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_100879_pir__S06879 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) C - maize
                  >gi_295853_emb_CAA33620 (X15596) GAPDH [Zea mays]
Seq. No.
                  307848
Seq. ID
                  uC-zmflmo17033b09a1
Method
                  BLASTN
NCBI GI
                  g2984708
BLAST score
                  38
                  4.0e-12
E value
Match length
                  54
                  93
% identity
NCBI Description
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
Seq. No.
                  307849
Seq. ID
                  uC-zmflmo17033b09b2
Method
                  BLASTX
```

% identity

NCBI GI g2984709 BLAST score 340 E value 3.0e-32 Match length 98

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 307850

Seq. ID uC-zmflmo17033c03b2

71



Method BLASTX
NCBI GI g1709619
BLAST score 306
E value 2.0e-28
Match length 86
% identity 72

NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /

DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE

(GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)

>gi_2146814_pir__S69181 protein disulfide isomerase (EC
5.3.4.1) precursor - maize >gi_625148 (L39014) protein

disulfide isomerase [Zea mays]

Seq. No. 307851

Seq. ID uC-zmflmo17033c08b2

Method BLASTX
NCBI GI g832876
BLAST score 277
E value 1.0e-29
Match length 83
% identity 83

NCBI Description (L41345) ascorbate free radical reductase [Solanum

lycopersicum] >gi_1097368_prf__2113407A ascorbate free

radical reductase [Lycopersicon esculentum]

Seq. No. 307852

Seq. ID uC-zmflmo17033c11b2

Method BLASTX
NCBI GI g3482967
BLAST score 177
E value 2.0e-13
Match length 66
% identity 50

NCBI Description (AL031369) Protein phosphatase 2C-like protein [Arabidopsis

thaliana] >qi 4559345 qb AAD23006.1 AC006585 1 (AC006585)

protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 307853

Seq. ID uC-zmflmo17033c12b2

Method BLASTX
NCBI GI g1946355
BLAST score 220
E value 3.0e-18
Match length 87
% identity 57

NCBI Description (U93215) maize transposon MuDR mudrA protein isolog

[Arabidopsis thaliana] >gi 2880040 (AC002340) maize

transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 307854

Seq. ID uC-zmflmo17033d07b2

Method BLASTX
NCBI GI g3292826
BLAST score 333
E value 4.0e-31
Match length 97
% identity 62

```
NCBI Description
                  (AL031018) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  307855
Seq. ID
                  uC-zmflmo17033d11b2
Method
                  BLASTX
NCBI GI
                  q4115377
BLAST score
                  164
E value
                  1.0e-11
Match length
                  78
% identity
NCBI Description
                  (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  307856
Seq. ID
                  uC-zmflmo17033e02b2
Method
                  BLASTN
NCBI GI
                  g1213278
BLAST score
                  39
E value
                  5.0e-13
Match length
                  75
% identity
                  88
NCBI Description
                  Z.mays ZEMb gene
Seq. No.
                  307857
Seq. ID
                  uC-zmflmo17033e03b2
Method
                  BLASTX
NCBI GI
                  q4006879
BLAST score
                  188
E value
                  9.0e-25
Match length
                  87
% identity
NCBI Description
                  (Z99707) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  307858
                  uC-zmflmo17034e08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171967
BLAST score
                  149
E value
                  1.0e-09
Match length
                  57
% identity
                  53
NCBI Description
                  P4-6 PROTEIN >gi 2137635 pir I48711 phosphodiesterase -
                  mouse >gi 467578 emb CAA49481 (X69827) phosphodiesterase
                  [Mus musculus]
                  307859
Seq. No.
```

uC-zmflmo17035a01b1 Seq. ID

Method BLASTN NCBI GI g22332 BLAST score 280 E value 1.0e-156 Match length 363 % identity 94

NCBI Description Z.mays HRGP gene

Seq. No. 307860

Seq. ID uC-zmflmo17035a02b1

Method BLASTN

43734

79.



```
NCBI GI
                   q22332
BLAST score
                   71
E value
                   1.0e-31
Match length
                   119
% identity
                   92
NCBI Description
                  Z.mays HRGP gene
                   307861
Seq. No.
```

Seq. ID uC-zmflmo17035a04b1 Method BLASTX NCBI GI g112994 BLAST score 428 E value 2.0e-42 Match length 85 % identity 99

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

> >>gi_82685 pir S04536 embryonic abundant protein, glycine-rich - maize >gi 22313 emb CAA31077 (X12564)

ABA-inducible gene protein [Zea mays]

>gi 226091 prf 1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 307862

Seq. ID uC-zmflmo17035b12b1

Method BLASTX NCBI GI g2129648 BLAST score 227 E value 8.0e-19 Match length 60 % identity 73

NCBI Description MYB-related protein 33,3K - Arabidopsis thaliana

>gi 1263095 emb CAA90809 (Z54136) MYB-related protein

[Arabidopsis thaliana]

Seq. No. 307863

Seq. ID uC-zmflmo17035d05b1

Method BLASTN NCBI GI g507770 BLAST score 66 E value 1.0e-28 Match length 234 % identity 88

NCBI Description Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete

Seq. No. 307864

Seq. ID uC-zmflmo17035f02b1

Method BLASTX NCBI GI q4538967 BLAST score 408 E value 7.0e-40 Match length 125 % identity 70

NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis

thaliana]

Seq. No. 307865

```
uC-zmflmo17036a02b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1053057
BLAST score
                  182
                  1.0e-13
E value
Match length
                  77
% identity
                  55
NCBI Description
                  (U38422) histone H3 [Triticum aestivum]
                  307866
Seq. No.
Seq. ID
                  uC-zmflmo17036a07b2
Method
                  BLASTX
NCBI GI
                  g2459445
BLAST score
                  195
                  7.0e-15
E value
Match length
                  89
                  47
% identity
NCBI Description
                  (AC002332) putative ribonucleoprotein [Arabidopsis
                  thaliana]
Seq. No.
                  307867
Seq. ID
                  uC-zmflmo17036c07b2
Method
                  BLASTX
NCBI GI
                  g3142298
BLAST score
                  249
E value
                  3.0e-21
                  126
Match length
% identity
                  42
NCBI Description
                  (AC002411) Strong similarity to protein SBT1 gb_X98929 from
                  Lycopersicum esculentum. [Arabidopsis thaliana]
Seq. No.
                  307868
Seq. ID
                  uC-zmflmo17036e12b2
Method
                  BLASTX
NCBI GI
                  q602292
BLAST score
                  144
E value
                  5.0e-14
Match length
                  111
% identity
                  46
NCBI Description
                  (U17987) RCH2 protein [Brassica napus]
                  307869
Seq. No.
Seq. ID
                  uC-zmflmo17036g01b2
                  BLASTN
                  g4140643
                  170
```

Method NCBI GI BLAST score E value 1.0e-90 Match length 190 97

NCBI Description

Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No.

% identity

307870

Seq. ID

uC-zmflmo17036g04b2

Method BLASTX NCBI GI g82426 BLAST score . 752



```
E value
                      3.0e-80
   Match length
                      155
   % identity
                      46
   NCBI Description
                      ubiquitin precursor - barley (fragment)
                      >gi 755763 emb CAA27751 (X04133) ubiquitin polyprecursor
                      (171 aa) [Hordeum vulgare]
                      307871
Seq. No.
   Seq. ID
                      uC-zmflmo17036h01a1
   Method
                      BLASTN
   NCBI GI
                      g22292
   BLAST score
                      94
                      9.0e-46
   E value
   Match length
                      110
   % identity
                      96
   NCBI Description
                     Z.mayş mRNA for glycine-rich protein
   Seq. No.
                      307872
                      uC-zmflmo17036h01b2
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      q82696
   BLAST score
                      365
   E value
                      4.0e-35
   Match length
                      80
   % identity
                      89
   NCBI Description
                      glycine-rich protein - maize >gi 22293 emb CAA43431
                      (X61121) glycine-rich protein [Zea mays]
   Seq. No.
                      307873
   Seq. ID
                      uC-zmflmo17036h07b2
   Method
                      BLASTX
   NCBI GI
                      g3236253
   BLAST score
                      164
   E value
                      3.0e-24
   Match length
                      112
   % identity
                      54
   NCBI Description
                      (AC004684) receptor-like protein kinase [Arabidopsis
                      thaliana]
   Seq. No.
                      307874
   Seq. ID
                      uC-zmflmo17036h09b2
   Method
                      BLASTX
                      g4585879
   NCBI GI
   BLAST score
                      170
   E value
                      5.0e-12
   Match length
                      131
   % identity
                      37
   NCBI Description
                      (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis
                      thaliana]
```

Seq. No. 307875 Seq. ID uC-zmflmo17037b09b1

Method BLASTN

NCBI GI g3821780 BLAST score 36 5.0e-11 E value Match length 36

```
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  307876
Seq. No.
                  uC-zmflmo17037c06b1
Seq. ID
Method
                  BLASTX
                  g1296805
NCBI GI
BLAST score
                  280
E value
                  8.0e-25
Match length
                  80
% identity
                  72
NCBI Description
                  (X90929) C-terminal peptidase of the D1 protein [Hordeum
                  vulgare]
                  307877
Seq. No.
Seq. ID
                  uC-zmflmo17037d03b1
Method
                  BLASTX
NCBI GI
                  g3004565
BLAST score
                  266
E value
                  1.0e-25
Match length
                  122
% identity
                  52
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  307878
Seq. ID
                  uC-zmflmo17037e09b1
Method
                  BLASTN
NCBI GI
                  g218121
BLAST score
                  58
E value
                  8.0e-24
Match length
                  154
                  84
% identity
NCBI Description Rice mRNA for U2 small nuclear RNA-associated B antigen
Seq. No.
                  307879
Seq. ID
                  uC-zmflmo17037f09b1
Method
                  BLASTX
NCBI GI
                  g2244965
BLAST score
                  227
E value
                  1.0e-18
Match length
                  119
                <u>√;</u> 50
% identity
NCBI Description (Z97340) unnamed protein product [Arabidopsis thaliana]
                  307880
Seq. No.
                  uC-zmflmo17038a11a1
Seq. ID
Method
                  BLASTX
```

NCBI GI g4539453 BLAST score 235 7.0e-20 E value Match length 63 % identity 63

NCBI Description (ALO49500) putative protein [Arabidopsis thaliana]

Seq. No. 307881

uC-zmflmo17038b05b1Seq. ID

Method BLASTX

43738

```
NCBI GI
                  a4097880
BLAST score
                  143
E value
                  5.0e-11
Match length
                  100
% identity
                  46
NCBI Description
                  (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  307882
Seq. ID
                  uC-zmflmo17038c03b1
Method
                  BLASTX
NCBI GI
                  g2827536
BLAST score
                  208
E value
                  2.0e-16
Match length
                  85
% identity
                  42
NCBI Description
                  (AL021633) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  307883
                  uC-zmflmo17038c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g138364
BLAST score
                  649
E value
                  4.0e-68
Match length
                  141
% identity
                  91
NCBI Description
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >qi 210812
                  (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  307884
Seq. ID
                  uC-zmflmo17038d04a1
Method
                  BLASTN
NCBI GI
                  g1906603
BLAST score
                  110
E value
                  6.0e-55
Match length
                  217
% identity
                  88
                  Zea mays ACCase gene, intron containing colonist1 and
NCBI Description
                  colonist2 retrotransposons and reverse transcriptase
                  pseudogene, complete sequence
Seq. No.
                  307885
Seq. ID
                  uC-zmflmo17038d04b1
Method
                  BLASTX
NCBI GI
                  q2735008
BLAST score
                  385
                  2.0e-37
```

E value Match length 114

NCBI Description (U81960) kinase associated protein phosphatase [Zea mays]

Seq. No. Seq. ID

% identity

uC-zmflmo17038d06a1

307886

Method BLASTN NCBI GI g22192 BLAST score 38



```
E value
                   4.0e-12
Match length
                  54
% identity
                  93
NCBI Description Z.mays B-I gene for B transcriptional activator
                  307887
Seq. No.
Seq. ID
                  uC-zmflmo17038e10a1
Method
                  BLASTX
NCBI GI
                  g3212866
BLAST score
                  166
E value
                  1.0e-11
Match length
                  73
% identity
                  45
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  307888
Seq. ID
                  uC-zmflmo17038f02b1
Method
                  BLASTX
NCBI GI
                  q138364
BLAST score
                  289
E value
                  5.0e-26
Match length
                  108
% identity
                  56
NCBI Description
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (stratn Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  307889
Seq. ID
                  uC-zmflmo17038g08b1
Method
                  BLASTX
NCBI GI
                  g3287695
BLAST score
                  616
E value
                  3.0e-64
Match length
                  154
% identity
                  78
NCBI Description
                  (AC003979) Similar to hypothetical protein C34B7.2
                  gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis
                  thaliana]
Seq. No.
                  307890
Seq. ID
                  uC-zmflmo17038g10b1
Method
                  BLASTX
NCBI GI
                  g138364
BLAST score
                  390
E value
                  3.0e-43
Match length
                  125
% identity
                  77
```

NCBI Description

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

. F.

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No.

307891

Seq. ID

uC-zmflmo17038g11b1

BLASTX g3176714

Method NCBI GI



BLAST score 272 E value 5.0e-24 Match length 108 % identity 55

NCBI Description (AC002392) putative tRNA-splicing endonuclease positive effector [Arabidopsis thaliana]

Seq. No. 307892

Seq. ID uC-zmflmo17038g12a1

Method BLASTN
NCBI GI 9758354
BLAST score 41
E value 3.0e-14
Match length 65
% identity 91

NCBI Description Z.mays mRNA for plasma membrane H+ ATPase

Seq. No. 307893

Seq. ID uC-zmflmo17038g12b1

Method BLASTX
NCBI GI g2641619
BLAST score 283 E value 2.0e-25
Match length 86
% identity 64

NCBI Description (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea

mays]

Seq. No. 307894

Seq. ID uC-zmflmo17039a04b1

Method BLASTX
NCBI GI g4544457
BLAST score 267
E value 3.0e-23
Match length 68
% identity 74

NCBI Description (AC006592) putative MADS box protein [Arabidopsis thaliana]

Seq. No. 307895

Seq. ID uC-zmflmo17039a10b1

Method BLASTX
NCBI GI g3319340
BLAST score 143
E value 6.0e-09
Match length 121
% identity 34

NCBI Description (AF077407) contains similarity to E. coli cation transport

protein ChaC (GB:D90756) [Arabidopsis thaliana]

Seq. No. 307896

Seq. ID uC-zmflmo17039b08b1

Method BLASTX
NCBI GI g2444178
BLAST score 176
E value 6.0e-15
Match length 128
% identity 45





```
NCBI Description
                   (U94784) unconventional myosin [Helianthus annuus]
                   307897
Seq. No.
Seq. ID
                   uC-zmflmo17039d09b1
Method
                   BLASTX
NCBI GI
                   g3126967
BLAST score
                   510
E value
                   8.0e-52
Match length
                  136
                   13
% identity
NCBI Description
                  (AF061807) polyubiquitin [Elaeagnus umbellata]
Seq. No.
                   307898
                   uC-zmflmo17039d12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g266578
BLAST score
                   245
E value
                   1.0e-20
Match length
                   56
                   79
% identity
NCBI Description
                  METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir__$17560
                  metallothionein-like protein - maize >gi_236730 bbs 57629
                   (S57628) metallothionein homologue [Zea mays, Peptide, 76
                   aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186)
                  metallothionein- like protein [Zea mays]
                  >gi_228095_prf__1717215A metallothionein-like protein [Zea
                  mays]
Seq. No.
                   307899
Seq. ID
                   uC-zmflmo17039e11b1
Method
                   BLASTX
NCBI GI
                   g4544412
BLAST score
                   350
E value
                   5.0e-33
Match length
                  146
% identity
                   45
NCBI Description
                  (AC006955) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   307900
Seq. ID
                  uC-zmflmo17039f02b1
Method
                  BLASTX
NCBI GI
                   g129591
BLAST score
                   476
                                                    . .
E value
                   9.0e-48
Match length
                   121
% identity
                  79
NCBI Description
                  PHENYLALANINE AMMONIA-LYASE >gi_295824 emb CAA34226
                   (X16099) phenylalanine ammonia-Tyase [Oryza sativa]
Seq. No.
                  307901
Seq. ID
                  uC-zmflmo17039f05b1
Method
                  BLASTX
NCBI GI
                  g2996096
BLAST score
                  190
E value
                  2.0e-14
```

58

62

Match length % identity



```
NCBI Description
                   (AF030517) translation elongation factor-1 alpha; EF-1
                   alpha [Oryza sativa]
 Seq. No.
                   307902
 Seq. ID
                   uC-zmflmo17039h05b1
Method
                   BLASTX
NCBI GI
                   g3337356
BLAST score
                   170
E value
                   2.0e-17
Match length
                   85
% identity
                   67
NCBI Description
                   (AC004481) putative protein transport protein SEC61 alpha
                   subunit [Arabidopsis thaliana]
Seq. No.
                   307903
Seq. ID
                   uC-zmflmo17039h06b1
Method
                   BLASTX
NCBI GI
                   g2213643
BLAST score
                   214
E value
                   3.0e-17
Match length
                   67
% identity
                   61
                   (U57338) glossyl homolog [Oryza sativa]
NCBI Description
Seq. No.
                   307904
Seq. ID
                   uC-zmflmo17039h10b1
Method
                   BLASTX
NCBI GI
                   g3337356
BLAST score
                   292
E value
                   3.0e-36
Match length
                   101
% identity
                   82
NCBI Description
                   (AC004481) putative protein transport protein SEC61 alpha
                   subunit [Arabidopsis thaliana]
Seq. No.
                   307905
Seq. ID
                   uC-zmflmo17040b08b1
Method
                   BLASTX
NCBI GI
                   g2809246
BLAST score
                   283
E value
                   4.0e-25
Match length
                   150
% identity
                   41
NCBI Description
                   (AC002560) F2401.15 [Arabidopsis thaliana]
Seq. No.
                   307906
Seq. ID
                   uC-zmflmo17040c05b1
Method
                   BLASTX
NCBI GI
                   g112994
BLAST score
                   271
E value
                   6.0e-24
Match length
                   81
```

% identity 72

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

> >gi_82685_pir_ S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb CAA31077 (X12564)

ABA-inducible gene protein [Zea mays]

43743



>gi_226091_prf__1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 307907

Seq. ID uC-zmflmo17040g03a1

Method BLASTN
NCBI GI g22174
BLAST score 69
E value 1.0e-30
Match length 89
% identity 94

NCBI Description Maize Aux311 gene for auxin-binding protein

Seq. No. 307908

Seq. ID uC-zmflmo17040h06b1

Method BLASTN
NCBI GI g22332
BLAST score 213
E value 1.0e-116
Match length 409
% identity 94

NCBI Description Z.mays HRGP gene

Seq. No. 307909

Seq. ID uC-zmflmo17041a05b1

Method BLASTX
NCBI GI g4510363
BLAST score 222
E value 2.0e-18
Match length 85

% identity 56
NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 307910

Seq. ID uC-zmflmo17041b01b1

Method BLASTX
NCBI GI g3746059
BLAST score 145
E value 3.0e-09
Match length 66
% identity 47

NCBI Description (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis

thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative

cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 307911

Seq. ID uC-zmflmo17041b08b1

Method BLASTX
NCBI GI g4538939
BLAST score 288
E value 7.0e-26
Match length 84
% identity 65

NCBI Description (AL049483) Col-O casein kinase I-like protein [Arabidopsis

thaliana]



```
Seq. No.
                   307912
Seq. ID
                   uC-zmflmo17041e12b1
Method
                   BLASTX
NCBI GI
                   g3688598
BLAST score
                   241
E value
                   3.0e-20
Match length
                   66
% identity
                 . 61
NCBI Description (AB009029) Cycloartenol Synthase [Panax ginseng]
Seq. No.
                   307913
Seq. ID
                   uC-zmflmo17041g02b1
Method
                   BLASTX
NCBI GI
                   g283051
BLAST score
                   156
E value
                   3.0e-10
Match length
                   80
% identity
                   51
NCBI Description
                  RNA-directed DNA polymerase (EC 2.7.7.49) - maize
                   transposon (fragment)
Seq. No.
                   307914
Seq. ID
                   uC-zmflmo17041g08b1
Method
                   BLASTN
NCBI GI
                   g1098664
BLAST score
                   43
Evalue
                   9.0e-15
Match length
                   107
% identity
                   85
NCBI Description Zea mays phytoene synthase (Y1) gene, complete cds
Seq. No.
                   307915
Seq. ID
                   uC-zmflmo17041h12b1
Method
                   BLASTX
NCBI GI
                   g1332579
BLAST score
                   445
E value
                   3.0e-44
Match length
                   116
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                   307916
Seq. ID
                   uC-zmflmo17042a08a1
Method
                   BLASTN
NCBI GI
                   g22275
BLAST score
                   62
E value
                   1.0e-26
Match length
                   143
% identity
                   85
NCBI Description Maize mRNA for ferritin (clone FM1)
Seq. No.
                   307917
Seq. ID
                  uC-zmflmo17042c08a1
```

Method BLASTN NCBI GI g4079797 BLAST score 35 E value 2.0e-10



Match length 59 % identity 90

NCBI Description Oryza sativa 23 kDa polypeptide of photosystem II mRNA,

complete cds

Seq. No. 307918

Seq. ID uC-zmflmo17042c10b1

Method BLASTX
NCBI GI g2252844
BLAST score 509
E value 1.0e-51
Match length 162
% identity 64

NCBI Description (AF013293) belongs to the cytochrome p450 family

[Arabidopsis thaliana]

Seq. No. 307919

Seq. ID uC-zmflmo17042g05b1

Method BLASTX
NCBI GI g3319208
BLAST score 197
E value 4.0e-15
Match length 70
% identity 63

NCBI Description (U68751) ubiquitin-carboxyl extension [Daucus carota]

Seq. No. 307920

Seq. ID uC-zmflmo17042g06b1

Method BLASTX
NCBI GI 94314378
BLAST score 157
E value 2.0e-10
Match length 62
% identity 55

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 307921

Seq. ID uC-zmflmo17042g12a1

Method BLASTN
NCBI GI g902583
BLAST score 123
E value 9.0e-63
Match length 297
% identity 83

NCBI Description Zea mays clone MubG1 ubiquitin gene, complete cds

Seq. No. 307922

Seq. ID uC-zmflmo17042h02a1

Method BLASTN
NCBI GI g22091
BLAST score 128
E value 8.0e-66
Match length 217
% identity 90

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 307923

```
Seq. ID
                   uC-zmflmo17042h04b1
Method
                   BLASTX
NCBI GI
                   a3163946
BLAST score
                   478
E value
                   4.0e-48
Match length
                   90
% identity
                   98
NCBI Description
                  (AJ005599) alpha-tubulin 1 [Eleusine indica]
Seq. No.
                   307924
Seq. ID
                   uC-zmflmo17043a06a1
Method
                   BLASTN
NCBI GI
                   q4160401
BLAST score
                   136
E value
                   2.0e-70
Match length
                   196
% identity
                   92
NCBI Description
                  Zea mays eIF-5 gene, exons 1-2
Seq. No.
                   307925
Seq. ID
                   uC-zmflmo17043b02b1
Method
                   BLASTX
NCBI GI
                   g3426064
BLAST score
                   229
E value
                   8.0e-19
Match length
                   128
% identity
                   41
NCBI Description
                   (AJ007588) monooxygenase [Arabidopsis thaliana]
                   >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2)
                   [Arabidopsis thaliana]
Seq. No.
                   307926
Seq. ID
                   uC-zmflmo17043c07b1
Method
                   BLASTN
NCBI GI
                   q3043528
BLAST score
                   175
                   8.0e-94
E value
Match length
                   299
% identity
                   91
NCBI Description
                  Zea mays mRNA for flavin containing polyamine oxidase (PAO)
                   307927
                  uC-zmflmo17043d07b1
                  BLASTN
                  g22169
```

Seq. No. Seq. ID Method NCBI GI BLAST score 59 2.0e-24 E value Match length 202

84

NCBI Description Maize nuclear ARS1 DNA autonomously replicating in yeast

Seq. No. 307928 Seq. ID uC-zmflmo17043e01b1 Method BLASTX NCBI GI g3135543 BLAST score 586

∘ 1.0e-60

% identity

E value



307929

```
Match length 141
% identity 81
NCBI Description (AF
```

Description (AF062393) aquaporin [Oryza sativa]

Seq. No. Seq. ID

uC-zmflmo17043h10b1

Method BLASTX
NCBI GI g3335355
BLAST score 582
E value 2.0e-60
Match length 120
% identity 27

NCBI Description (AC004512) Match to polyubiquitin DNA gb_L05401 from A.

thaliana. Contains insertion of mitochondrial NADH

dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene with an expressed insert. EST gb_AA586248 comes from this

region. [Arabi

Seq. No.

× 30

307930

Seq. ID uC-zmflmo17044a09a1

Method BLASTX
NCBI GI g2618691
BLAST score 394
E value 3.0e-38
Match length 113
% identity 62

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 307931

Seq. ID uC-zmflmo17044b08b1

Method BLASTX
NCBI GI g3738324
BLAST score 194
E value 8.0e-15
Match length 75
% identity 47

NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No. 307932

Seq. ID uC-zmflmo17044d05b1

Method BLASTX
NCBI GI g2623301
BLAST score 301
E value 3.0e-27
Match length 98
% identity 62

NCBI Description (AC002409) putative kinase [Arabidopsis thaliana]

Seq. No. 307933

Seq. ID uC-zmflmo17044e03b1

Method BLASTX
NCBI GI g113621
BLAST score 547
E value 4.0e-56
Match length 151
% identity 96



NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir_ ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850 emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf 1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 307934

Seq. ID uC-zmflmo17044e09b1

Method BLASTX
NCBI GI g4263704
BLAST score 152
E value 8.0e-10
Match length 83
% identity 40

NCBI Description (AC006223) putative sugar starvation-induced protein

[Arabidopsis thaliana]

Seq. No. 307935

Seq. ID uC-zmflmo17044f03a1

Method BLASTX
NCBI GI g2244799
BLAST score 166
E value 1.0e-11
Match length 121
% identity 30

NCBI Description (Z97336) carnitine racemase homolog [Arabidopsis thaliana]

Seq. No. 307936

Seq. ID uC-zmflmo17044f07b1

Method BLASTX
NCBI GI g3482974
BLAST score 549
E value 2.0e-56
Match length 138
% identity 80

NCBI Description (AL031369) ATP-dependent Clp proteinase-like protein

[Arabidopsis thaliana]

Seq. No. 307937

Seq. ID uC-zmflmo17044f08b1

Method BLASTX
NCBI GI 94587615
BLAST score 209
E value 2.0e-31
Match length 102
% identity 69

NCBI Description (AC006951) putative acyl-CoA synthetase [Arabidopsis

thaliana]

Seq. No. 307938

Seq. ID uC-zmflmo17044g02b1

Method BLASTX
NCBI GI g3212871
BLAST score 618
E value 2.0e-64
Match length 139



% identity 86
NCBI Description (AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No. 307939
Seq. ID uC-zmflmo17044h08b1
Method BLASTX
NCBI GI g4544403
BLAST score 183

BLAST score 183
E value 2.0e-13
Match length 60
% identity 55
NCBI Description (AC00704

NCBI Description (AC007047) putative glucan endo-1,3-beta-D-glucosidase

precursor [Arabidopsis thaliana]

Seq. No. 307940

Seq. ID uC-zmflmo17045a07b1

Method BLASTX
NCBI GI g2055374
BLAST score 308
E value 5.0e-28
Match length 66
% identity 89

NCBI Description (U29095) serine-threonine protein kinase [Triticum

aestivum]

Seq. No. 307941

Seq. ID uC-zmflmo17045b01b1

Method BLASTX
NCBI GI 94559342
BLAST score 277
E value 1.0e-24
Match length 61
% identity 85

NCBI Description (AC007087) putative copper methylamine oxidase [Arabidopsis

thaliana]

Seq. No. 307942

Seq. ID uC-zmflmo17045b02b1

Method BLASTX
NCBI GI g3643609
BLAST score 507
E value 2.0e-51
Match length 109
% identity 75

NCBI Description (AC005395) putative Cys3His zinc finger protein

[Arabidopsis thaliana]

Seq. No. 307943

Seq. ID uC-zmflmo17045b10b1

Method BLASTX
NCBI GI g4587533
BLAST score 238
E value 6.0e-20
Match length 77
% identity 58

NCBI Description (AC007060) EST gb AA721821 comes from this gene.



[Arabidopsis thaliana]

```
Seq. No.
                   307944
Seq. ID
                   uC-zmflmo17045d07a1
Method
                   BLASTN
NCBI GI
                   q4007864
BLAST score
                   92
E value
                   1.0e-44
Match length
                   123
% identity
                   94
NCBI Description Zea mays HRGP gene, AC1503 line
Seq. No.
                   307945
Seq. ID
                   uC-zmflmo17045d07b1
Method
                   BLASTN
NCBI GI
                   g22332
BLAST score
                   216
E value
                   1.0e-118
Match length
                   347
% identity
                   91
NCBI Description Z.mays HRGP gene
Seq. No.
                   307946
Seq. ID
                   uC-zmflmo17045d09a1
Method
                   BLASTN
NCBI GI
                   g22292
BLAST score
                   151·
E value
                   1.0e-79
Match length
                   260
% identity
                   90
NCBI Description Z.mays mRNA for glycine-rich protein
Seq. No.
                   307947
Seq. ID
                   uC-zmflmo17045e08b1
Method
                   BLASTX
                   g4585985
NCBI GI
BLAST score
                   379
E value
                   2.0e-36
Match length
                   156
% identity
                   47
                  (AC005287) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  307948
Seq. ID
                  uC-zmflmo17045e09b1
Method
                  BLASTN
NCBI GI
                  g4007864
BLAST score
                  243
E value
                  1.0e-134
Match length
                  309
% identity
                  98
NCBI Description Zea mays HRGP gene, AC1503 line
```

Ţ.,

Seq. No. 307949

Seq. ID uC-zmflmo17045e10b1

Method BLASTN NCBI GI g3851527 91

BLAST score

```
E value
                   2.0e-43
Match length
                   158
% identity
                   89
NCBI Description
                  Hordeum vulgare cultivar Bomi starch branching enzyme IIb
                   (sbeIIb) gene, nuclear gene encoding plastid protein,
Seq. No.
                  307950
Seq. ID
                  uC-zmflmo17045f02b1
Method
                  BLASTX
NCBI GI
                  g1360090
BLAST score
                  249
E value
                  1.0e-21
Match length
                  84
% identity
NCBI Description
                  (X95576) C1C-Nt1 [Nicotiana tabacum]
Seq. No.
                  307951
Seq. ID
                  uC-zmflmo17045f07b1
Method
                  BLASTX
NCBI GI
                  g170354
BLAST score
                  538
E value
                  3.0e-55
Match length
                  124
% identity
NCBI Description
                  (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
Seq. No.
                  307952
Seq. ID
                  uC-zmflmo17045g10b1
Method
                  BLASTX
NCBI GI
                  g4468992
BLAST score
                  260
E value
                  2.0e-22
Match length
                  87
% identity
                  55
NCBI Description
                  (AL035605) putative protein [Arabidopsis thaliana]
Seq. No.
                  307953
Seq. ID
                  uC-zmflmo17046a05b1
Method
                  BLASTX
                  g4584957
NCBI GI
BLAST score
                  564
E value
                  3.0e-58
Match length
                  123
% identity
                  95
NCBI Description
                  (AF077337) heat shock protein 101; 101 kDa heat shock
                  protein [Zea mays]
Seq. No.
                  307954
Seq. ID
                  uC-zmflmo17046b05b1
                  BLASTX
```

Method

NCBI GI g557472 BLAST score 191 E value 2.0e-14 Match length 123 % identity 41

NCBI Description (U15178) arabinosidase [Bacteroides ovatus]

```
Seq. No.
                   307955
Seq. ID
                   uC-zmflmo17046d06a1
Method
                   BLASTN
NCBI GI
                   g4160401
BLAST score
                   34
E value
                   2.0e-09
Match length
                   50
% identity
                   92
NCBI Description Zea mays eIF-5 gene, exons 1-2
Seq. No.
                  307956
Seq. ID
                  uC-zmflmo17046d09b1
Method
                  BLASTX
NCBI GI
                  g4588012
BLAST score
                  144
E value
                   4.0e-09
Match length
                   45
% identity
NCBI Description
                   (AF085717) putative callose synthase catalytic subunit
                   [Gossypium hirsutum]
Seq. No.
                  307957
Seq. ID
                  uC-zmflmo17046e06b1
Method
                  BLASTN
NCBI GI
                  g287829
BLAST score
                  53
E value
                  9.0e-21
Match length
                  220
% identity
                  88
NCBI Description Z.mays gene for polygalacturonase
Seq. No.
                  307958
Seq. ID
                  uC-zmflmo17046q10b1
Method
                  BLASTX
NCBI GI
                  g548774
BLAST score
                  175
E value
                  6.0e-13
Match length
                  81
% identity
                  51
NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal
                  protein L7a - rice >gi_303855_dbj_BAA02156 (D12631)
                  ribosomal protein L7A [Oryza sativa]
Seq. No.
                  307959
Seq. ID
                  uC-zmflmo17046h09b1
Method
                  BLASTX
                  g2344889
```

NCBI GI BLAST score 187 E value 1.0e-21 Match length 157 % identity 36

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.

307960

Seq. ID

uC-zmflmo17047f01a1

Method BLASTN



```
NCBI GI
                   g168490
BLAST score
                   41
                   7.0e-14
E value
Match length
                   121
% identity
                   83
NCBI Description
                  Maize glutathione S-transferase (GST-I) mRNA, complete cds
Seq. No. o
                   307961
Seq. ID
                   uC-zmflmo17048b02b1
Method
                   BLASTN
NCBI GI
                   g257040
BLAST score
                   115
E value
                   5.0e-58
Match length
                   235
% identity
                   87
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
Seq. No.
                   307962
Seq. ID
                   uC-zmflmo17048b09b1
Method
                   BLASTX
NCBI GI
                   g1906828
BLAST score
                  171
E value
                   2.0e-12
Match length
                   66
% identity
                   56
NCBI Description (Y11828) heat shock protein [Arabidopsis thaliana]
Seq. No.
                   307963
Seq. ID
                   uC-zmflmo17048b10b1
Method
                  BLASTN
                   g22332
NCBI GI
BLAST score
                   272
E value
                  1.0e-151
Match length
                   458
% identity
                   90
NCBI Description
                  Z.mays HRGP gene
Seq. No.
                   307964
Seq. ID
                  uC-zmflmo17048c02b1
Method
                  BLASTX
NCBI GI
                  q1800217
BLAST score
                   666
E value
                  5.0e-70
Match length
                  161
% identity
                  84
NCBI Description
                  (U56730) Phytochrome B [Sorghum bicolor]
Seq. No.
                  307965
Seq. ID
                  uC-zmflmo17048d01b1
Method
                  BLASTN
NCBI GI
                  g22332
BLAST score
                  291
E value
                  1.0e-163
Match length
                  397
% identity
                  93
```

NCBI Description Z.mays HRGP gene



```
Seq. No.
                   307966
Seq. ID
                   uC-zmflmo17048e01b1
Method
                   BLASTX
                   g2660677
NCBI GI
BLAST score
                   229
E value
                   8.0e-19
Match length
                   86
% identity
                   59
NCBI Description
                  (AC002342) unknown protein [Arabidopsis thaliana]
Seq. No.
                   307967
Seq. ID
                   uC-zmflmo17048e09b1
Method
                   BLASTN
NCBI GI
                   g949979
BLAST score
                   85
E value
                   7.0e-40
Match length
                   136
% identity
                   91
NCBI Description
                  Z.mays Glossy2 locus DNA
                   307968
Seq. No.
Seq. ID
                   uC-zmflmo17048g02b1
Method
                   BLASTN
NCBI GI
                   g1906603
                   136
BLAST score
E value
                   3.0e-70
Match length
                   332
% identity
                   85
NCBI Description
                   Zea mays ACCase gene, intron containing colonist1 and
                   colonist2 retrotransposons and reverse transcriptase
                   pseudogene, complete sequence
Seq. No.
                   307969
Seq. ID
                   uC-zmflmo17048g11b1
Method
                   BLASTX
NCBI GI
                   g2773154
BLAST score
                   196
E value
                   5.0e-15
Match length
                   55
% identity
                   65
NCBI Description
                   (AF039573) abscisic acid- and stress-inducible protein
                   [Oryza sativa]
Seq. No.
                   307970
Seq. ID
                  uC-zmflmo17048h02b1
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                  149
E value
                  8.0e-22
Match length
                  83
% identity
                  72
```

NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_ (X61121) glycine-rich protein [Zea mays]

Seq. No.

307971

Seq. ID

uC-zmflmo17048h12b1

Method

BLASTX

```
NCBI GI
                   g1346957
BLAST score
                   197
E value
                   4.0e-15
Match length
                   67
% identity
                   66
NCBI Description
                  RAS-RELATED PROTEIN RAB-2-B >gi 722328 (U22433) GTP binding
                   protein [Zea mays]
Seq. No.
                   307972
Seq. ID
                   uC-zmflmo17049c03a1
Method
                   BLASTN
NCBI GI
                   g949979
BLAST score
                   44
E value
                   1.0e-15
Match length
                   104
% identity
                   86
NCBI Description . Z.mays Glossy2 locus DNA
                   307973
Seq. No.
Seq. ID
                   uC-zmflmo17050b09b2
                  BLASTX 🥳
Method
NCBI GI
                   q1076746
BLAST score
                   589
E value
                   3.0e-61
Match length
                   118
% identity
                   96
                  heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                  307974
Seq. ID
                  uC-zmflmo17050b11b2
Method
                  BLASTX
NCBI GI
                  g3176690
BLAST score
                  164
E value
                  1.0e-17
Match length
                  93
% identity
                  57
NCBI Description
                  (AC003671) Similar to ubiquitin ligase gb D63905 from S.
                  cerevisiae. EST gb_R65295 comes from this gene.
                   [Arabidopsis thaliana]
                  307975
Seq. No.
Seq. ID
                  uC-zmflmo17050c06b2
Method
                  BLASTX
NCBI GI
                  g4378875
BLAST score
                  556
E value
                  3.0e-57
                  123
                  82
NCBI Description
                  (AF124360) delta-12 desaturase [Brassica carinata]
```

Match length % identity

Seq. No. Seq. ID

307976

uC-zmflmo17050c10b2 Method BLASTX

NCBI GI g2498883 BLAST score 236

```
E value 8.0e-20
Match length 95
% identity 54
NCBI Description SPLICEO
```

CBI Description SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150)

>gi_1173905 (U41371) spliceosome associated protein [Homo

- ...

sapiens]

Seq. No. 307977

Seq. ID uC-zmflmo17050d11b2

Method BLASTN
NCBI GI g2921303
BLAST score 136
E value 2.0e-70
Match length 371
% identity 85

NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA,

complete cds

Seq. No. 307978

Seq. ID uC-zmflmo17050d12b2

Method BLASTX
NCBI GI g3927830
BLAST score 287
E value 1.0e-25
Match length 116
% identity 55

NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No. 307979

Seq. ID uC-zmflmo17050e04b2

Method BLASTX
NCBI GI g310317
BLAST score 205
E value 3.0e-16
Match length 88
% identity 56

NCBI Description (L19598) beta-tubulin [Oryza sativa]

Seq. No. 307980

Seq. ID uC-zmflmo17050e08b2

Method BLASTX
NCBI GI g1170937
BLAST score 347
E value 9.0e-33
Match length 142
% identity 56

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 307981

Seq. ID uC-zmflmo17050e11b2

Method BLASTX
NCBI GI g3236237
BLAST score 274
E value 3.0e-24

43757

₹,



```
Match length
                   96
% identity
                   58
NCBI Description
                   (AC004684) putative ribotol dehydrogenase [Arabidopsis
                   thaliana]
                   307982
Seq. No.
Seq. ID
                   uC-zmflmo17050f04b2
Method
                   BLASTX
NCBI GI
                   g18732
BLAST score
                   200
E value
                   2.0e-15
Match length
                   49
% identity
                   80
NCBI Description
                   (X52492) DNA-directed RNA polymerase [Glycine max]
Seq. No.
                   307983
Seq. ID
                   uC-zmflmo17050g12b2
Method
                   BLASTX
NCBI GI
                   q4101722
BLAST score
                   262
E value
                   9.0e-23
Match length
                   102
% identity
                   46
NCBI Description
                   (AF006602) histone deacetylase mHDA1 [Mus musculus]
Seq. No.
                   307984
Seq. ID
                   uC-zmflmo17050h07b2
Method
                   BLASTX
NCBI GI
                   q3834307
BLAST score
                   241
E value
                   3.0e-20
Match length
                   54
% identity
                   83
NCBI Description
                   (AC005679) Strong similarity to gene T10I14.120 gi 2832679
                   putative protein from Arabidopsis thaliana BAC gb \overline{\text{AL}}021712.
                   ESTs gb_N65887 and gb_N65627 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   307985
Seq. ID
                   uC-zmflmo17051a04b1
Method
                   BLASTX
NCBI GI
                   g2759997
BLAST score
                   260
E value
                   1.0e-22
Match length
                   80
% identity
                   76
NCBI Description
                  (AJ003134) fimbriata-associated protein [Citrus sinensis]
Seq. No.
                   307986
Seq. ID
                   uC-zmflmo17051b07b1
Method
                  BLASTN
NCBI GI
                   g4416300
```

Method BLASTN
NCBI GI g4416300
BLAST score 52
E value 3.0e-20
Match length 257
% identity 84

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster



region, complete sequence

```
Seq. No.
                   307987
Seq. ID
                   uC-zmflmo17051b11b1
Method
                   BLASTX
NCBI GI
                   g3695023
BLAST score
                   178
E value
                   4.0e-13
Match length
                   77
% identity
                   49
NCBI Description
                  (AF055850) unknown [Arabidopsis thaliana]
Seq. No.
                   307988
Seq. ID
                   uC-zmflmo17051c08b1
Method
                   BLASTN
                   g940880
NCBI GI
BLAST score
                   86
E value
                   1.0e-40
Match length
                   205
% identity
                   92
NCBI Description
                  Z.mays zag2 gene
Seq. No.
                   307989
                   uC-zmflmo17051d09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4105131
BLAST score
                   322
E value
                   3.0e-37
Match length
                   141
% identity
                   69
NCBI Description
                  (AF043539) ClpC protease [Spinacia oleracea]
Seq. No.
                   307990
Seq. ID
                   uC-zmflmo17051g09b1
Method
                   BLASTX
                   g4006829
NCBI GI
BLAST score
                   190
E value
                   2.0e-14
Match length
                   43
% identity
                   86
NCBI Description
                   (AC005970) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   307991
Seq. ID
                   uC-zmflmo17051h07b1
Method
                   BLASTX
NCBI GI
                   q1513298
BLAST score
                   167
E value
                   1.0e-11
Match length
                   117
% identity
                   35
NCBI Description (U66526) AbcA [Dictyostelium discoideum]
Seq. No.
                   307992
```

Seq. ID uC-zmflmo17052b04b1

Method BLASTX NCBI GI g1488297 BLAST score 282

43759

, s^y+

```
E value
                   3.0e-25
Match length
                   75
% identity
                   73
NCBI Description
                  (U63530) osRAD23 [Oryza sativa]
Seq. No.
                   307993
Seq. ID
                   uC-zmflmo17052c01b1
Method
                   BLASTX
NCBI GI
                   q2826786
BLAST score
                   174
E value
                   1.0e-12
Match length
                   60
% identity
                   63
NCBI Description
                  (Y10905) RAPB protein [Oryza sativa]
Seq. No.
                   307994
Seq. ID
                  uC-zmflmo17052c08a1
Method
                  BLASTX
NCBI GI
                   q2244784
BLAST score
                   223
E value
                   2.0e-28
Match length
                  127
% identity
                   54
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  307995
Seq. ID
                  uC-zmflmo17052c08b1
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  33
E value
                  3.0e-09
Match length
                  33
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  307996
Seq. ID
                  uC-zmflmo17052d07b1
Method
                  BLASTX
NCBI GI
                  g3881138
BLAST score
                  165
E value
                  2.0e-11
Match length
                  65
% identity
                  52
NCBI Description (AL023846) Y52B11C.1 [Caenorhabditis elegans]
Seq. No.
                  307997
Seq. ID
                  uC-zmflmo17052e02b1
Method
                  BLASTX
NCBI GI
                  g1002800
BLAST score
                  398
E value
                  1.0e-38
Match length
                  103
% identity
                  69
NCBI Description
                 (U33917) Cpm7 [Craterostigma plantagineum]
```

uC-zmflmo17052e03b1

307998

Seq. No.

Seq. ID

```
Method
                    BLASTX
 NCBI GI
                    g2995384
 BLAST score
                    212
 E value
                    5.0e-17
 Match length
                    68
 % identity
                    65
 NCBI Description
                   (AJ004810) cytochrome P450 monooxygenase [Zea mays]
                   307999
 Seq. No.
                   uC-zmflmo17052f09b1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2914700
 BLAST score
                   155
 E value
                   2.0e-10
 Match length
                   43
 % identity
                   74
                    (AC003974) tRNA-processing protein SEN3-like [Arabidopsis *
 NCBI Description
                   thaliana]
                   308000
 Seq. No.
                   uC-zmflmo17052g12a1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2924509
 BLAST score
                   331
 E value
                   6.0e-31
 Match length
                   137
 % identity
                   50
                   (AL022023) subtilisin proteinase - like [Arabidopsis
 NCBI Description
                   thaliana]
 Seq. No.
                   308001
 Seq. ID
                   uC-zmflmo17053b09a1
 Method
                   BLASTN
 NCBI GI
                   g22229
 BLAST score
                   35
 E value
                   2.0e-10
 Match length
                   67
 % identity
                   88
                   Z.mays cab-m7 gene for light harvesting chlorophyll a/b
 NCBI Description
                   binding protein
 Seq. No.
                   308002
 Seq. ID
                   uC-zmflmo17053b12a1
 Method
                   BLASTN
 NCBI GI
                   g342631
 BLAST score
                   99
 E value
                   1.0e-48
Match length
                   203
 % identity
                   87
 NCBI Description
                   Maize mitochondrial F-1-ATPase subunit-2 mRNA, complete cds
*Seq. No.
                   308003
 Seq. ID
                   uC-zmflmo17053c10b1
Method
                   BLASTX
```

Method BLASTX NCBI GI g1785621 BLAST score 493

BLAST score 493 E value 7.0e-50

BLAST score

Match length

% identity

E value

215

68

68

2.0e-17

```
Match length
% identity
                  74
                   (Z84202) AtPK2324 [Arabidopsis thaliana] >gi_2465927
NCBI Description
                   (AF024650) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana] >gi 4249408 (AC006072) putative
                  serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.
                  308004
Seq. ID
                  uC-zmflmo17053e05b1
Method
                  BLASTX
NCBI GI
                  g2914703
BLAST score
                  190
E value
                  2.0e-14
Match length
                  52
% identity
                  69
NCBI Description
                  (AC003974) unknown protein [Arabidopsis thaliana]
Seq. No.
                  308005
Seq. ID
                  uC-zmflmo17053e11b1
Method
                  BLASTN .
NCBI GI
                  g4007864
BLAST score
                  260
E value
                  1.0e-144
Match length
                  381
% identity .
                  98
NCBI Description Zea mays HRGP gene, AC1503 line
Seq. No.
                  308006
Seq. ID
                  uC-zmflmo17053q09b1
Method
                  BLASTX
NCBI GI
                  g629843
BLAST score
                  393
E value
                  2.0e-38
Match length
                  107
% identity
                  76
                  heat shock protein hsp70-4 - maize (fragment)
NCBI Description
                  >gi_498773_emb_CAA55183 (X78414) heat shock protein 70 kDa
                  [Zea mays]
Seq. No.
                  308007
Seq. ID
                  uC-zmflmo17054a04b1
Method
                  BLASTX
NCBI GI
                  g113217
BLAST score
                  218
E value
                  1.0e-17
Match length
                  58
% identity
                  74
NCBI Description ACTIN 1 >gi_100149_pir__S07002 actin 1 - carrot
Seq. No.
                  308008
Seq. ID
                  uC-zmflmo17054a05b1
Method
                  BLASTX
NCBI GI
                  g1076678
```

```
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
 Seq. No.
                   308009
 Seq. ID
                   uC-zmflmo17054b01b1
                   BLASTN
 Method
 NCBI GI
                   g3821780
 BLAST score
                   36
 E value
                   1.0e-10
Match length
                   36
 % identity
                   100
 NCBI Description Xenopus laevis cDNA clone 27A6-1
 Seq. No.
                   308010
```

Seq. ID uC-zmflmo17054b04b1 Method BLASTN NCBI GI g3452293 : BLAST score 49 § . E value 2.0e-18

Match length 65 % identity 94

NCBI Description Zea mays retrotransposon Ji-1 5' LTR, partial sequence

Seq. No. 308011

Seq. ID uC-zmflmo17054b09b1

Method BLASTN NCBI GI g3821780 BLAST score 36 E value 1.0e-10 Match length 36 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 308012

Seq. ID uC-zmflmo17054c04b1

Method BLASTX NCBI GI g100551 BLAST score 141 E value 3.0e-09 Match length 50 % identity 60

NCBI Description tubulin beta chain - oat

Seq. No. 308013

Seq. ID uC-zmflmo17054c09a1

Method BLASTX NCBI GI g1353193 BLAST score 188 E value 2.0e-14Match length 47 % identity 70

NCBI Description O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070

(L14063) O-methyltransferase [Zea mays]

Seq. No. 308014

Seq. ID uC-zmflmo17054d01b1

Method BLASTX

```
NCBI GI
                   q4056489
BLAST score
                   192
E value
                   2.0e-14
Match length
                  120
% identity
                   44
NCBI Description
                  (AC005896) putative white protein [Arabidopsis thaliana]
Seq. No.
                  308015
Seq. ID
                  uC-zmflmo17054e05b1
Method
                  BLASTX
NCBI GI
                  g3913427
BLAST score
                  175
E value
                  1.0e-12
Match length
                  84
% identity
                  50
NCBI Description
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                  (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767)
                  S-adenosylmethionine decarboxylase [Zea mays]
Seq. No.
                  308016
Seq. ID
                  uC-zmflmo17054h02b1
Method
                  BLASTX
NCBI GI
                  g4220538
BLAST score
                  348
E value
                  7.0e-33
Match length
                  138
% identity
                  50
                  (AL035356) NADPH-ferrihemoprotein reductase ATR1
NCBI Description
                  [Arabidopsis thaliana]
                  308017
                  uC-zmflmo17054h08b1
```

Seq. No. Seq. ID Method BLASTX

NCBI GI g2668742 BLAST score 263 E value 4.0e-23 Match length 89 % identity 63

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 308018

Seq. ID uC-zmflmo17055b04b1

Method BLASTX NCBI GI q282430 BLAST score 209 E_value 2.0e-16 Match length 67 % identity 61

NCBI Description leucine--tRNA ligase (EC 6.1.1.4) - Bacillus subtilis

>gi_143148 (M88581) transfer RNA-Leu synthetase [Bacillus

subtilis]

Seq. No. 308019

Seq. ID uC-zmflmo17055b12b1

Method BLASTX NCBI GI g3287695 BLAST score 229



E value 6.0e-19
Match length 106
% identity 43

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis

thaliana]

Seq. No. 308020

Seq. ID uC-zmflmo17055d02b1

Method BLASTX
NCBI GI g115815
BLAST score 520
E value 5.0e-53
Match length 113
% identity 87

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-M9) (LHCP) >gi_100866_pir__\$13098 chlorophyll

a/b-binding protein precursor - maize

>gi_22355 emb CAA39376 (X55892) light-harvesting

chlorophyll a/b binding protein [Zea mays]

Seq. No. 308021

Seq. ID uC-zmflmo17055d06b1

Method BLASTX
NCBI GI g2062169
BLAST score 268
E value 2.0e-23
Match length 132
% identity 42

NCBI Description (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis

thaliana]

Seq. No. 308022

Seq. ID uC-zmflmo17055f06b1

Method BLASTX
NCBI GI g2150029
BLAST score 240
E value 8.0e-21
Match length 63
% identity 70

NCBI Description (AF001270) cytosolic NADP-malic enzyme [Lycopersicon

esculentum]

Seq. No. 308023

Seq. ID uC-zmflmo17055f09a1

Method BLASTX
NCBI GI g4539344
BLAST score 279
E value 7.0e-25
Match length 89
% identity 62

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 308024

Seq. ID uC-zmflmo17055g08b1

Method BLASTX NCBI GI g1619300

```
BLAST score
E value
                   2.0e-23
Match length
                   61
% identity
                   77
NCBI Description
                   (X95269) LRR protein [Lycopersicon esculentum]
Seq. No.
                   308025
Seq. ID
                   uC-zmflmo17057a08a1
Method
                   BLASTX
NCBI GI
                   g2914703
BLAST score
                   362
E value
                   2.0e-34
Match length
                   80
% identity
                   81
NCBI Description
                   (AC003974) unknown protein [Arabidopsis thaliana]
Seq. No.
                   308026
Seq. ID
                   uC-zmflmo17057a12b1
Method
                   BLASTX
NCBI GI
                   g2760844
BLAST score
                   158
E value
                   1.0e-10
Match length
                   59
% identity
                   53
NCBI Description
                   (AC003105) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   308027
Seq. ID
                   uC-zmflmo17057c07b1
Method
                   BLASTX
NCBI GI
                   g4204232
BLAST score
                   262
E value
                   7.0e-23
Match length
                   109
% identity
                   54
NCBI Description
                   (AF035378) MADS-box protein 1 [Lolium temulentum]
Seq. No.
                   308028
Seq. ID
                   uC-zmflmo17057d10a1
Method
                   BLASTN
NCBI GI
                   g577824
BLAST score
                   162
E value
                   6.0e-86
Match length
                   189
                   95
% identity
NCBI Description
                  Z.mays gene for H2B histone (gH2B3)
Seq. No.
                   308029
Seq. ID
                   uC-zmflmo17057f09b1
Method
                   BLASTX
NCBI GI
                   g2911068
BLAST score
                   175
E value
                   1.0e-12
Match length
                   35
% identity
                   91
NCBI Description
                  (AL021960) G10-like protein [Arabidopsis thaliana]
```

Seq. No. 308030

```
Seq. ID
                   uC-zmflmo17057g12b1
Method
                   BLASTX
                   g82696
NCBI GI
BLAST score
                   279
E value
                   5.0e-25
Match length
                   73
% identity
                   74
NCBI Description
                   glycine-rich protein - maize >qi 22293 emb CAA43431
                   (X61121) glycine-rich protein [Zea mays]
                   308031
Seq. No.
Seq. ID
                   uC-zmflmo17057h04b1
Method
                   BLASTX
NCBI GI
                   q1084476
BLAST score
                   332
E value
                   4.0e-31
Match length
                   70
% identity
                   93
NCBI Description
                   catalase (EC 1.11.1.6) - maize >gi 311239 emb CAA42720
                   (X60135) catalase-1 [Zea mays]
Seq. No.
                   308032
Seq. ID
                   uC-zmflmo17057h07a1
Method
                   BLASTX
NCBI GI
                   g2979552
BLAST score
                   329
E value
                   1.0e-30
Match length
                   95
% identity
NCBI Description
                   (AC003680) unknown protein [Arabidopsis thaliana]
Seq. No.
                   308033
Seq. ID
                   uC-zmflmo17058a07b1
Method
                   BLASTX
NCBI GI
                   g2497542
BLAST score
                   167
E value
                   8.0e-13
Match length
                   60
% identity
                   70
NCBI Description
                   PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR
                   >gi_629696 pir S44287 pyruvate kinase, plastid - common
                   tobacco >gi 482938 emb CAA82223 (Z28374) Pyruvate kinase;
                   plastid isozyme [Nicotiana tabacum]
Seq. No.
                   308034
Seq. ID
                   uC-zmflmo17058b05a1
```

Method BLASTN -NCBI GI g257040 BLAST score 33 E value 3.0e-09 Match length .77 . % identity 86

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 308035

Seq. ID uC-zmflmo17058c06b1

Method BLASTX

```
NCBI GI
                   q1143188
BLAST score
                   420
E value
                   2.0e-41
Match length
                   130
% identity
                   26
NCBI Description
                  (U32627) ubiquitin precursor [Candida albicans]
                   308036
Seq. No.
Seq. ID
                   uC-zmflmo17058d12b1
Method
                   BLASTX
NCBI GI
                   g3885884
BLAST score
                   218
                   1.0e-17
E value
Match length
                   89
% identity
                   52
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
Seq. No.
                   308037
Seq. ID
                   uC-zmflmo17058e03a1
Method
                   BLASTX
NCBI GI
                   g4468985
BLAST score
                   144
E value
                   5.0e-09
Match length
                   57
% identity
                   53
NCBI Description
                  (AL035605) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   308038
Seq. ID
                   uC-zmflmo17058f05a1
Method
                  BLASTX
NCBI GI
                   q4468814
BLAST score
                  198
E value
                   2.0e-15
Match length
                  128
% identity
                   38
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                  308039
Seq. ID
                  uC-zmflmo17058f06b1
Method
                  BLASTX
NCBI GI
                  g2506277
BLAST score
                  298
E value
                  6.0e-27
Match length
                  77
% identity
                  79
NCBI Description
                  RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60
                  KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi 806808
                   (U21139) chaperonin precursor [Pisum sativum]
Seq. No.
                  308040
Seq. ID
                  uC-zmflmo17058q06b1
Method
                  BLASTX
NCBI GI
                  g2511531
BLAST score
                  206
E value
                  2.0e-16
Match length
```

55

73

% identity



NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica] >gi 3163944 emb_CAA06618 (AJ005598) alpha-tubulin 1 [Eleusine indica] 308041 Seq. No. Seq. ID uC-zmflmo17058h06b1 Method BLASTX NCBI GI g123650 BLAST score 209 E value 6.0e-17 Match length 76 % identity 66 NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN >gi 82245 pir S03250 heat shock protein 70 (clone pMON9743) - garden petunia >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70 [Petunia x hybrida] Seq. No. 308042 Seq. ID uC-zmflmo17059b05b1 Method BLASTX NCBI GI g3914005 BLAST score 522 E value 3.0e-53 Match length 135 % identity 79 NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 1816586 (U85494) LON1 protease [Zea mays] Seq. No. 308043 Seq. ID uC-zmflmo17059d01b1 Method BLASTX NCBI GI g3355471 BLAST score 303 E value 1.0e-27 Match length 115 % identity 50 NCBI Description (AC004218) putative lysophospholipase [Arabidopsis thaliana] 308044 uC-zmflmo17059f07b1 BLASTX g3309082 226 1.0e-18 Match length 67 % identity 63

Seq. No. Seq. ID Method NCBI GI BLAST score E value

NCBI Description (AF076251) calcineurin B-like protein 1 [Arabidopsis thaliana]

Seq. No. 308045

Seq. ID uC-zmflmo17059f12b1 Method BLASTN

NCBI GI q3821780 BLAST score 36 E value 1.0e-10 Match length 36



```
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   308046
Seq. ID
                   uC-zmflmo17059q09b1
Method
                   BLASTN
NCBI GI
                   g3955064
BLAST score
                   63
                   8.0e-27
E value
Match length
                   195
% identity
                   84
                  Zea mays PHYT I gene for acidic phytase
NCBI Description
Seq. No.
                   308047
Seq. ID
                   uC-zmflmo17059g10b1
Method
                   BLASTX
NCBI GI
                   q806299
BLAST score
                   249
E value
                   3.0e-21
Match length
                   96
% identity
                   48
NCBI Description
                  (M25427) unknown protein [Zea mays]
Seq. No.
                   308048
Seq. ID
                  uC-zmflmo17059g12b1
Method
                  BLASTN
NCBI GI
                   g602605
BLAST score
                   66
E value
                  1.0e-28
Match length
                  114
% identity
                  90
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
                  308049
Seq. No.
                  uC-zmflmo17059h04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982328
BLAST score
                  514
E value
                  2.0e-52
Match length
                  103
% identity
                  95
NCBI Description
                  (AF051249) pyruvate dehydrogenase E1 beta subunit [Picea
                  mariana]
Seq. No.
                  308050
Seq. ID
                  uC-zmflmo17060a03a1
Method
                  BLASTX
                  g1773330
                  202
```

NCBI GI BLAST score E value 7.0e-16 Match length 67 % identity 58

NCBI Description (U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No. 308051

Seq. ID uC-zmflmo17060a04b1

Method BLASTN

% identity

NCBI Description

```
NCBI GI
                  g168436
BLAST score
                  44
E value
                  2.0e-15
Match length
                  80
                  89
% identity
                  Zea mays catalase (Cat3) gene, complete cds
NCBI Description
Seq. No.
                  308.052
                  uC-zmflmo17060c02b1
Seq. ID
                  BLASTX
Method
                  g548770
NCBI GI
BLAST score
                  190
E value
                  2.0e-14
Match length
                  64
% identity
                  62
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal
                  protein L3 - rice >gi 303853 dbj BAA02155 (D12630)
                  ribosomal protein L3 [Oryza sativa]
                  308053
Seq. No.
Seq. ID
                  uC-zmflmo17060c10b1
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  387
E value
                  1.0e-37
Match length
                  81
% identity
                  95
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091_prf 1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  308054
Seq. ID
                  uC-zmflmo17060d01b1
Method
                  BLASTX
NCBI GI
                  q2499903
BLAST score
                  553
E value
                  2.0e-58
Match length
                  180
% identity
                  62
NCBI Description
                  PUROMYCIN-SENSITIVE AMINOPEPTIDASE (PSA) >gi 1184161
                  (U35646) aminopeptidase [Mus musculus]
                  >gi_1585925_prf__2202260A puromycin sensitive
                  aminopeptidase [Mus musculus]
Seq. No.
                  308055
Seq. ID
                  uC-zmflmo17060d04b1
Method
                  BLASTX
NCBI GI
                  q2244785
BLAST score
                  228
E value
                  4.0e-19
Match length
                  87
```

(Z97335) hypothetical protein [Arabidopsis thaliana]

```
308056
   Seq. No.
   Seq. ID
                     uC-zmflmo17060g01b1
  Method
                     BLASTX
  NCBI GI
                     q3687235
  BLAST score
                     359
  E value
                     5.0e-34
  Match length
                     111
  % identity
                     68
  NCBI Description
                     (AC005169) putative copia-like transposable element
                     [Arabidopsis thaliana]
  Seq. No.
                     308057
   Seq. ID
                     uC-zmflmo17060h02b1
  Method
                     BLASTN
                     g311238
  NCBI GI
  BLAST score
                     36
  E value
                     7.0e-11
  Match length
                     72
  % identity
                     88
  NCBI Description Z.mays cat1 gene for catalase
                     308058
  Seq. No.
                     uC-zmflmo17060h04b1
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g2345085
  BLAST score
                     212
  E value
                     1.0e-116
  Match length
                     364
                     90
   % identity
  NCBI Description Zea mays ribosomal RNA intergenic spacer, partial sequence
                     308059
  Seq. No.
                     uC-zmflmo17061a09b1
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g3914557
  BLAST score
                     300
  E value
                     4.0e-27
  Match length
                     61
  % identity
                     98
  NCBI Description
                     RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED
                     PROTEIN) >gi_1155265 (U40219) possible apospory-associated
                     protein [Pennisetum ciliare]
  Seq. No.
                     308060
  Seq. ID
                     uC-zmflmo17061c05b1
  Method
                     BLASTX
  NCBI GI
                     q3450889
  BLAST score
                     173
                     2.0e-12
  E value
  Match length
                     72
  % identity
NCBI Description
                     (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
```

Seq. No. 308061

Seq. ID uC-zmflmo17061h06b1

Method BLASTX 92735931

```
BLAST score 275
E value 8.0e-42
Match length 128
% identity 69
NCBI Description (AF014813 nidulans)
```

NCBI Description (AF014813) DNA replication licensing factor [Emericella

Seq. No. 308062

Seq. ID uC-zmflmo17062f07a1

Method BLASTN
NCBI GI g4140643
BLAST score 184
E value 3.0e-99
Match length 299
% identity 91

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 308063

Seq. ID uC-zmflmo17064a08a1

Method BLASTX
NCBI GI g1871187
BLAST score 255
E value 4.0e-22
Match length 82
% identity 61

NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 308064

Seq. ID uC-zmflmo17064e02a1

Method BLASTN
NCBI GI g22371
BLAST score 104
E value 1.0e-51
Match length 140
% identity 94

NCBI Description Maize Mu4 transposable element DNA

Seq. No. 308065

Seq. ID uC-zmflmo17065d01a1

Method BLASTN
NCBI GI g22292
BLAST score 121
E value 9.0e-62
Match length 214
% identity 89

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 308066

Seq. ID uC-zmflmo17065f02a1

Method BLASTN
NCBI GI 922371
BLAST score 66
E value 6.0e-29
Match length 110
% identity 90

NCBI Description Maize Mu4 transposable element DNA

· Andrews

```
Seq. No.
                   308067
Seq. ID
                   uC-zmflmo17065g01a1
Method
                   BLASTN
NCBI GI
                   q1532072
BLAST score
                   156
E value
                   1.0e-82
Match length
                  188
% identity
                  96
NCBI Description
                  Z.mays mRNA for S-adenosylmethionine decarboxylase
Seq. No.
                   308068
Seq. ID
                  uC-zmflmo17065g01b1
Method
                  BLASTX
                  g3913427
NCBI GI
BLAST score
                  236
E value
                  8.0e-20
Match length
                  51
% identity
                  96
NCBI Description
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                   (SAMDC) >gi 1532073 emb CAA69075 (Y07767)
                  S-adenosylmethionine decarboxylase [Zea mays]
Seq. No.
                  308069
Seq. ID
                  uC-zmflmo17065g06b1
Method
                  BLASTX
                                                                -74.
NCBI GI
                  g4538959
BLAST score
                  167
E value
                  5.0e-12
Match length
                  62
% identity
                  53
NCBI Description
                  (AL049488) putative protein [Arabidopsis thaliana]
Seq. No.
                  308070
Seq. ID
                  uC-zmflmo17066a02b1
Method
                  BLASTN
NCBI GI
                  g4007864
BLAST score
                  60
E value
                  4.0e-25
Match length
                  100
% identity
                  92
NCBI Description
                  Zea mays HRGP gene, AC1503 line
Seq. No.
                  308071
Seq. ID
                  uC-zmflmo17066b07b1
Method
                  BLASTX
NCBI GI
                  g282946
BLAST score
                  171
E value
                  3.0e-12
Match length
                  111
% identity
                  37
NCBI Description
                  Ca2+-transporting ATPase (EC 3.6.1.38) - tomato
                  >gi_423783_pir__A46284 Ca(2+)-ATPase, LCA1 -
                  Lycopersicon=tomatoes >gi_170378 (M96324) Ca2+-ATPase
```

43774

Ca2+ ATP synthase [Lycopersicon esculentum]

[Lycopersicon esculentum] >gi_4206311 (AF050495) Ca2+ ATP synthase [Lycopersicon esculentum] >gi_4206313 (AF050496)

Method

NCBI GI



```
Seq. No.
                   308072
Seq. ID
                   uC-zmflmo17066b08b1
Method
                   BLASTX
NCBI GI
                   q2660669
BLAST score
                   678
E value
                   2.0e-71
Match length
                   143
% identity
                   92
NCBI Description
                   (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   308073
Seq. ID
                   uC-zmflmo17066b11b1
Method
                   BLASTN
                   g257040
NCBI GI
BLAST score
                   217
E value
                   1.0e-119
Match length
                   265
% identity
                   95
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
Seq. No.
                   308074
Seq. ID
                   uC-zmflmo17066c05b1
Method
                  BLASTX
NCBI GI
                   g4263787
BLAST score
                   295
E value
                   9.0e-27
Match length
                  78
% identity
                   68
NCBI Description
                  (AC006068) unknown protein [Arabidopsis thaliana]
Seq. No.
                  308075
Seq. ID
                  uC-zmflmo17066d11a1
Method
                  BLASTX
                  g4416302
NCBI GI
                 ~ 556
BLAST score
                  3.0e-57
E value
Match length
                  139
% identity
                  78
NCBI Description (AF105716) copia-type pol polyprotein [Zea mays]
Seq. No.
                  308076
Seq. ID
                  uC-zmflmo17066d11b1
Method
                  BLASTX
NCBI GI
                  q4416302
BLAST score
                  752
E value
                  3.0e-80
Match length
                  146
% identity
                  97
NCBI Description (AF105716) copia-type pol polyprotein [Zea mays]
Seq. No.
                  308077
Seq. ID
```

g1498384 BLAST score 748

BLASTX

uC-zmflmo17066e02b1



E value 1.0e-79 Match length 151 % identity 98

NCBI Description (U60508) actin [Zea mays]

308078 Seq. No.

uC-zmflmo17066q07b1 Seq. ID

Method BLASTN NCBI GI q4007864 BLAST score 251 E value 1.0e-139 Match length 405 % identity 25

NCBI Description Zea mays HRGP gene, AC1503 line

Seq. No. 308079

uC-zmflmo17066h12b1 Seq. ID

Method BLASTX NCBI GI g2369714 BLAST score 281 E value 3.0e-25 Match length 80 69

% identity

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

. 6-

Seq. No. -308080

Seq. ID uC-zmflmo17067a05a1

Method BLASTN NCBI GI q1220422 BLAST score 83 E value 3.0e-39 Match length 119

% identity 92

NCBI Description Zea mays ubiquitin (MUB14) mRNA, 3' end

Seq. No. 308081

Seq. ID uC-zmflmo17067a05b1

Method BLASTX NCBI GI g1362008 BLAST score 486 E value 4.0e-49 Match length 106 % identity 19

NCBI Description ubiquitin-like protein 12 - Arabidopsis thaliana

Seq. No. 308082

Seq. ID uC-zmflmo17067a11b1

Method BLASTX NCBI GI g2984709 BLAST score 342 E value 3.0e-32 . Match length 71 % identity 93

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 308083

uC-zmflmo17067b06b1 ಿSeq. ID

```
Method
                   BLASTX
NCBI GI
                   g2317910
BLAST score
                   445
E value
                   2.0e-44
Match length
                   111
% identity
                   71
NCBI Description
                   (U89959) CER1 protein [Arabidopsis thaliana]
                   308084
Seq. No.
                   uC-zmflmo17067c02a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3551951
BLAST score
                   36
E value
                   7.0e-11
Match length
                   56
% identity
                   91
                  Hemerocallis hybrid cultivar senescence-associated protein
NCBI Description
                   4 (SA4) mRNA, complete cds
Seq. No.
                   308085
                   uC-zmflmo17067c06b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3452291
BLAST score
                   185
                   1.0e-99
E value
Match length
                   216
% identity
                   97
NCBI Description
                  Zea mays retrotransposon Huck-2 3' LTR, partial sequence
                  308086
Seq. No.
Seq. ID
                  uC-zmflmo17067c07a1
Method
                  BLASTN
NCBI GI
                   g22091
BLAST score
                   90
E value
                   3.0e-43
Match length
                  147
% identity
                   91
NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein
Seq. No.
                  308087
Seq. ID
                  uC-zmflmo17067c07b1
Method
                  BLASTN
NCBI GI
                  g257040
BLAST score
                  129
E value
                  3.0e-66
Match length
                  325
                  94
% identity
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
Seq. No.
                  308088
Seq. ID
                  uC-zmflmo17067c08b1
Method
                  BLASTN
NCBI GI
```

43777

q22292

74 1.0e-33

202

85

BLAST score

E value Match length

% identity

A 8.2



```
NCBI Description
                  Z.mays mRNA for glycine-rich protein
                   308089
Seq. No.
                   uC-zmflmo17067d07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g123593
BLAST score
                   391
E value
                   5.0e-38
                                                                   140
Match length
                   78
% identity
                   95
NCBI Description
                  HEAT SHOCK 70 KD PROTEIN >gi_82697_pir__A25089 heat shock
                   protein 70 - maize
Seq. No.
                   308090
                   uC-zmflmo17067e09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3859534
BLAST score
                   146
E value
                   1.0e-09
Match length
                   74
% identity
                   45
NCBI Description
                   (AF095452) asparagine synthetase [Arabidopsis thaliana]
Seq. No.
                   308091
Seq. ID
                   uC-zmflmo17067f12b1
Method
                   BLASTX
NCBI GI
                   g123593
BLAST score
                   179
                   3.0e-13
E value
Match length
                   69
% identity
                   58
NCBI Description
                  HEAT SHOCK 70 KD PROTEIN >gi_82697_pir__A25089 heat shock
                  protein 70 - maize
Seq. No.
                   308092
Seq. ID
                   uC-zmflmo17067h05b1
Method
                   BLASTX
NCBI GI
                   g129591
BLAST score
                   207
E value
                   6.0e-17
Match length
                   69
% identity
                   59
                  PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   308093
Seq. ID
                  uC-zmflmo17068a10b2
Method
                  BLASTN
NCBI GI
                  g1905943
BLAST score
                  72
E value
                   2.0e-32
```

E value 2.0e-32 Match length 140 % identity 88

NCBI Description Sorghum bicolor MADS box transcription factor SbMADS1 mRNA,

complete cds

Seq. No. 308094

```
uC-zmflmo17068b03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2224846
BLAST score
                  187
                  3.0e-14
E value
Match length
                  50
% identity
                  80
NCBI Description
                  (Y13905) anionic peroxidase [Zea mays]
Seq. No.
                  308095
Seq. ID
                  uC-zmflmo17068e08b2
Method
                  BLASTX
NCBI GI
                  g118104
BLAST score
                  190
E value
                  5.0e-29
Match length
                  126
% identity
                  60
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays] 🔅
Seq. No.
                  308096
Seq. ID
                  uC-zmflmo17068e09b2
Method
                  BLASTX
                  g267072
NCBI GI
BLAST score
                  195
E value
                  5.0e-15
Match length
                  118
% identity
                  42
NCBI Description
                  TUBULIN BETA-1 CHAIN >gi 100072 pir S20868 tubulin beta-1
                  chain - garden pea >gi 20758 emb CAA38613 (X54844)
                  beta-tubulin 1 [Pisum sativum]
Seq. No.
Seq. ID
                  308097
                  uC-zmflmo17068f03a1
Method
                  BLASTN
NCBI GI
                  q22091
BLAST score
                  356
E value
                  0.0e + 00
Match length
                  408
% identity
NCBI Description
                  Z.diploperennis gene for hydroxyproline-rich glycoprotein
Seq. No.
                  308098
Seq. ID
                  uC-zmflmo17068g01b2
Method
                  BLASTX
NCBI GI
                  g3341699
BLAST score
                  164
E value
                  3.0e-11
                  77
Match length
% identity
                  43
NCBI Description
                  (AC003672) putative giberellin beta-hydroxylase
```

Seq. No.

[Arabidopsis thaliana]

BLAST score

E value

241

1.0e-31

```
Seq. ID
                    uC-zmflmo17068h02b2
  Method
                   BLASTN
  NCBI GI
                    g535743
  BLAST score
                    51
                    1.0e-19
  E value
 Match length
                    83
                    90
  % identity
  NCBI Description Oryza sativa unknown ORF mRNA, complete cds
                    308100
  Seq. No.
                    uC-zmflmo17069a01b1
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    g1143864
  BLAST score
                    140
  E value
                    4.0e-09
 Match length
                    43
  % identity
                    65
  NCBI Description
                    (U28047) beta glucosidase [Oryza sativa]
  Seq. No.
                    308101
                    uC-zmflmo17069a04b1
  Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g2305013
 BLAST score
                    43
E value
                    3.0e-15
 Match length
                    55
  % identity
                    95
  NCBI Description
                    Musa acuminata S-adenosyl-L-methionine synthetase homolog
                    mRNA, complete cds
  Seq. No.
                    308102
  Seq. ID
                    uC-zmflmo17069b03b1
 Method
                    BLASTX
 NCBI GI
                    g1703380
  BLAST score
                    182
 E value
                    5.0e-14
 Match length
                    44
  % identity
                    86
 NCBI Description
                    ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
                    ADP-ribosylation factor [Oryza sativa]
  Seq. No.
                    308103
  Seq. ID
                    uC-zmflmo17069c07b1
 Method
                    BLASTX
 NCBI GI
                    g4455287
 BLAST score
                    211
 E value
                    8.0e-17
 Match length
                    105
  % identity
                    51
 NCBI Description
                    (AL035527) putative protein [Arabidopsis thaliana]
 Seq. No.
                    308104
  Seq. ID
                    uC-zmflmo17069d01b1
 Method
                    BLASTX
 NCBI GI
                    q4206122
```

```
99
 Match length
% identity
                    71
 NCBI Description
                    (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
                    crystallinum]
                    308105
 Seq. No.
 Seq. ID
                    uC-zmflmo17069d02b1
 Method
                    BLASTX
 NCBI GI
                    q3298539
 BLAST score
                    292
 E value
                    3.0e-26
 Match length
                    146
 % identity
                    (AC004681) NPK1-related protein kinase [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    308106
 Seq. ID
                    uC-zmflmo17069f05b1
 Method
                    BLASTX
                    q3859548
NCBI GI
 BLAST score
                    435
                    4.0e-47
 E value
 Match length
                    116
 % identity
                    85
                    (AF097182) protein phosphatase 2A catalytic subunit [Oryza
 NCBI Description
                    sativa]
 Seq. No.
                    308107
                    uC-zmflmo17069g02b1
                    BLASTX
                    q4538939
                    735
                    4.0e-78
                    180
```

Seq. ID Method NCBI GI

BLAST score E value Match length % identity

NCBI Description (AL049483) Col-O casein kinase I-like protein [Arabidopsis

thaliana]

Seq. No. 308108

Seq. ID uC-zmflmo17070a01b1

Method BLASTX NCBI GI g2668742 BLAST score 380 E value 9.0e-37 86 Match length % identity 88

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

308109 Seq. No.

uC-zmflmo17070a03b1 Seq. ID

Method BLASTN NCBI GI g22332 BLAST score 163 E value 1.0e-86 Match length 354 % identity 86

NCBI Description Z.mays HRGP gene

Seq. ID

Method

```
Seq. No.
                    308110
 Seq. ID
                   uC-zmflmo17070b05b1
 Method
                   BLASTX
 NCBI GI
                    q3914423
 BLAST score
                   393
                   3.0e-38
 E value
Match length
                   84
 % identity
                   85
 NCBI Description PROFILIN 4 >gi 2642324 (AF032370) profilin [Zea mays]
Seq. No.
                   308111
 Seq. ID
                   uC-zmflmo17070b08b1
 Method
                   BLASTX
 NCBI GI
                    g4455299
 BLAST score
                   251
 E value
                    6.0e-31
 Match length
                   98
 % identity
                    64
 NCBI Description
                   (AL035528) putative protein [Arabidopsis thaliana]
                   308112
 Seq. No.
 Seq. ID
                   uC-zmflmo17070b12a1
                   BLASTX
 Method
 NCBI GI
                   g629844
 BLAST score
                   254
 E value
                    6.0e-22
 Match length
                    66
                   79
 % identity
 NCBI Description
                   heat shock protein hsp70-5 - maize (fragment)
                   >gi_498775_emb_CAA55184_ (X78415) heat shock protein 70 kDa
                    [Zea mays]
 Seq. No.
                   308113
 Seq. ID
                   uC-zmflmo17070c10a1
 Method
                   BLASTN
 NCBI GI
                   `g602252
 BLAST score
                   52
 E value
                   3.0e-20
 Match length
                   76
 % identity
                   92
 NCBI Description Zea mays enolase (eno2) mRNA, complete cds
 Seq. No.
                   308114
 Seq. ID
                   uC-zmflmo17070d01b1
 Method
                   BLASTX
 NCBI GI
                   g3337389
 BLAST score
                   199
                   2.0e-15
 E value
 Match length
                   102
 % identity
                   45
 NCBI Description
                   (AC004682) pre-mRNA splicing factor (PRP16)(KIAA0224) [Homo
                   sapiens]
 Seq. No.
                   308115
```

43782

uC-zmflmo17070e04b1

BLASTX

ů.

```
NCBI GI
                    q3298540
  BLAST score
                    401
  E value
                    4.0e-39
  Match length
                    106
  % identity
                    73
  NCBI Description
                    (AC004681) unknown protein [Arabidopsis thaliana]
                    308116
  Seq. No.
                    uC-zmflmo17070e12b1
  Seq. ID
  Method
                    BLASTX
 NCBI GI
                    q168404
  BLAST score
                    561
 E value
                    7.0e-58
 Match length
                    124
  % identity
                    90
 NCBI Description
                    (J01238) actin [Zea mays]
Seq. No.
                    308117
 Seq. ID
                    uC-zmflmo17070f01b1
 Method
                    BLASTX
 NCBI GI
                    g2760839
 BLAST score
                    331
 E value
                    5.0e-31
 Match length
                    86
  % identity
                    73
 NCBI Description
                    (AC003105) putative receptor kinase [Arabidopsis thaliana]
 Seq. No.
                    308118
 Seq. ID
                    uC-zmflmo17070f03b1
 Method
                    BLASTX
 NCBI GI
                    q1890575
 BLAST score
                    487
 E value
                    4.0e-49
 Match length
                    113
  % identity
                    80
 NCBI Description
                    (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
                    vulgare]
 Seq. No.
                    308119
 Seq. ID
                    uC-zmflmo17070f04b1
 Method
                    BLASTX
 NCBI GI
                    q82696
 BLAST score
                    332
 E value
                    4.0e-31
 Match length
                    85
 % identity
                    76
 NCBI Description
                    glycine-rich protein - maize >gi 22293 emb CAA43431
                    (X61121) glycine-rich protein [Zea mays]
 Seq. No.
                    308120
```

Seq. ID uC-zmflmo17070f12b1

Method BLASTX NCBI GI q3757521 BLAST score 416 E value 9.0e-41 Match length 148 % identity 52



```
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
                  308121
Seq. No.
                  uC-zmflmo17070g04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455338
BLAST score
                  142
E value
                  8.0e-09
Match length
                  34
                  74
% identity
NCBI Description
                  (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                  308122
Seq. ID
                  uC-zmflmo17070g05a1
Method
                  BLASTN
NCBI GI
                  g22312
BLAST score
                  159
E value
                  4.0e-84
Match length
                  183
% identity
                  97
NCBI Description
                  Maize ABA_inducible gene for glycine-rich protein ( ABA =
                  abscisic acid)
Seq. No.
                  308123
Seq. ID
                  uC-zmflmo17070h08b1
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  347
E value
                  6.0e-33
Match length
                  94
                  76
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  308124
Seq. ID
                  uC-zmflmo17071a05b1
Method
                  BLASTX
NCBI GI
                  g464986
BLAST score
                  337
E value
                  2.0e-31
Match length
                  67
% identity
                  93
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi 297884 emb_CAA78714_ (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                  enzyme E2 [Arabidopsis thaliana]
```

Seq. No. 308125

ligase UBC9 [Arabidopsis thaliana]

>gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein



```
Seq. ID
                   uC-zmflmo17071b09b1
Method
                   BLASTN
NCBI GI
                   q22332
BLAST score
                   356
E value
                   0.0e+00
Match length
                   434
% identity
                   95
NCBI Description
                  Z.mays HRGP gene
                   308126
Seq. No.
                  uC-zmflmo17071c04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3126967
BLAST score
                   428
E value
                   3.0e-42
Match length
                   105
% identity -
                   15
NCBI Description
                  (AF061807) polyubiquitin [Elaeagnus umbellata]
Seq. No.
                  308127
                  uC-zmflmo17071d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2829910
BLAST score
                   208
E value
                   2.0e-16
Match length
                  131
% identity
                   40
NCBI Description
                   (AC002291) Unknown protein, contains regulator of
                   chromosome condensation motifs [Arabidopsis thaliana]
Seq. No.
                   308128
                  uC-zmflmo17071e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2493965
BLAST score
                  174
E value
                   2.0e-12
Match Tength
                  90
% identity
                   42
NCBI Description
                  XANTHINE DEHYDROGENASE (PURINE HYDROXYLASE I)
                  >gi_1078636_pir__A55875 xanthine dehydrogenase (EC
                   1.1.1.204) - Emericella nidulans >gi_577731_emb_CAA58034_
                   (X82827) xanthine dehydrogenase [Emericella nidulans]
Seq. No.
                   308129
Seq. ID
                  uC-zmflmo17071e05a1
Method
                  BLASTN
NCBI GI
                  g902524
BLAST score
                  137
E value
                  2.0e-71
Match length
                  173
% identity
                  95
NCBI Description
                  Zea mays clone MubG10 ubiquitin fusion protein gene,
                  complete cds
```

Seq. No. 308130

Seq. ID uC-zmflmo17071e09b1

Method BLASTX

```
NCBI GI
                     g2854049
  BLAST score
                     328
  E value
                     2.0e-30
  Match length
                     126
   % identity
                     57
                     (AF044260) receptor serine/threonine kinase; protein kinase
  NCBI Description
                     [Oryza sativa]
  Seq. No.
                     308131
  Seq. ID
                     uC-zmflmo17071e11b1
  Method
                     BLASTN
  NCBI GI
                     g902524
  BLAST score
                     50
  E value
                     3.0e-19
  Match length
                     90
   % identity
                     89
                     Zea mays clone MubG10 ubiquitin fusion protein gene,
  NCBI Description
                     complete cds
   Seq. No.
                     308132
   Seq. ID
                     uC-zmflmo17071f02b1
  Method
                     BLASTX
  NCBI GI
                     q4417304
  BLAST score
                     346
  E value
                     7.0e-33
  Match length
                     103
   % identity
   NCBI Description
                      (AC006446) putative beta-1,4-mannosyl-glycoprotein
                     beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis
                     thaliana]
   Seq. No.
                     308133
                     uC-zmflmo17071f09b1
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g1707011
   BLAST score
                     227
   E value
                     9.0e-19
   Match length
                     47
   % identity
   NCBI Description
                      (U78721) auxin-repressed protein isolog [Arabidopsis
                     thaliana]
                     308134
   Seq. No.
                     uC-zmflmo17071q08b1
  Seq. ID
  Method
                     BLASTX
   NCBI GI
                     g4588001
  BLAST score
                     243
  E value
                     2.0e-20
  Match length
                     97
   % identity
                     43
                      (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis
   NCBI Description
\leq 2_{\rm sc}
                     thaliana]
                     308135
   Seq. No.
```

Seq. ID uC-zmflmo17071h06b1

Method BLASTX NCBI GI g2651310

```
BLAST score
                  313
E value
                  9.0e-29
Match length
                  90
% identity
                  61
                  (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
                  308136
Seq. No.
Seq. ID
                  uC-zmflmo17071h09b1
Method
                  BLASTX
NCBI GI
                  g2578033
BLAST score
                  194
E value
                  9.0e-15
Match length
                  65
% identity
                  58
NCBI Description
                 (X97016) omega-6 desaturase [Gossypium hirsutum]
                  308137
Seq. No.
Seq. ID
                  uC-zmflmo17072b01b1
Method
                  BLASTX
NCBI GI
                  g2829688
BLAST score
                  537
                  7.0e-55
E value
Match length
                  115
% identity
                  95
NCBI Description
                  CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)
                  (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                  >gi_1076798 pir S52738 cysteine synthase (EC 4.2.99.8)
                  precursor - maize >gi 758353 emb CAA59798 (X85803)
                  cysteine synthase [Zea mays]
                  308138
Seq. No.
Seq. ID
                  uC-zmflmo17072c05b1
Method
                  BLASTX
NCBI GI
                  g4539335
                  140 🍦
BLAST score
E value
                  4.0e-09
Match length
                  53
% identity
                  57
NCBI Description
                  (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                  308139
Seq. ID
                uC-zmflmo17072e10b1
Method
                  BLASTX
NCBI GI
                  g82698
BLAST score
                  155
E value
                  2.0e-10
Match length
                  67
% identity
```

NCBI Description hydroxyproline-rich glycoprotein precursor - maize >gi_257041_bbs_115226 (S45164) hydroxyproline-rich

glycoprotein, HRGP [maize, Peptide, 328 aa] [Zea mays] >gi_4007865_emb_CAA10387_ (AJ131535) Hydroxyproline-rich

Glycoprotein (HRGP) [Zea mays]

308140 Seq. No.

Seq. ID uC-zmflmo17072g06b1

```
Method
                   BLASTX
NCBI GI
                   g3080738
                   $89
BLAST score
E value
                   2.0e-14
Match length
                   74
                   53
 % identity
NCBI Description
                   (U77365) pasticcino 1-A [Arabidopsis thaliana]
Seq. No.
                   308141
                   uC-zmflmo17072h02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1181673
BLAST score
                   399
E value
                   5.0e-39
                   100
Match length
 % identity
                   88
NCBI Description
                   (U41652) heat shock protein cognate 70 [Sorghum bicolor]
Seq. No.
                   308142
                   uC-zmflmo17072h04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1575130
BLAST score
                   493
E value
                   1.0e-63
Match length
                   151
% identity
                   86
NCBI Description
                   (U58209) lumenal binding protein cBiPe3 [Zea mays]
Seq. No.
                   308143
Seq. ID
                   uC-zmflmo17072h06b1
Method
                   BLASTX
NCBI GI
                   g3309243
BLAST score
                   181
E value
                   1.0e-25
Match length
                   106
% identity
                   60
NCBI Description
                   (AF073507) aconitase-iron regulated protein 1 [Citrus
                   limon]
Seq. No.
                   308144
Seq. ID
                   uC-zmflmo17073f01b1
Method
                   BLASTX
NCBI GI
                   g4376158
BLAST score
                   391
E value
                   4.0e-38
Match length
                   94
% identity
                   80
NCBI Description
                   (X98873) aspartate kinase [Arabidopsis thaliana]
Seq. No.
                   308145
                   uC-zmflmo17073f05b1
Seq. ID
```

Method BLASTX
NCBI GI 94467138
BLAST score 275
E value 2.0e-24
Match length 68
% identity 82

Seq. ID

Method

```
NCBI Description
                    (AL035540) probable H+-transporting ATPase [Arabidopsis
                    thaliana]
  Seq. No.
                    308146
  Seq. ID
                    uC-zmflmo17073f09b1
  Method
                    BLASTX
  NCBI GI
                    q2914703
 BLAST score
                    257
 E valué
                    3.0e-22
 Match length
                    111
% identity
                    (AC003974) unknown protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                    308147
  Seq. ID
                    uC-zmflmo17073g07b1
 Method
                    BLASTX
 NCBI GI
                    g2281637
 BLAST score
                    157
 E value
                    1.0e-10
 Match length
                    44
  % identity
                    66
                    (AF003099) AP2 domain containing protein RAP2.6
  NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    308148
 Seq. ID
                    uC-zmflmo17073g09b1
 Method
                    BLASTX
 NCBI GI
                    q4455351
 BLAST score
                    212
 E value
                    5.0e-17
 Match length
                    60
 % identity
                    60
 NCBI Description
                    (AL035524) putative protein [Arabidopsis thaliana]
 Seq. No.
                    308149
 Seq. ID
                    uC-zmflmo17073h09b1
 Method
                    BLASTX
 NCBI GI
                    g2213620
 BLAST score
                    357
 E value
                    4.0e-34
 Match length
                    104
 % identity
                    63
 NCBI Description
                    (AC000103) F21J9.13 [Arabidopsis thaliana]
                    308150
 Seq. No.
 Seq. ID
                    uC-zmflmo17074a09b1
 Method
                    BLASTX
 NCBI GI
                    g4091008
 BLAST score
                    187
 E value
                    4.0e-14
 Match length
                    95
 % identity
                    52
 NCBI Description
                    (AF040700) methionyl-tRNA synthetase [Oryza sativa]
 Seq. No.
                    308151
```

43789

uC-zmflmo17074b03b1

BLASTX

.

E value

2.0e-11



```
NCBI GI
                   q3292817
BLAST score
                  - 145
                   1.0e-09
E value
Match length
                   58
% identity
                   53
                   (AL031018) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   308152
Seq. ID
                   uC-zmflmo17074c05b1
Method
                   BLASTX
NCBI GI
                   g2827664
BLAST score
                   242
E value
                   8.0e-21
Match length
                   84
% identity
                   56
                   (AL021637) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_2982427_emb_CAA18236_ (AL0222224) hypothetical protein
                   [Arabidopsis thaliana]
Seq. No.
                   308153
Seq. ID
                   uC-zmflmo17074c09b1
Method
                   BLASTX
NCBI GI
                   g4490330
BLAST score
                   178
E value
                   6.0e-13
Match length
                   139
% identity
                   33
                   (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   308154
Seq. ID
                   uC-zmflmo17074c12b1
Method
                   BLASTN
NCBI GI
                   g2773153
BLAST score
                   48
E value
                   7.0e-18
Match length
                   175
% identity
                   83
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
                  308155
Seq. No.
Seq. ID
                  uC-zmflmo17074e01b1
Method
                  BLASTX
NCBI GI
                  g2425066
BLAST score
                  190
E value
                  1.0e-14
Match length
                  81
% identity
                  54
NCBI Description
                  (AF019147) cysteine proteinase Mir3 [Zea mays]
Seq. No.
                  308156
Seq. ID
                  uC-zmflmo17074e03b1
Method
                  BLASTN
NCBI GI
                  g22149
BLAST score
                  37
```

```
Match length
                  121
% identity
                  83
NCBI Description Z.mays mRNA for alpha-tubulin
                  308157
Seq. No.
                  uC-zmflmo17074e04b1
Seq. ID
Method
                  BLASTN
                  g257040
NCBI GI
BLAST score
                  190
E value
                  1.0e-102
Match length
                  436
% identity
                  32
NCBI Description
                  hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
Seq. No.
                  308158
Seq. ID
                  uC-zmflmo17074e06b1
Method
                  BLASTX
NCBI GI
                  q4309728
BLAST score
                  269
E value
                  1.0e-23
Match length
                  100
% identity
                  57
                  (AC006439) putative ADP-ribosylation factor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  308159
Seq. ID
                  uC-zmflmo17074h11b1
Method
                  BLASTX
NCBI GI
                  g417154
BLAST score
                  219
E value
                  1.0e-19
Match length
                  107
% identity
                  61
NCBI Description
                  HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
Seq. No.
                  308160
Seq. ID
                  uC-zmflmo17074h12b1
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                  251
E value
                  5.0e-33
Match length
                  85
                  91
% identity
NCBI Description
                  glycine-rich protein - maize >gi 22293 emb CAA43431
                  (X61121) glycine-rich protein [Zea mays]
Seq. No.
                  308161
Seq. ID
                  uC-zmflmo17075a09b2
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  34
E value
                  1.0e-09
Match length
                  34
% identity
                  100
```